

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 19:58:50 ; Search time 125 Seconds
(without alignments)
83.540 Million cell updates/sec

Title: US-10-627-685a-1
Perfect score: 120
Sequence: 1 CXIXNQCXQXLDCCSXXCNXXKCV 27

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	27	2	AAW35723 Kappa-con
2	120	100.0	27	4	AAU10200 Snail Kap
3	120	100.0	27	4	AAU10195 Snail Kap
4	120	100.0	27	4	AAU10208 Snail Kap
5	120	100.0	27	4	AAU10205 Snail Kap
6	120	100.0	27	4	AAU10199 Snail Kap
7	120	100.0	27	4	AAU10196 Snail Kap
8	120	100.0	27	4	AAU10202 Snail Kap
9	120	100.0	27	4	AAU10197 Snail Kap
10	120	100.0	27	4	AAU10206 Snail Kap
11	120	100.0	27	4	AAU10207 Snail Kap
12	120	100.0	27	4	AAU10201 Snail Kap
13	120	100.0	27	4	AAU10204 Snail Kap
14	120	100.0	27	4	AAU10218 Snail Kap
15	120	100.0	27	4	AAU10203 Snail Kap
16	120	100.0	27	6	AAE38342 Conus pur
17	120	100.0	27	6	AAE38344 Conus pur
18	120	100.0	27	6	AAE38336 Conus pur
19	120	100.0	27	6	AAE38339 Conus pur
20	120	100.0	27	6	AAE38345 Conus pur
21	120	100.0	27	6	AAE38337 Conus pur
22	120	100.0	27	6	AAE38340 Conus pur
23	120	100.0	27	6	AAE38335 Conus pur
24	120	100.0	27	6	AAE38346 Conus pur
25	120	100.0	27	6	AAE38343 Conus pur

26	120	100.0	27	6	AAE38358 Conus pur
27	120	100.0	27	6	AAE38341 Conus pur
28	120	100.0	27	6	AAE38347 Conus pur
29	120	100.0	27	6	AAE38348 Conus pur
30	117	97.5	27	4	AAU10212 Snail Kap
31	117	97.5	27	6	AAE38352 Conus pur
32	116	96.7	27	4	AAU10217 Snail Kap
33	116	96.7	27	6	AAE38357 Conus pur
34	115	95.8	27	4	AAU10214 Snail Kap
35	115	95.8	27	4	AAU10198 Snail Kap
36	115	95.8	27	6	AAE38338 Conus pur
37	115	95.8	27	6	AAE38354 Conus pur
38	114	95.0	27	4	AAU10216 Snail Kap
39	114	95.0	27	4	AAU10210 Snail Kap
40	114	95.0	27	6	AAE38356 Conus pur
41	114	95.0	27	6	AAE38350 Conus pur
42	112	93.3	27	4	AAU10213 Snail Kap
43	112	93.3	27	4	AAU10209 Snail Kap
44	112	93.3	27	4	AAU10219 Snail Kap
45	112	93.3	27	4	AAU10215 Snail Kap
46	112	93.3	27	4	AAU10211 Snail Kap
47	112	93.3	27	6	AAE38353 Conus pur
48	112	93.3	27	6	AAE38351 Conus pur
49	112	93.3	27	6	AAE38355 Conus pur
50	112	93.3	27	6	AAE38349 Conus pur
51	112	93.3	27	6	AAE38359 Conus pur
52	81	67.5	26	2	AAE38359 Conus pur
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54	81	67.5	26	2	AAE38359 Conus pur
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57	81	67.5	26	2	AAE38359 Conus pur
58	81	67.5	26	2	AAE38359 Conus pur
59	81	67.5	26	2	AAE38359 Conus pur
60	81	67.5	26	2	AAE38359 Conus pur
61	81	67.5	26	2	AAE38359 Conus pur
62	81	67.5	26	2	AAE38359 Conus pur
63	77	64.2	26	2	AAE38359 Conus pur
64	77	64.2	26	2	AAE38359 Conus pur
65	77	64.2	26	2	AAE38359 Conus pur
66	77	64.2	26	2	AAE38359 Conus pur
67	77	64.2	26	2	AAE38359 Conus pur
68	77	64.2	26	2	AAE38359 Conus pur
69	77	64.2	26	2	AAE38359 Conus pur
70	77	64.2	26	2	AAE38359 Conus pur
71	77	64.2	26	2	AAE38359 Conus pur
72	77	64.2	26	2	AAE38359 Conus pur
73	77	64.2	26	2	AAE38359 Conus pur
74	74	61.7	26	5	ABE36786 Omega-con
75	72	60.0	26	8	ADL26915 Xenopus s
76	70	58.3	26	5	ABE36790 Omega-con
77	69	57.5	26	2	AAE38359 Conus pur
78	69	57.5	26	2	AAE38359 Conus pur
79	69	57.5	26	2	AAE38359 Conus pur
80	69	57.5	26	2	AAE38359 Conus pur
81	69	57.5	26	2	AAE38359 Conus pur
82	69	57.5	26	2	AAE38359 Conus pur
83	69	57.5	26	2	AAE38359 Conus pur
84	69	57.5	26	2	AAE38359 Conus pur
85	69	57.5	26	2	AAE38359 Conus pur
86	69	57.5	26	2	AAE38359 Conus pur
87	69	57.5	26	2	AAE38359 Conus pur
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89	69	57.5	26	2	AAE38359 Conus pur
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93	69	57.5	26	2	AAE38359 Conus pur
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96	69	57.5	26	2	AAE38359 Conus pur
97	69	57.5	26	2	AAE38359 Conus pur
98	68.5	57.1	342	8	ADP04517 Sea equir

XX AC AAU10195;
 XX DT 16-JAN-2002 (first entry)
 XX DE Snail Kappa-conotoxin PVIIA analogue #1.
 XX KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma.
 XX OS Conus purpurascens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 2
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Misc-difference 4
 FT /label= OTHER
 FT /note= "Other= Pro or Hydroxyproline"
 FT Misc-difference 7
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Misc-difference 9
 FT /label= OTHER
 FT /note= "Other= Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr,
 FT mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
 FT nitro-Tyr, (D,L)-Trp, neo-Trp or (D,L)-halo-Trp"
 FT Misc-difference 11
 FT /label= OTHER
 FT /note= "Other= His or halo-His"
 FT Misc-difference 18
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Misc-difference 19
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Misc-difference 22
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Misc-difference 23
 FT /label= OTHER
 FT /note= "Other= Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr,
 FT mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
 FT nitro-Tyr, (D,L)-Trp, neo-Trp or (D,L)-halo-Trp"
 FT Misc-difference 25
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX WO200121648-A1.
 XX 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025827.
 XX 22-SEP-1999; 99US-0155135P.
 XX 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX Jones RR;
 XX WPI; 2001-648090/74.
 XX Treating disorders associated with radical depolarization of excitable
 FT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises
 FT activating a KATP channel by administering to an individual a kappa-
 FT conotoxin PVIIA peptide.
 XX Claim 1; Page 27; 46pp; English.
 XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX SQ Sequence 27 AA;
 Query Match 100.0%; Score 120; DB 4; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.00084;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CXIXNOXCXQXLDCCSXCNXXNXXCV 27
 Db 1 CXIXNOXCXQXLDCCSXCNXXNXXCV 27
 RESULT 4
 AAU10208
 ID AAU10208 standard; peptide; 27 AA.
 XX AC AAU10208;
 XX DT 16-JAN-2002 (first entry)
 XX Snail Kappa-conotoxin PVIIA analogue H1A.
 DE Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; H1A.
 XX OS Conus purpurascens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX WO200121648-A1.
 XX 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025827.
 XX 22-SEP-1999; 99US-0155135P.
 XX 20-JUL-2000; 2000US-0219438P.
 XX (COGN-) COGNETIX INC.
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX Jones RR;

[illegible]

AC	AAU10201;
XX	
DT	16-JAN-2002 (first entry)
DE	
DE	Snail Kappa-conotoxin PVIIA analogue F9A.
XX	
KW	Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW	cardioactive; antisthmatic; KATP channel activation; cardiac ischaemia;
KW	cerebral ischaemia; ocular ischaemia; asthma; F9A.
XX	
OS	Conus purpurascens.
OS	Synthetic.
XX	
FH	Key
FT	Modified-site 4
FT	Location/Qualifiers
FT	/note= "Hydroxyproline"
FT	27
FT	Modified-site
FT	/note= "The C-terminus is either a carboxyl group or an
FT	amide group"
XX	
PN	WO200121648-A1.
XX	
PD	29-MAR-2001.
XX	
PF	21-SEP-2000; 2000WO-US025827.
XX	
PR	22-SEP-1999; 99US-0155135P.
PR	20-JUL-2000; 2000US-0219438P.
XX	
PA	(COGN-) COGNETIX INC.
XX	
PI	Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI	Jones RR;
XX	
DR	WPI; 2001-648090/74.
XX	
PT	Treating disorders associated with radical depolarization of excitable
PT	membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
PT	activating a KATP channel by administering to an individual a kappa-
PT	conotoxin PVIIA peptide.
XX	
PS	Claim 1; Page 27; 46pp; English.
XX	
CC	The invention relates to treating disorders associated with radical
CC	depolarisation of excitable membrane by activating a KATP channel
CC	comprising administering to an individual a kappa-conotoxin PVIIA (kappa
CC	PVIIA) peptide or its analogue, derivative or physiologically active
CC	salt. The conotoxins are used for treating disorders associated with
CC	radical depolarisation of excitable membrane by activating a KATP
CC	channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC	ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
CC	analogue of the invention
XX	
SQ	Sequence 27 AA;
	Query Match 100.0%; Score 120; DB 4; Length 27;
	Best Local Similarity 66.7%; Pred. No. 0.00084;
	Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps
Qy	1 CXTXNQXCXQXLDCCSCXCNXXNXCXV 27
	: : : : : : : : : : : : : : : : : :
Db	1 CRXNQKCAQHLDCCSCRCNRFNKCXV 27
RESULT 13	
AAU10204	
ID	AAU10204 standard; peptide; 27 AA.
XX	
AC	AAU10204;
XX	
DT	16-JAN-2002 (first entry)
XX	
DE	Snail Kappa-conotoxin PVIIA analogue K7A.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; K7A.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 4
 FT Modified-site 27 /note= "Hydroxyproline"
 FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX
 PN WO200121648-A1.
 XX
 XX 29-MAR-2001.
 PD
 XX
 XX 21-SEP-2000; 2000WO-US025827.
 PF
 XX
 XX 22-SEP-1999; 99US-0155135P.
 PR
 XX 20-JUL-2000; 2000US-0219438P.
 PR
 XX (COGN-) COGNETIX INC.
 PA
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 PI
 XX WPI; 2001-648090/74.
 DR
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.
 XX
 PS Claim 1; Page 28; 46pp; English.
 XX
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 120; DB 4; Length 27;
 Best Local Similarity 66.7%; Pred. No. 0.00084;
 Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQXLDCCSXKCNXXKCV 27
 Db 1 CRIANQKCFQHLDDCCSRKCNRFNKCV 27
 RESULT 14
 AAU10218
 ID AAU10218 standard; peptide; 27 AA.
 XX
 AC AAU10218;
 XX
 XX 16-JAN-2002 (first entry)
 DT
 XX
 DE Snail Kappa-conotoxin PVIIA analogue O4A.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; O4A.
 XX

OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 4
 FT Modified-site 27 /note= "Hydroxyproline"
 FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX
 PN WO200121648-A1.
 XX
 XX 29-MAR-2001.
 PD
 XX
 XX 21-SEP-2000; 2000WO-US025827.
 PF
 XX
 XX 22-SEP-1999; 99US-0155135P.
 PR
 XX 20-JUL-2000; 2000US-0219438P.
 PR
 XX (COGN-) COGNETIX INC.
 PA
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 PI
 XX WPI; 2001-648090/74.
 DR
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.
 XX
 PS Claim 1; Page 28; 46pp; English.
 XX
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 120; DB 4; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.00084;
 Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQXLDCCSXKCNXXKCV 27
 Db 1 CRIANQKCFQHLDDCCSRKCNRFNKCV 27
 RESULT 15
 AAU10203
 ID AAU10203 standard; peptide; 27 AA.
 XX
 AC AAU10203;
 XX
 XX 16-JAN-2002 (first entry)
 DT
 XX
 DE Snail Kappa-conotoxin PVIIA analogue R2K.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; R2K.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 4

PT use of a compound binding to kappa-PVIIA-binding site.

PS Disclosure; Page 7; 32pp; English.

CC The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue peptide

XX Sequence 27 AA;

Query Match 100.0%; Score 120; DB 6; Length 27;

Best Local Similarity 63.0%; Pred. No. 0.00084;

Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXINQXCXQXLDCCSKXCNXXKCV 27

Db 1 CRIPNOKCFQHLDDCCSRKCNRFNKCV 27

RESULT 20

ID AAE38345 standard; peptide; 27 AA.

AC AAE38345;

DT 20-NOV-2003 (first entry)

DE Conus purpurascens kappa-PVIIA analogue peptide, P9M.

KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

FX Key Location/Qualifiers

FT Modified-site 4 /label= Hyp

PT WO2003063782-A2.

PN 07-AUG-2003.

PD 28-JAN-2003; 2003WO-US002384.

PP 29-JAN-2002; 2002US-0352219P.

PR (COGN-) COGNETIX INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;

PI Olivera BW;

DR WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.

PS Disclosure; Page 7; 32pp; English.

CC The invention relates to kappa-PVIIA-related conotoxins and their use as

CC organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue peptide

XX Sequence 27 AA;

Query Match 100.0%; Score 120; DB 6; Length 27;

Best Local Similarity 63.0%; Pred. No. 0.00084;

Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXINQXCXQXLDCCSKXCNXXKCV 27

Db 1 CRIPNOKCFQHLDDCCSRKCNRFNKCV 27

RESULT 21

AAE38337

ID AAE38337 standard; peptide; 27 AA.

AC AAE38337;

DT 20-NOV-2003 (first entry)

DE Conus purpurascens kappa-PVIIA analogue peptide, R22A.

KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

FX Key Location/Qualifiers

FT Modified-site 4 /label= Hyp

PN WO2003063782-A2.

PD 07-AUG-2003.

PP 28-JAN-2003; 2003WO-US002384.

PR 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;

PI Olivera BW;

DR WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.

PS Disclosure; Page 6; 32pp; English.

CC The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury,

CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;

Query Match 100.0%; Score 120; DB 6; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.00084;
 Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXXCNXXNCV 27
 Db 1 CRIPNQKCFQHLDDCCSRKCNFAPKCV 27

RESULT 22
 AAE38340
 ID AAE38340 standard; peptide; 27 AA.

XX AC AAE38340;

XX DT 20-NOV-2003 (first entry)

XX DE Conus purpurascens kappa-PVIIA analogue peptide, R2A.

XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

XX OS Conus purpurascens.

XX FH Key Location/Qualifiers
 FT Modified-site 4
 FT /label= Hyp

PN W02003063782-A2.

PD 07-AUG-2003.

XX PF 28-JAN-2003; 2003WO-US002384.

XX PR 29-JAN-2002; 2002US-0352219P.

XX PA (COGN-) COGNETIX INC.

XX FA (UTAH) UNIV UTAH RES FOUND.

XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;

XX DR WPI; 2003-679464/64.

XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
 XX use of a compound binding to kappa-PVIIA-binding site.

XX PS Disclosure; Page 7; 32pp; English.

CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present

CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;

Query Match 100.0%; Score 120; DB 6; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.00084;
 Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXXCNXXNCV 27
 Db 1 CAIPNQKCFQHLDDCCSRKCNFAPKCV 27

RESULT 23
 AAE38335

ID AAE38335 standard; peptide; 27 AA.

XX AC AAE38335;

XX DT 20-NOV-2003 (first entry)

XX DE Conus purpurascens kappa-PVIIA peptide.

XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

XX OS Conus purpurascens.

XX FH Key Location/Qualifiers

FT Misc-difference 2 /label= Arg, Orn, Lys, His, OTHER

FT /note= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys,
 N-N-N-trimethyl-Lys, any synthetic basic amino acid, halo
 -His; preferably Arg"

FT Misc-difference 4 /label= Pro, Hyp

FT Misc-difference 7

FT /label= Arg, Orn, Lys, His, OTHER
 /note= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys,
 N-N-N-trimethyl-Lys, any synthetic basic amino acid, halo
 -His; preferably Lys"

FT Misc-difference 9

FT /label= Phe, Tyr, OTHER
 /note= "OTHER = Meta-Tyr, ortho-Tyr, nor-Tyr, mono- halo-
 Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr,
 D or L-Trp, neo-Trp, D or L-halo-Trp or any synthetic
 aromatic amino acid; preferably Phe"

FT Misc-difference 11

FT /label= His, OTHER
 /note= "OTHER = Halo-His; preferably His"

FT Misc-difference 18

FT /label= Arg, Orn, Lys, His, OTHER
 /note= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys,
 N-N-N-trimethyl-Lys, any synthetic basic amino acid, halo
 -His; preferably Arg"

FT Misc-difference 19

FT /label= Arg, Orn, Lys, His, OTHER
 /note= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys,
 N-N-N-trimethyl-Lys, any synthetic basic amino acid, halo
 -His; preferably Lys"

FT Misc-difference 22

FT /label= Arg, Orn, Lys, His, OTHER
 /note= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys,
 N-N-N-trimethyl-Lys, any synthetic basic amino acid, halo
 -His; preferably Arg"

FT Misc-difference 23

FT /label= Phe, Tyr, OTHER
 /note= "OTHER = Meta-Tyr, ortho-Tyr, nor-Tyr, mono- halo-
 Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr,

FT	D or L-Trp, nso-Trp, D or L-halo-Trp or any synthetic aromatic amino acid; preferably Phe"
FT	Misc-difference 25
FT	/label= Arg, Orn, Lys, His, OTHER
FT	/note= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys, N-N-N-trimethyl-Lys, any synthetic basic amino acid, halo
FT	-His; preferably Lys"
XX	
PN	WO2003063782-A2.
XX	
PD	07-AUG-2003.
XX	
PF	28-JAN-2003; 2003WO-US002384.
XX	
PR	29-JAN-2002; 2002US-0352219P.
XX	
PA	(COGN-) COGNETIX INC.
PA	(UTAH) UNIV UTAH RES FOUND.
XX	
PI	Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
PI	Oliviera BM;
XX	
DR	WPI; 2003-679464/64.
XX	
PT	Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
PT	
XX	
PS	Disclosure; Page 5; 32pp; English.
XX	
CC	The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA peptide.
XX	
SQ	Sequence 27 AA;
	Query Match 100.0%; Score 120; DB 6; Length 27;
	Best Local Similarity 100.0%; Pred. No. 0.00084;
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CXIXNQXCQXQLDDCCSXXCNXXKCV 27
Db	1 CXIXNQXCQXQLDDCCSXXCNXXKCV 27
RESULT 24	
AAE38346	ID AAE38346 standard; peptide; 27 AA.
XX	
AC	AAE38346;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Conus purpurascens kappa-PVIIA analogue peptide, P9Y.
XX	
KW	Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
OS	Conus purpurascens.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 4


```

XX PF 28-JAN-2003; 2003WO-US002384.
XX PF AAE38358
XX PR 29-JAN-2002; 2002US-0352219P.
XX PA (COGN-) COGNETIX INC.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
XX PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
XX PT use of a compound binding to kappa-PVIIA-binding site.
XX PS Disclosure; Page 7; 32pp; English.
XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
XX CC organ protectants. The invention also relates to a method of arresting,
XX CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
XX CC related conotoxins. The conotoxins can also be used for arresting,
XX CC protecting or preserving somatic cells. The invention is for the
XX CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
XX CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
XX CC peripheral circulation disturbances, hypertension, angina, cerebral
XX CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
XX CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
XX CC ischaemic heart disease, asthma and congestive heart failure. The present
XX CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX CC peptide
XX SQ Sequence 27 AA;
XX Query Match 100.0%; Score 120; DB 6; Length 27;
XX Best Local Similarity 63.0%; Pred. No. 0.00084;
XX Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQXLDCCSXXCNXXKCV 27
Db 1 CKIPNQKCFQHLDDCCSRKCNFKVCV 27
XX
RESULT 26
AAE38358
ID AAE38358 standard; peptide; 27 AA.
AC AAE38358;
XX 20-NOV-2003 (first entry)
XX Conus purpurascens kappa-PVIIA analogue peptide, Q4A.
XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX congestive heart failure; neuropathy; nephropathy; CABG.
XX OS Conus purpurascens.
XX WO2003063782-A2.
XX 07-AUG-2003.
XX 28-JAN-2003; 2003WO-US002384.
XX PR 29-JAN-2002; 2002US-0352219P.
XX PA (COGN-) COGNETIX INC.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
XX PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
XX PT use of a compound binding to kappa-PVIIA-binding site.
XX PS Disclosure; Page 8; 32pp; English.
XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
XX CC organ protectants. The invention also relates to a method of arresting,
XX CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
XX CC related conotoxins. The conotoxins can also be used for arresting,
XX CC protecting or preserving somatic cells. The invention is for the
XX CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
XX CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
XX CC peripheral circulation disturbances, hypertension, angina, cerebral
XX CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
XX CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
XX CC ischaemic heart disease, asthma and congestive heart failure. The present
XX CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX CC peptide
XX SQ Sequence 27 AA;
XX Query Match 100.0%; Score 120; DB 6; Length 27;
XX Best Local Similarity 63.0%; Pred. No. 0.00084;
XX Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQXLDCCSXXCNXXKCV 27
Db 1 CRIANQKCFQHLDDCCSRKCNFKVCV 27
XX
RESULT 27
AAE38341
ID AAE38341 standard; peptide; 27 AA.
XX AAE38341;
XX 20-NOV-2003 (first entry)
XX Conus purpurascens kappa-PVIIA analogue peptide, F9A.
XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX congestive heart failure; neuropathy; nephropathy; CABG.
XX OS Conus purpurascens.
XX Key Location/Qualifiers
XX Modified-site 4 /label= Hyp
XX WO2003063782-A2.
XX 07-AUG-2003.
XX 28-JAN-2003; 2003WO-US002384.
XX PR 29-JAN-2002; 2002US-0352219P.
XX PA (COGN-) COGNETIX INC.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
XX PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises

```


The invention relates to kappa-PVIIA-related conotoxins and their use as

CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;

Query Match 100.0%; Score 120; DB 6; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.00084;
 Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCSXKXCNXKCV 27
 Db 1 CRIPNQKCFQALDDCCSRKCNRFKCV 27

RESULT 30
 AAU10212
 ID AAU10212 standard; peptide; 27 AA.
 XX
 AC AAU10212;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Snail Kappa-conotoxin PVIIA analogue S17A.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; S17A.
 XX
 OS Conus purpurascens.
 OS Synthetic.

Key Location/Qualifiers
 Modified-site 4 /note= "Hydroxyproline"
 Modified-site 27 /note= "The C-terminus is either a carboxyl group or an amide group"

WO200121648-A1.
 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-US025927.
 XX
 PR 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX
 PA (COGN-) COGNETIX INC.
 XX
 PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX
 DR WPI; 2001-648090/74.
 XX
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.
 XX
 PS Claim 1; Page 28; 46pp; English.
 XX
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular

CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 SQ Sequence 27 AA;

Query Match 97.5%; Score 117; DB 4; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.0015;
 Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCSXKXCNXKCV 27
 Db 1 CRIXNQKCFQHLDDCCARKCNRFKCV 27

RESULT 31
 AAE38352
 ID AAE38352 standard; peptide; 27 AA.
 XX
 AC AAE38352;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Conus purpurascens kappa-PVIIA analogue peptide, S17A.
 XX
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 OS Conus purpurascens.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT
 XX
 PN WO2003063782-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 28-JAN-2003; 2003WO-US002384.
 XX
 PR 29-JAN-2002; 2002US-0352219P.
 XX
 PA (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX
 DR WPI; 2003-679464/64.
 XX
 PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX
 PS Disclosure; Page 7; 32pp; English.
 XX
 CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral,
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;

Query Match 97.5%; Score 117; DB 6; Length 27;
 Best Local Similarity 59.3%; Pred. No. 0.0015;
 Matches 16; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXCKXQXLDCCSXXCNXXNKC 27
 Db 1 CRIPNKCFOHLDCCCKRKNRNCV 27

RESULT 32

AAU10217
 ID AAU10217 standard; peptide; 27 AA.
 AC AAU10217;
 XX
 XX
 DT 16-JAN-2002 (first entry)
 DE Snail Kappa-conotoxin PVIIA analogue V27A.
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiaethmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; V27A.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 FT
 XX
 XX WO200121648-A1.
 XX
 XX 29-MAR-2001.
 XX
 XX
 XX 21-SEP-2000; 2000WO-US025827.
 XX
 XX 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX
 XX (COGN-) COGNETIX INC.
 XX
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX
 XX WPI; 2001-648090/74.
 DR
 XX
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.
 XX
 XX Claim 1; Page 28; 46pp; English.
 PS
 XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 XX Sequence 27 AA;

Query Match 96.7%; Score 116; DB 4; Length 27;
 Best Local Similarity 65.4%; Pred. No. 0.0019;
 Matches 17; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXCKXQXLDCCSXXCNXXNKC 26

Db 1 CRIXNOKCFOHLDCCSRKCNRENKC 26

RESULT 33

AAE38357
 ID AAE38357 standard; peptide; 27 AA.
 XX
 AC AAE38357;
 XX
 XX
 DT 20-NOV-2003 (first entry)
 DE Conus purpurascens kappa-PVIIA analogue peptide, V27A.
 XX
 XX
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 OS Conus purpurascens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4
 FT /label= Hyp
 FT
 XX
 XX WO2003063782-A2.
 XX
 XX 07-AUG-2003.
 XX
 XX 28-JAN-2003; 2003WO-US002384.
 XX
 XX 29-JAN-2002; 2002US-0352219P.
 XX
 XX (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX
 XX WPI; 2003-679464/64.
 DR
 XX
 XX Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX
 XX Disclosure; Page 8; 32pp; English.
 XX
 XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 XX Sequence 27 AA;

Query Match 96.7%; Score 116; DB 6; Length 27;
 Best Local Similarity 61.5%; Pred. No. 0.0019;
 Matches 16; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXCKXQXLDCCSXXCNXXNKC 26

Db 1 CRIPNKCFOHLDCCSRKCNRENKC 26

RESULT 34

AAU10214
ID AAU10214 standard; peptide

XX
AC AAU10211;

XX
DT 16-JAN-02 15:31:00

DE Snail 1, Xin 1
XX
DE

XX	Smart	1	XX
XX			
KW	Purp	1	120

KW	Fulp.
KW	carc.
KW	Ce

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COUNCIL

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tion/.

$$H_n = \mathbb{C}$$
$$L_n = \epsilon$$

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[illegible]

“T”	“C”	“A”	“S”	“E”	“M”	“L”	“D”	“U”	“N”	“I”	“O”	“P”	“Q”	“R”	“S”	“T”	“U”	“V”	“W”	“X”	“Y”	“Z”
“T”	“C”	“A”	“S”	“E”	“M”	“L”	“D”	“U”	“N”	“I”	“O”	“P”	“Q”	“R”	“S”	“T”	“U”	“V”	“W”	“X”	“Y”	“Z”

1. The first group of people who are not allowed to enter the country are those who are on the "no-fly" list. This list is maintained by the Department of Homeland Security and includes individuals who are suspected of being involved in terrorism or other activities that could threaten the security of the United States.

U.S. DEPARTMENT OF AGRICULTURE
BUREAU OF PLANT INDUSTRY
WASHINGTON, D. C.

11

11

1951

10

FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 PN WO200121648-A1.
 XX 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025827.
 XX 22-SEP-1999; 99US-0155135P.
 XX 20-JUL-2000; 2000US-0219438P.
 XX (COGN-) COGNETIX INC.
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX Jones RR;
 XX WPI; 2001-648090/74.
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.
 XX Claim 1; Page 28; 46pp; English.
 XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX Sequence 27 AA;
 SQ Query Match 95.0%; Score 114; DB 4; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.0028;
 Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQXLDCCSXXCNXXNXCXV 27
 Db 1 CRXNQRKCFQHLDDCCSRKCNRFNKCXV 27
 RESULT 39
 AAU10210
 ID AAU10210 standard; peptide; 27 AA.
 XX AC AAU10210;
 XX 16-JAN-2002 (first entry)
 DE Snail Kappa-conotoxin PVIIA analogue Q6A.
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; Q6A.
 XX Conus purpurascens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX WO200121648-A1.
 XX

PD 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025827.
 XX 22-SEP-1999; 99US-0155135P.
 XX 20-JUL-2000; 2000US-0219438P.
 XX (COGN-) COGNETIX INC.
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX Jones RR;
 XX WPI; 2001-648090/74.
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.
 XX Claim 1; Page 28; 46pp; English.
 XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX Sequence 27 AA;
 SQ Query Match 95.0%; Score 114; DB 4; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.0028;
 Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQXLDCCSXXCNXXNXCXV 27
 Db 1 CRXNQRKCFQHLDDCCSRKCNRFNKCXV 27
 RESULT 40
 AAU10210
 ID AAU10210 standard; peptide; 27 AA.
 XX AC AAU10210;
 XX 20-NOV-2003 (first entry)
 DE Conus purpurascens kappa-PVIIA analogue peptide, Q10A.
 XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX Conus purpurascens.
 OS Conus purpurascens.
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /label= Hyp
 FT WO2003063782-A2.
 XX 07-AUG-2003.
 XX 28-JAN-2003; 2003WO-US002384.
 XX 29-JAN-2002; 2002US-0352219P.
 XX (COGN-) COGNETIX INC.
 XX

The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention

Sequence 27 AA;

Query Match 93.3%; Score 112; DB 4; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.0041;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXTXNQXCXYQLDDCCSXCNXXNKCVCV 27
| : | | | : | : | | | : | | | : | : | : |
Db 1 CRIXNQKCFOHLDACCSKCNRFNKCV 27

RESULT 44
AAU10219
ID AAU10219 standard; peptide; 27 AA.
AC AAU10219;
XX
DT 16-JAN-2002 (first entry)
DE
XE
DE Snail Kappa-conotoxin PVIIA analogue NSA.
XX
KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
XX cerebral ischaemia; ocular ischaemia; asthma; NSA.
XX
OS Conus purpurascens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT FT /note= "Hydroxyproline"
FT Modified-site 27
FT FT /note= "The C-terminus is either a carboxyl group or an amide group"
XX
PN WO200121648-A1.
XX
XX
PD 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-US025827.
XX
PR 22-SEP-1999; 99US-015513SP.
PR 20-JUL-2000; 2000US-0219438P.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
PI
DR WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.

Claim 1; Page 28; 45pp; English.

The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue derivative or physiologically active salt.

CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
CC analogue of the invention
XX
XX Sequence 27 AA;
SQ
Query Match 93.3%; Score 112; DB 4; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.0041;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CXIXNQXCXQLDDCCSXCNXXNKCVCV 27
Db 1 CRIXAQKCFQHLDDCCSRKCNRFNKCVCV 27
RESULT 45
AAU10215
ID AAU10215 standard; peptide; 27 AA.
XX AC AAU10215;
XX AC
XX 16-JAN-2002 (first entry)
XX Snail Kappa-conotoxin PVIIA analogue D13A.
XX DE
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; D13A.
XX
XX Conus purpurascens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27
FT /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX
XX WO200121648-A1.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-US025827.
XX
XX 22-SEP-1999; 99US-0155135P.
XX 20-JUL-2000; 2000US-0219438P.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
PT activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.
XX
XX Claim 1; Page 28; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
CC analogue of the invention

XX SQ Sequence 27 AA;
Query Match 93.3%; Score 112; DB 4; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.0041;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CXIXNQXCXQLDDCCSXCNXXNKCVCV 27
Db 1 CRIXNQKCFQHLDDCCSRKCNRFNKCVCV 27
RESULT 46
AAU10211
ID AAU10211 standard; peptide; 27 AA.
XX AC AAU10211;
XX AC
XX 16-JAN-2002 (first entry)
XX Snail Kappa-conotoxin PVIIA analogue N21A.
XX DE
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; N21A.
XX
XX Conus purpurascens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27
FT /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX
XX WO200121648-A1.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-US025827.
XX
XX 22-SEP-1999; 99US-0155135P.
XX 20-JUL-2000; 2000US-0219438P.
XX
XX (COGN-) COGNETIX INC.
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
PT activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.
XX
XX Claim 1; Page 28; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
CC analogue of the invention
XX
XX Sequence 27 AA;
Query Match 93.3%; Score 112; DB 4; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.0041;

KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 OS Conus purpurascens.

FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 XX

PN WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JW;
 PI Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises
 FT use of a compound binding to kappa-PVIA-binding site.

XX Disclosure; Page 8; 32pp; English.

XX The invention relates to kappa-PVIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIA analogue
 XX peptide

XX Sequence 27 AA;

Query Match 93.3%; Score 112; DB 6; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.0041;

Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXCNXXNKCXV 27

Db 1 CRIXAQKCFQHLDDCCSRKCNRFNKCXV 27

RESULT 52

AAR39628

ID AAR39628 standard; peptide; 26 AA.

XX AAR39628;

XX 25-MAR-2003 (revised)

DT 20-DEC-1993 (first entry)

XX SNX-202.

XX Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
 KW calcium channel; neurone; contraction; guinea pig; ileum; MWIIA;
 KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
 KW narcotics.

XX Synthetic.

FH Key Location/Qualifiers
 FT Disulfide-bond 1. .16
 FT Disulfide-bond 8. .20
 FT Disulfide-bond 15. .26
 FT Modified-site 26
 XX /note= "Amidated C-terminal"

PN WO9313128-A1.

XX 08-JUL-1993.

XX 30-DEC-1992; 92WO-US011349.

XX 30-DEC-1991; 91US-00814759.

XX (NEUR-) NEUREX CORP.

XX Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;

XX WPI; 1993-227270/28.

XX Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
 FT calcium channels - to induce analgesia, enhance opiate analgesics, treat
 FT pain etc.

XX Claim 1; Fig 2; 90pp; English.

XX The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
 CC derivatives of these, which may be used to produce analgesia in a mammal.
 CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
 CC tissue. This is shown by the peptides ability to stimulate contraction in
 CC guinea pig ileum and to bind to OCT MWIIA binding sites present in
 CC neuronal tissue. OCTs are components of peptide toxins derived from
 CC marine snails of the genus Conus, and act as calcium channel blockers.
 CC These OCTs may be used to replace opiods in the treatment of chronic pain
 CC or to reduce the opiod dosage required. This helps to reduce dependence
 CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
 CC PN field.)

XX Sequence 26 AA;

Query Match 67.5%; Score 81; DB 2; Length 26;
 Best Local Similarity 34.6%; Pred. No. 2;

Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXCNXXNXC 26

Db 1 CKLKGQSCSRMLYDCCSGSGRSGKC 26

RESULT 53

AAR37774

ID AAR37774 standard; peptide; 26 AA.

XX AAR37774;

XX 25-MAR-2003 (revised)

DT 08-SEP-1993 (first entry)

XX SNX-202.

XX Ischaemia; neuronal; omega-conotoxin; OCT; MWIIA; MWIIC; MWIID; MWIIB;
 KW GVIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment;
 KW antihistamine; blood pressure; N-type voltage-gated Ca currents;
 KW N-channel mediated neurotransmitter release.

XX Synthetic.

FH Key Location/Qualifiers
 FT Disulfide-bond 1. .16
 FT Disulfide-bond 8. .20

XX Disulfide-bond 15. .26

PN W09310145-A1.
 XX 27-MAY-1993.
 PD 12-NOV-1992; 92WO-US009766.
 XX 12-NOV-1991; 91US-00789913.
 PR 17-JUL-1992; 92US-00916478.
 XX (NEUR-) NEUREX CORP.
 XX Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;
 PI Yamashiro DH;
 XX WPI; 1993-182487/22.
 DR Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
 PT bind specifically to omega-conotoxin MVIIA binding sites.
 XX Disclosure; Fig 2; 103pp; English.
 CC The C-terminal is amidated. Ischaemia-related neuronal damage in mammals
 CC is reduced by admin., 4-24 hr after onset of ischaemia, of a cpd. (I)
 CC which binds selectively to an omega-conotoxin (OCT) MVIIA site in
 CC neuronal tissue. (I) has selectivity at least 100 expressed as ratio of
 CC binding affinity for the MVIIA site to that for the MVIIC site. (I) is
 CC one of the OCTs MVIIA, MVIIB, GVIA, GVIIA or RVIA or it is the cpd. SNX-
 CC 207. (I) is esp. used to reduce neuronal damage caused by stroke. By
 CC delaying admin. for some time (compare US051403 where cpds. are given
 CC within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage
 CC is achieved. (I) is admin. e.g. by intracerebroventricular (ICV)
 CC injection at 0.1-20 microg/kg, but can also be given i.v. (opt. after
 CC treatment with antihistamines to minimise redn. in blood pressure caused
 CC by (I)). (I) is also at least as effective as the specified conotoxins
 CC for (1) selective inhibition of N-type voltage-gated Ca currents in
 CC neuronal tissue and (2) selective inhibition of N-channel mediated
 CC neurotransmitter release in neuronal tissue. Primary sequences of omega-
 CC conopeptides are given in AAR37752-62. Several analog omega-conopeptides
 CC are given in AAR37763-76. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 26 AA;
 SQ Query Match 67.5%; Score 81; DB 2; Length 26;
 Best Local Similarity 34.6%; Pred. No. 2;
 Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXOXLDCCSCXXCNXXNC 26
 DB 1 CKLQGSCSLMYDCCSGCGRGKC 26
 RESULT 54
 AAW19570
 ID AAW19570 standard; peptide; 26 AA.
 AC AAW19570;
 XX 14-OCT-1997 (first entry)
 DT SNX-202, omega conopeptide derivative used for pain relief.
 DE Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;
 XX N-type voltage-sensitive calcium channel; block; Conus.
 KW Synthetic.
 OS Key Location/Qualifiers
 FT Modified-site 26
 FT /note= "amidated"
 XX W09701351-A1.
 XX 16-JAN-1997.

XX 26-JUN-1996; 96WO-US011041.
 XX 27-JUN-1995; 95US-00496847.
 PR 08-MAR-1996; 96US-00613400.
 XX (NEUR-) NEUREX CORP.
 XX Amstutz GA, Bowersox SS, Gohl K, Adriaenssens PI, Kristipati R;
 PI Gadbois T, Pettus MR, Luther RR;
 XX WPI; 1997-100012/09.
 DR Stable omega conopeptide compositions - for producing analgesia and for
 XX inhibiting progression of neuropathic pain disorders.
 XX Disclosure; Fig 4; 47pp; English.
 CC AAW19555-W19572 are omega conopeptides (OCs) derived from natural
 CC peptides from Conus sp. (cone snails). The peptides and their analogues
 CC are used as analgesics acting by blocking N-type voltage-sensitive
 CC calcium channels. The OCs can be used to treat neuropathic pain as a
 CC result of e.g. insult to the spinal cord or peripheral nerves, cancer,
 CC bone degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes
 CC zoster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or
 CC hyperalgesia. The OCs are preferably administered in a medicament via an
 CC epidural route in a continuous infusion or sustained release formulation.
 CC The OCs can provide pain relief when administered epidurally in the
 CC absence of a premedication enhancer, at doses that are comparable to
 CC effective analgesic doses using intrathecal administration. OC
 CC formulations comprising an OC and a carboxylic acid buffer anti-oxidant.
 CC They also confer stability to solutions containing them for prolonged
 CC treatment methods and long-term storage
 XX SQ Sequence 26 AA;
 SQ Query Match 67.5%; Score 81; DB 2; Length 26;
 Best Local Similarity 34.6%; Pred. No. 2;
 Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXOXLDCCSCXXCNXXNC 26
 DB 1 CKLQGSCSLMYDCCSGCGRGKC 26
 RESULT 55
 AAW12985
 ID AAW12985 standard; peptide; 26 AA.
 XX AAW12985;
 XX 25-MAR-2003 (revised)
 DT 22-APR-1997 (first entry)
 XX Omega conopeptide SNX-202.
 DE Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition;
 XX neuronal damage; schizoprenia; tardive dyskinesia; analgesia;
 KW acute dystonic reactions; inflammation; epilepsy.
 XX Synthetic.
 OS US5587454-A.
 XX 24-DEC-1996.
 PD 15-APR-1993; 93US-00049794.
 XX 30-DEC-1991; 91US-00814759.
 PR 30-DEC-1992; 92WO-US011349.
 XX (NEUR-) NEUREX CORP.
 XX

PI Gohil KC, Miljanich GP, Valentino KL, Justice A, Singh T;
 DR WPI; 1997-064830/06.
 XX
 XX Omega cono:peptide(s) - useful as analgesics, esp. for treating
 PT neuropathic pain.
 PT
 XX
 PS Disclosure; Col 51-52; 59pp; English.
 XX
 CC The present peptide is an omega conopeptide, useful as an analgesic,
 CC especially for treating neuropathic pain. The peptide, which can be
 CC prepared by solid phase synthesis, can also be used to inhibit neuronal
 CC damage and treat schizophrenia, tardive dyskinesia, acute dystonic
 CC reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
 CC PF field.)
 XX
 XX
 SQ Sequence 26 AA;
 Query Match 67.5%; Score 81; DB 2; Length 26;
 Best Local Similarity 34.6%; Pred. No. 2;
 Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXQLDDCCSXCNXXNXC 26
 Db 1 CLKKGQSCRLMYDCCSGCGSGK 26
 RESULT 56
 AAW72625
 ID AAW72625 standard; peptide; 26 AA.
 AC AAW72625;
 XX
 XX 27-AUG-2003 (revised)
 DT 06-JAN-1999 (first entry)
 XX
 DE Conus genus analogue omega-conopeptide SNX-202.
 XX
 XX Conus genus; marine snail; cone snail; omega-conopeptide; analgesia;
 KW nociceptive pain; neuropathic pain; neuronal tissue; conotoxin;
 KW inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction;
 KW rheumatoid arthritis; epilepsy.
 XX
 OS Conus.
 XX
 XX US5824645-A.
 PN 20-OCT-1998.
 XX
 XX 01-NOV-1996; 96US-00742774.
 XX
 XX 30-DEC-1991; 91US-00814759.
 PR 15-APR-1993; 93US-00049794.
 XX
 XX 03-JUL-1996; 96US-00675354.
 XX
 XX (NEUR-) NEUREX CORP.
 PA
 XX Miljanich GP, Valentino KL, Gohil KC, Justice A, Singh T;
 PI WPI; 1998-582596/49.
 XX
 XX Treatment of inflammation, comprises administration of omega-conopeptide
 PT - effective to block voltage-gated calcium channels, bind with high
 PT affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
 PT release.
 XX
 XX Disclosure; Fig 2; 59pp; English.
 PS
 XX A method has been developed for the treatment of inflammation in a
 CC subject. The method comprises administration of an omega-conopeptide
 CC effective to: (i) block voltage-gated calcium channels; (ii) bind with
 CC high affinity to an omega-conopeptide binding site; and (iii) inhibit
 CC neurotransmitter release from nervous tissue. The method is used to treat

BEST LOCAL SIMILARITY 34.6%; PRED: NO. 2;
Matches 9: Conservative 13: Mismatches 4: Indels 0: Gaps 0:

0v 1 CXIXNOXCXOXLDCCSXXCNXXNXC 26

[illegible]

PF 03-JUL-1996; 96US-00675354.
 XX
 PR 30-DEC-1991; 91US-00814759.
 PR 15-APR-1993; 93US-00049794.
 XX
 XX (NEUR-) NEUREX CORP.
 PA
 PI Miljanich GP, Gohil KC, Valentino KL, Justice A, Singh T;
 XX WPI; 1999-120002/10.
 DR
 XX Production of analgesia in mammal - by administration of omega cono-
 PT peptide(s).
 PT
 XX Disclosure; Fig 1B; 59pp; English.
 PS
 CC Sequences AAW5564-573 represent primary sequences of natural omega-
 CC conopeptides. Omega-conopeptides are components of peptide toxins
 CC produced by marine snails of the genus Conus, and which act as calcium
 CC channel blockers. The invention relates to a method of producing
 CC analgesia in a mammal that comprises administering an omega conopeptide
 CC having activities in (a) inhibiting electrically stimulated contraction
 CC of guinea pig ileum and (b) selectively binding to omega conopeptide
 CC MWIIA binding sites in neuronal tissue, where these activities are within
 CC the ranges of those of omega-conotoxins MWIIA and TVIA. The method is
 CC used for treating chronic pain, especially neuropathic pain
 XX
 SQ Sequence 26 AA;
 Query Match 64.2%; Score 77; DB 2; Length 26;
 Best Local Similarity 34.6%; Pred. No. 4.4;
 Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQLDCCSXCNXXNC 26
 DB 1 CKLKGQSCRKTSYDCSGSGRSGKC 26
 RESULT 69
 AAY56480
 ID AAY56480 standard; peptide; 26 AA.
 AC AAY56480;
 XX
 DT 16-FEB-2000 (first entry)
 XX
 DE Natural omega conopeptide SVIB/SNX-183.
 XX
 KW Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin;
 KW marine snail; peptide toxin; inflammation; binding;
 KW voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline;
 KW anti-inflammatory.
 XX
 OS Conus sp.
 XX
 PN US5994305-A.
 XX
 PD 30-NOV-1999.
 XX
 PF 21-AUG-1998; 98US-00138439.
 XX
 PR 30-DEC-1991; 91US-00814759.
 PR 15-APR-1993; 93US-00049794.
 PR 03-JUL-1996; 96US-00675354.
 PR 01-NOV-1996; 96US-00742774.
 XX
 PA (ELAN-) ELAN PHARM INC.
 XX
 PI Justice A, Singh T, Valentino KL, Miljanich GP, Gohil KC;
 XX WPI; 2000-038270/03.
 DR
 XX Measuring the activity of test compounds in blocking voltage-gated
 PT

PT calcium channels, binding to the omega conopeptide binding site and
 PT inhibiting norepinephrine (noradrenaline) release for treating
 PT inflammation.
 XX
 PS Disclosure; Fig 1; 47pp; English.
 XX
 CC A method has been developed of selecting a test compound for treating
 CC inflammation. The method comprises measuring the activity of the test
 CC compound in blocking voltage-gated calcium channels, binding to the omega
 CC conopeptide binding site and inhibiting norepinephrine (noradrenaline)
 CC release from nervous tissue. The method is useful for selecting compounds
 CC for treating inflammation. The selected compounds are capable of
 CC producing analgesia in a mammalian subject with chronic or intractable
 CC pain. Analgesia caused by selected compounds may reduce the reliance on
 CC opioid analgesic agents of the prior art which cause dependency and
 CC tolerance, requiring potentially dangerous increases in opioid doses to
 CC achieve the analgesic effect. The present sequence represents an omega
 CC conopeptide given in the present invention
 XX
 SQ Sequence 26 AA;
 Query Match 64.2%; Score 77; DB 3; Length 26;
 Best Local Similarity 34.6%; Pred. No. 4.4;
 Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQLDCCSXCNXXNC 26
 DB 1 CKLKGQSCRKTSYDCSGSGRSGKC 26
 RESULT 70
 AAB14359
 ID AAB14359 standard; peptide; 26 AA.
 AC AAB14359;
 XX
 DT 06-DEC-2000 (first entry)
 XX
 DE Omega-conopeptide SVIB/SNX-183.
 XX
 KW Marine snail; omega-conopeptide; calcium channel blocker; SVIB; SNX-183;
 KW toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic;
 KW norepinephrine release inhibitor; schizophrenia; tardive dyskinesia;
 KW acute dystonic reaction; inflammation; epilepsy.
 XX
 OS Conus sp.
 XX
 PN US6087091-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 23-APR-1999; 99US-00298017.
 XX
 PR 30-DEC-1991; 91US-00814759.
 PR 15-APR-1993; 93US-00049794.
 PR 03-JUL-1996; 96US-00675354.
 PR 01-NOV-1996; 96US-00742774.
 PR 21-AUG-1998; 98US-00138439.
 XX
 PA (ELAN-) ELAN PHARM INC.
 XX
 PI Singh T, Gohil KC, Valentino KL, Miljanich GP, Justice A;
 XX WPI; 2000-490177/43.
 DR
 XX Selecting a compound for producing analgesia involves measuring activity
 PT

PT of test compound in blocking voltage-gated calcium channels, binding to
 XX omega conopeptide binding site and inhibiting norepinephrine release.
 PS Example 4; Fig 1; 58pp; English.
 CC The present sequence is an omega-conopeptide from marine snails of the
 CC genus Conus. Omega-conopeptides are components of peptide toxins produced
 CC by the cone snails, and which act as calcium channel blockers. Natural
 CC omega-conopeptides and their derivatives may be useful for producing
 CC analgesia in nociceptive and neuropathic pain. The peptides bind to omega
 CC -conopeptide binding sites, which are present mainly in neuronal tissue,
 CC and inhibit norepinephrine release from nervous tissue. Conopeptides such
 CC as MWIIA and TVIA are effective as therapeutic agents for treating
 CC neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
 CC dystonic reactions, inflammation and epilepsy
 XX
 SQ Sequence 26 AA;
 Query Match 64.2%; Score 77; DB 3; Length 26;
 Best Local Similarity 34.6%; Pred. No. 4.4;
 Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXOXLDCCSXCNXNXC 26
 DB 1 CKLKGQSCRKTSYDCCSGSGCRSGKC 26
 RESULT 71
 AAB92221
 ID AAB92221 standard; peptide; 26 AA.
 AC AAB92221;
 XX
 XX 22-JUN-2001 (first entry)
 DE Toxin peptide SEQ ID NO:1397.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 KW
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200069900-A2.
 XX
 XX 23-NOV-2000.
 XX
 XX 17-MAY-2000; 2000WO-US013576.
 XX
 XX 17-MAY-1999; 99US-0134406P.
 XX 10-SEP-1999; 99US-0153406P.
 XX 15-OCT-1999; 99US-0159783P.
 XX
 XX (CONJ-) CONJUCHEM INC.
 XX
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 XX peptidase degradation, useful for increasing length of in vivo activity.
 XX
 XX Disclosure; Page 653-654; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in

CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 26 AA;
 Query Match 64.2%; Score 77; DB 4; Length 26;
 Best Local Similarity 34.6%; Pred. No. 4.4;
 Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXOXLDCCSXCNXNXC 26
 DB 1 CKLKGQSCRKTSYDCCSGSGCRSGKC 26
 RESULT 72
 AAB19449
 ID AAB19449 standard; peptide; 26 AA.
 XX
 XX AAB19449;
 XX
 XX 06-MAR-2001 (first entry)
 XX
 XX Primary sequence of a natural omega-conopeptide SVIB/SNX-183.
 XX
 KW Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic;
 KW peptide toxin; opiate; pain; neuronal damage; ischemic condition;
 KW schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
 KW epilepsy.
 XX
 OS Conus sp.
 XX
 XX Key Location/Qualifiers
 XX Disulfide-bond 1..15
 XX Disulfide-bond 8..19
 XX Disulfide-bond 15..26
 XX Modified-site 26
 XX /note= "amidated C-terminal"
 XX
 XX US6136786-A.
 XX
 XX 24-OCT-2000.
 XX
 XX 09-SEP-1999; 99US-00392979.
 XX
 XX 30-DEC-1991; 91US-00814759.
 XX 15-APR-1993; 93US-00049794.
 XX 23-JUN-1993; 93US-00081863.
 XX 03-JUL-1996; 96US-00675354.
 XX 01-NOV-1996; 96US-00742774.
 XX 21-AUG-1998; 98US-00138439.
 XX 23-APR-1999; 99US-00298017.
 XX
 XX (ELAN-) ELAN PHARM INC.
 XX
 XX Singh T, Gohil KC, Valentino KL, Miljanich GP, Justice A;
 XX WPI; 2001-030946/04.
 XX
 XX Enhancing analgesia produced by opiates by administering an omega-
 XX conopeptide that inhibits electrically stimulated contraction of guinea
 XX pig ilium and binds to omega-conopeptide MWIIA binding sites in neuronal
 XX tissues.
 XX
 XX Disclosure; Fig 1; 58pp; English.
 PS
 XX The present sequence represents an omega-conopeptide. Omega-conopeptides

CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB9698-A3B9806 represent omega-conopeptide
 CC generic toxin sequences
 XX
 SQ Sequence 26 AA; .

Query Match 58.3%; Score 70; DB 5; Length 26;
 Best Local Similarity 34.6%; Pred. No. 18;
 Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXIXNQXCKXLDCCSXXCNXXNC 26
 Db 1 CKLKGQSCRKTXDCCSGSCGRGKC 26

RESULT 77
 AAR39616
 ID AAR39616 standard; peptide; 26 AA.

AC AAR39616;

DT 25-MAR-2003 (revised)
 DT 20-DEC-1993 (first entry)

DE MVIIC/SNX230.

KW Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
 KW calcium channel; neurone; contraction; guinea pig; ileum; MVIIC;
 KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
 KW narcotics.

OS Synthetic.

FH Key Location/Qualifiers
 FT Disulfide-bond 1. .16
 FT Disulfide-bond 8. .20
 FT Disulfide-bond 15. .26

PN WO9313128-A1.

PD 08-JUL-1993.

PF 30-DEC-1992; 92WO-US011349.

PR 30-DEC-1991; 91US-00814759.

PA (NEUR-) NEUREX CORP.

PI Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;

DR WPI; 1993-227270/28.

PT Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
 PT calcium channels - to induce analgesia, enhance opiate analgesics, treat
 PT pain etc.

PS Claim 1; Fig 1; 90pp; English.

XX The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
 CC derivatives of these, which may be used to produce analgesia in a mammal.
 CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
 CC tissue. This is shown by the peptides ability to stimulate contraction in
 CC guinea pig ileum and to bind to OCT MVIIC binding sites present in
 CC neuronal tissue. OCTs are components of peptide toxins derived from
 CC marine snails of the genus Conus, and act as calcium channel blockers.
 CC These OCTs may be used to replace opiods in the treatment of chronic pain
 CC or to reduce the opiod dosage required. This helps to reduce dependence
 CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
 CC PN field.)

XX

SQ Sequence 26 AA;

Query Match 57.5%; Score 69; DB 2; Length 26;
 Best Local Similarity 30.8%; Pred. No. 22;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCKXLDCCSXXCNXXNC 26
 Db 1 CKGKGFPCRKTYDCCSGSCGRGKC 26

RESULT 78

AAR39617
 ID AAR39617 standard; peptide; 26 AA.

AC AAR39617;

DT 25-MAR-2003 (revised)

DT 20-DEC-1993 (first entry)

DE SNX231.

KW Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
 KW calcium channel; neurone; contraction; guinea pig; ileum; MVIIC;
 KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
 KW narcotics.

OS Synthetic.

FH Key Location/Qualifiers
 FT Disulfide-bond 1. .16
 FT Modified-site 7 /note="4Hyp"
 FT Disulfide-bond 8. .20
 FT Disulfide-bond 15. .26

PN WO9313128-A1.

PD 08-JUL-1993.

PF 30-DEC-1992; 92WO-US011349.

PR 30-DEC-1991; 91US-00814759.

PA (NEUR-) NEUREX CORP.

PI Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;

DR WPI; 1993-227270/28.

PT Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
 PT calcium channels - to induce analgesia, enhance opiate analgesics, treat
 PT pain etc.

PS Claim 1; Fig 1; 90pp; English.

XX The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
 CC derivatives of these, which may be used to produce analgesia in a mammal.
 CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
 CC tissue. This is shown by the peptides ability to stimulate contraction in
 CC guinea pig ileum and to bind to OCT MVIIC binding sites present in
 CC neuronal tissue. OCTs are components of peptide toxins derived from
 CC marine snails of the genus Conus, and act as calcium channel blockers.
 CC These OCTs may be used to replace opiods in the treatment of chronic pain
 CC or to reduce the opiod dosage required. This helps to reduce dependence
 CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
 CC PN field.)

SQ Sequence 26 AA;

Query Match 57.5%; Score 69; DB 2; Length 26;
 Best Local Similarity 30.8%; Pred. No. 22;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;


```

Query Match          57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNC 25
   | : : : : : | | | : : : | : : |
DB 1 CKGKAPCRKTMWDCSGSGCGRRGKC 25

RESULT 81
AAW19552
ID AAW19552 standard; peptide; 26 AA.
XX
AC AAW19552;
XX
DT 27-AUG-2003 (revised)
DT 13-OCT-1997 (first entry)
XX
DE Natural omega-conopeptide MWIIC/SNX-230 used for pain relief.
XX
KW Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;
KW N-type voltage-sensitive calcium channel; block; Conus.
XX
OS Conus.
XX
PN WO9701351-A1.
XX
PD 16-JAN-1997.
XX
PF 26-JUN-1996; 96WO-US011041.
XX
PR 27-JUN-1995; 95US-00496047.
PR 08-MAR-1996; 96US-00613400.
XX
PA (NEUR-) NEUREX CORP.
XX
PI Amstutz GA, Bowersox SS, Gohil K, Adriaenssens PI, Kristipati R;
PI Gadbois T, Pettus MR, Luther RR;
XX
DR WPI; 1997-100012/09.
XX
PT Stable omega conopeptide compositions - for producing analgesia and for
PT inhibiting progression of neuropathic pain disorders.
XX
PS Disclosure; Fig 2; 47pp; English.
XX
CC AAW19544-W19553 are naturally occurring omega conopeptides (OCs) isolated
CC from Conus sp. (cone snails). The peptides and their analogues are used
CC as analgesics acting by blocking N-type voltage-sensitive calcium
CC channels. The OCs can be used to treat neuropathic pain as a result of
CC e.g. insult to the spinal cord or peripheral nerves, cancer, bone
CC degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes zoster
CC neuropathy, diabetic neuropathy, hyperesthesia, allodynia or
CC hyperalgesia. The OCs are preferably administered in a medication via an
CC epidural route in a continuous infusion or sustained release formulation.
CC The OCs can provide pain relief when administered epidurally in the
CC absence of a permeation enhancer, at doses that are comparable to
CC effective analgesic doses using intrathecal administration. OC
CC formulations comprising an OC and a carboxylic acid buffer anti-oxidant.
CC They also confer stability to solutions containing them for prolonged
CC treatment methods and long-term storage. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 26 AA;

Query Match          57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNC 26
   | : : : : : | | | : : : | : : |
DB 1 CKGKAPCRKTMWDCSGSGCGRRGKC 26

RESULT 83
AAW72614
ID AAW72614 standard; peptide; 26 AA.
XX
AC AAW72614;
XX
DT 27-AUG-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE Conus genus natural omega-conopeptide MWIIC/SNX-230.

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RESULT 82
AAW12987
ID AAW12987 standard; peptide; 26 AA.
XX
AC AAW12987;
XX
DT 25-MAR-2003 (revised)
DT 22-APR-1997 (first entry)
XX
DE Omega conopeptide SNX-231.
XX
KW Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition;
KW neuronal damage; schizophrenia; tardive dyskinesia; analgesia;
KW acute dystonic reactions; inflammation; epilepsy.
XX
OS Synthetic.
XX
FH Key
FT Modified-site 7
FT FT /label= Hyp
XX
PN US5587454-A.
XX
PD 24-DEC-1996.
XX
PF 15-APR-1993; 93US-00049794.
XX
PR 30-DEC-1991; 91US-00814759.
PR 30-DEC-1992; 92WO-US011349.
XX
PA (NEUR-) NEUREX CORP.
XX
PI Gohil KC, Miljanich GP, Valentino KL, Justice A, Singh T;
PI WPI; 1997-064830/06.
XX
DR Omega conopeptide(s) - useful as analgesics, esp. for treating
DR neuropathic pain.
XX
PS Disclosure; Col 53-54; 58pp; English.
XX
CC The present peptide is an omega conopeptide, useful as an analgesic,
CC especially for treating neuropathic pain. The peptide, which can be
CC prepared by solid phase synthesis, can also be used to inhibit neuronal
CC damage and treat schizophrenia, tardive dyskinesia, acute dystonic
CC reactions, inflammation and epilepsy. In a rat paw formalin test, the
CC peptide had an ED50 of greater than 1.0 microg in phase 1, and greater
CC than 1.0 microg in phase 2 (by intrathecal administration). (Updated on
CC 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 26 AA;

Query Match          57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 22;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNC 26
   | : : : : : | | | : : : | : : |
DB 1 CKGKAPCRKTMWDCSGSGCGRRGKC 26

RESULT 83
AAW72614
ID AAW72614 standard; peptide; 26 AA.
XX
AC AAW72614;
XX
DT 27-AUG-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE Conus genus natural omega-conopeptide MWIIC/SNX-230.

```


FT	Modified-site	/note= "4-Hydroxyproline" 26	
FT		/note= "C-terminal amide"	
XX			
XX			
PN	US5859186-A.		
XX			
XX	12-JAN-1999.		
PD			
XX			
PF	03-JUL-1996;	96US-00675354.	
XX			
XX	30-DEC-1991;	91US-00814759.	
PR	15-APR-1993;	93US-00049794.	
XX			
XX	(NEUR-) NEUREX CORP.		
PA			
XX			
XX	Miljanich GP, Gohil KC, Valentino KL, Justice A, Singh T;		
XX			
DR	WPI; 1999-120002/10.		
XX			
PT	Production of analgesia in mammal - by administration of omega conopeptide(s).		
XX			
PS	Disclosure; Fig 1B; 59pp; English.		
XX			
CC	Sequences AAW95564-573 represent primary sequences of natural omega-conopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig ileum and (b) selectively binding to omega conopeptide MVIIA binding sites in neuronal tissue, where these activities are within the ranges of those of omega-conotoxins MVIIA and TVIA. The method is used for treating chronic pain, especially neuropathic pain		
XX			
XX	Sequence 26 AA;		
CC	Query Match	57.5%; Score 69; DB 2; Length 26;	
CC	Best Local Similarity	30.8%; Pred. No. 22;	
CC	Matches	8; Conservative 12; Mismatches	6; Indels 0; Gaps 0;
CC			
CC	QY	1 CXIXNQXCQXLDCCSXCNXXNC 26	
CC		: : : : : : : :	
CC	DB	1 CKGKAPCRKTYDCSGCGRRGKC 26	
CC		: : : : : : : :	
CC		1 CKGKAPCRKTYDCSGCGRRGKC 26	
XX			
XX	RESULT 87		
XX	AAW56482		
ID	AAW56482 standard; peptide; 26 AA.		
XX			
AC	AAW56482;		
XX			
XX	DT	16-FEB-2000 (first entry)	
XX			
DE	Natural omega conopeptide SNX-231.		
XX			
KW	Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin; marine snail; peptide toxin; inflammation; binding; voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline; anti-inflammatory.		
KW			
KW			
XX	Conus sp.		
XX			
OS			
XX	Key	Location/Qualifiers	
FH	Misc-difference 7	/note= "unspecified"	
FT			
FT			
XX	PN	US5994305-A.	
XX			
XX	PD	30-NOV-1999.	
XX			
XX	PP	21-AUG-1998;	98US-00138439.
XX			
PR	30-DEC-1991;	91US-00814759.	
PR	15-APR-1993;	93US-00049794.	
PR	03-JUL-1996;	96US-00675354.	
PR	01-NOV-1996;	96US-00742774.	
XX			
PA	(ELAN-) ELAN PHARM INC.		
XX			
XX	Justice A, Singh T, Valentino KL, Miljanich GP, Gohil KC;		
PI			
XX	WPI; 2000-038270/03.		
DR			
XX			

PT Measuring the activity of test compounds in blocking voltage-gated
PT calcium channels, binding to the omega conopeptide binding site and
PT inhibiting norepinephrine (noradrenaline) release for treating
PT inflammation.

XX Disclosure; Fig 1; 47pp; English.

XX A method has been developed of selecting a test compound for treating
CC inflammation. The method comprises measuring the activity of the test
CC compound in blocking voltage-gated calcium channels, binding to the omega
CC conopeptide binding site and inhibiting norepinephrine (noradrenaline)
CC release from nervous tissue. The method is useful for selecting compounds
CC for treating inflammation. The selected compounds are capable of
CC producing analgesia in a mammalian subject with chronic or intractable
CC pain. Analgesia caused by selected compounds may reduce the reliance on
CC opioid analgesic agents of the prior art which cause dependency and
CC tolerance, requiring potentially dangerous increases in opioid doses to
CC achieve the analgesic effect. The present sequence represents an omega
CC conopeptide given in the present invention

XX Sequence 26 AA;

Query Match 57.5%; Score 69; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 22;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCGSCXXCNXXNC 26
| : : : : : ||| : : : : :
Db 1 CKGKAXCRKTYDYCCSGCGRRGKC 26

RESULT 88

AAV56481
ID AAV56481 standard; peptide; 26 AA.

AC AAV56481;

XX 16-FEB-2000 (first entry)

DT Natural omega conopeptide MWIIC/SNX-230.

DE Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin;
KW marine snail; peptide toxin; inflammation; binding;
KW voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline;
KW anti-inflammatory.

XX Conus sp.

XX US5994305-A.

PN 30-NOV-1999.

XX 21-AUG-1998; 98US-00138439.

XX 30-DEC-1991; 91US-00814759.

PR 15-APR-1993; 93US-00049794.

PR 03-JUL-1996; 96US-00675354.

PR 01-NOV-1996; 96US-00742774.

XX (ELAN-) ELAN PHARM INC.

XX Justice A, Singh T, Valentino KL, Miljanich GP, Gohil KC;

XX WPI; 2000-038270/03.

XX Measuring the activity of test compounds in blocking voltage-gated
PT calcium channels, binding to the omega conopeptide binding site and
PT inhibiting norepinephrine (noradrenaline) release for treating
PT inflammation.

PS Disclosure; Fig 1; 47pp; English.

XX A method has been developed of selecting a test compound for treating

CC inflammation. The method comprises measuring the activity of the test
CC compound in blocking voltage-gated calcium channels, binding to the omega
CC conopeptide binding site and inhibiting norepinephrine (noradrenaline)
CC release from nervous tissue. The method is useful for selecting compounds
CC for treating inflammation. The selected compounds are capable of
CC producing analgesia in a mammalian subject with chronic or intractable
CC pain. Analgesia caused by selected compounds may reduce the reliance on
CC opioid analgesic agents of the prior art which cause dependency and
CC tolerance, requiring potentially dangerous increases in opioid doses to
CC achieve the analgesic effect. The present sequence represents an omega
CC conopeptide given in the present invention

SQ Sequence 26 AA;

Query Match 57.5%; Score 69; DB 3; Length 26;
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCGSCXXCNXXNC 26
| : : : : : ||| : : : : :
Db 1 CKGKAPCRKTYDYCCSGCGRRGKC 26

RESULT 89

AAV43715

ID AAV43715 standard; peptide; 26 AA.

AC AAV43715;

XX 11-FEB-2000 (first entry)

DT Amino acid sequence of an omega-conotoxin MWIIC.

DE Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;
KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX Conus magus.

XX WO9954350-A1.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-AU000288.

PR 16-APR-1998; 98AU-00002989.

PR 01-FEB-1999; 99AU-00008419.

XX (UYQU) UNIV QUEENSLAND.

XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX WPI; 2000-013226/01.

XX Novel peptides used for the treatment of disorders and diseases where
PT blockage of the N-type calcium channels is required.

PS Disclosure; Page 12; 81pp; English.

XX The present sequence represents an omega-conotoxin. Omega-conotoxins are
CC isolated from venoms of predatory marine snails, and have a selectivity
CC for N-type calcium channels over P/Q type channels, and so block N-type
CC calcium channels. The omega-conotoxins of the invention can be used in
CC any disease or disorder where blockage of N-type calcium channels is
CC required, e.g. in the reduction of neuronal damage following ischemia,
CC production of analgesia, or enhancement of opiate analgesia, in the
CC treatment of schizophrenia, stimulant induced psychoses, hypertension,
CC inflammation, and diseases which cause bronchotension, and also in the
CC inhibition of progression of neuropathic pain. They can also be used in a
CC screen to identify compounds with activity at N-type voltage sensitive
CC calcium channels

Query Match	57.5%;	Score 69;	DB 3;	Length 26;
Best Local Similarity	34.6%;	Pred. No. 22;		

Query Match 57.5%; Score 69; DB 4; Length 26;


```
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 1. .16
XX FT Disulfide-bond 8. .20
XX FT Disulfide-bond 15. .26
XX FT Modified-site 26
XX FT /note= "amidated"
XX PN JP2001253899-A.
XX PD 18-SEP-2001.
XX PF 13-MAR-2000; 2000JP-00068023.
XX PR 13-MAR-2000; 2000JP-00068023.
XX PA (MITU ) MITSUBISHI CHEM CORP.
XX DR WPI; 2002-044564/06.
XX PT Manufacturing peptide library, by introducing mutant amino acid in
XX PT peptide mixture for synthesizing peptide of interest and its variants,
XX PT forming intramolecular disulphide bonds between peptides and separating
XX PT them.
XX PS Example; Fig 1; 1lpp; Japanese.
XX CC The present invention describes a method for manufacturing a peptide
XX CC library comprising a peptide (I) having 2 or more intramolecular
XX CC disulphide (ID) bonds, and its variants (V). The method comprises
XX CC introducing mutant amino acid in the reaction mixture, a peptide mixture
XX CC containing two or more amino acids, for chemo-synthesising (I) and (V),
XX CC where the ID bonds are formed between the peptides by air oxidation, and
XX CC ID-containing peptides are separated. Also described are: (1) a peptide
XX CC library obtained by the above said method; (2) screening for mutant
XX CC peptide with an improved biological activity than its wild type,
XX CC comprising comparing the biological activities of the peptides in the
XX CC peptide library with a wild type peptide; (3) a mutant peptide obtained
XX CC by the above said screening method; and (4) a calcium channel blocker
XX CC containing Omega-conotoxin MV1IC peptide. The method is useful for
XX CC synthesising a peptide library, and for screening peptides with increased
XX CC biological activity than the wild type peptides. The method is suitable
XX CC for producing many number of variants for a given peptide,
XX CC simultaneously. The present sequence represents an omega-conotoxin MV1IC
XX CC peptide which is given in the exemplification of the present invention
XX SQ Sequence 26 AA;

Query Match 57.5%; Score 69; DB 5; Length 26;
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXOXLDCCSXNCNXXNC 26
| : : : : : | | | : : : |
Db 1 CKGKGPCKRTMYDCCSGCGRRGKC 26

RESULT 97
AAW12803
XX ID AAW12803 standard; peptide; 29 AA.
XX AC AAW12803;
XX DT 18-APR-1997 (first entry)
XX DE Full length omega-conotoxin MV1IC.
XX KW Omega-conotoxin; conus; Conus magus; alpha-conotoxin; mu-conotoxin;
XX KW nicotinic acetylcholine receptor; venom; skeletal muscle; inhibitor;
XX KW sodium ion channel; presynaptic neuronal calcium ion channel; therapy;
XX KW P-like subtype; N-type channel; respiratory rhythm; respiratory control;
XX KW neural developmental syndrome; respiratory crisis;
XX KW Lambert-Eaton myasthenic syndrome.
```

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XX OS Conus magus.
XX PN US5591821-A.
XX PD 07-JAN-1997.
XX PF 16-JUL-1993; 93US-00092215.
XX PR 16-JUL-1993; 93US-00092215.
XX PA (UTAH ) UNIV UTAH.
XX PI Monje VD, Imperial JS, Olivera BM, Hillyard DR;
XX DR WPI; 1997-086679/08.
XX PT New omega-conotoxin peptide(s) - which target P-type and N-type calcium
XX PT ion channels, used for distinguishing calcium channels or for diagnosis.
XX PS Example 1; Col 29-30; 2lpp; English.
XX CC AAW12800-W12804 represent omega-conotoxins isolated from Conus magus.
XX CC This sequence represents the MV1IC Conus magus omega-conotoxins. Conus
XX CC venom contains three types of disulphide rich peptides, these are the
XX CC alpha- conotoxins, mu-conotoxins and omega-conotoxins. The alpha-
XX CC conotoxins target and block the nicotinic acetylcholine receptors, and
XX CC the omega- conotoxins target and block the skeletal muscle sodium ion channels, and
XX CC ion channels. The omega-conotoxin peptides of the invention can target P-
XX CC like subtypes of calcium ion channels, as well as the N-type channels
XX CC (distinguishing them from previously known omega-conotoxins). These
XX CC sequences can also be used for distinguishing the types of calcium ion
XX CC channels. The presence or absence of sites for the peptides can be
XX CC determined in tissue sections, thereby characterising calcium ion channel
XX CC expressing cells into various types. As these sequences affect the
XX CC control of respiratory rhythms in vivo, they can be used to evaluate
XX CC abnormalities in respiratory control which are particularly severe in the
XX CC neonatal period. The peptides can also be used for assessing neural
XX CC developmental syndromes that result in respiratory crisis, and can be
XX CC used to diagnose the Lambert-Eaton myasthenic syndrome
XX SQ Sequence 29 AA;

Query Match 57.5%; Score 69; DB 2; Length 29;
Best Local Similarity 30.8%; Pred. No. 24;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXOXLDCCSXNCNXXNC 26
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Db 3 CKGKGPCKRTMYDCCSGCGRRGKC 28

RESULT 98
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XX ID ADP04517 standard; protein; 342 AA.
XX AC ADP04517;
XX DT 29-JUL-2004 (first entry)
XX DE Sea squirt protein with tissue specific expression in development Seq112.
XX KW sea squirt; regeneration medicine; gene therapy; cell proliferation;
XX KW differentiation; reproduction; environmental measurement; water survey.
XX OS Ciona intestinalis.
XX PN JP2004057129-A.
XX PD 26-FEB-2004.
XX PF 31-JUL-2002; 2002JP-00222593.
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PR	31-JAN-2001	2001US-0265412P
PR	31-JAN-2001	2001US-0265514P
PR	31-JAN-2001	2001US-0265517P
PR	02-FEB-2001	2001US-0265406P
PR	05-FEB-2001	2001US-0266767P
PR	07-FEB-2001	2001US-0266975P
PR	07-FEB-2001	2001US-0267057P
PR	08-FEB-2001	2001US-0267459P
PR	09-FEB-2001	2001US-0267823P
PR	15-FEB-2001	2001US-0268974P
PR	26-FEB-2001	2001US-02711664P
PR	27-FEB-2001	2001US-02711839P
PR	27-FEB-2001	2001US-0271855P
PR	02-MAR-2001	2001US-02727888P
PR	02-MAR-2001	2001US-02727806P
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PR	14-MAR-2001	2001US-0275989P
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PR	15-MAR-2001	2001US-0276450P
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PR	16-MAR-2001	2001US-0276768P
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PR	11-APR-2001	2001US-0283083P
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PR	23-APR-2001	2001US-0285743P
PR	03-MAY-2001	2001US-0288327P
PR	03-MAY-2001	2001US-0289504P
PR	29-MAY-2001	2001US-0289504P
PR	30-MAY-2001	2001US-0294473P
PR	08-JUN-2001	2001US-0296964P
PR	18-JUN-2001	2001US-0298959P
PR	19-JUN-2001	2001US-0299324P
PR	13-AUG-2001	2001US-0312020P
PR	16-AUG-2001	2001US-0312889P
PR	16-AUG-2001	2001US-0312908P
PR	21-AUG-2001	2001US-0313987P
PR	28-AUG-2001	2001US-0315470P
PR	31-AUG-2001	2001US-0315447P
PR	07-SEP-2001	2001US-0318115P
PR	07-SEP-2001	2001US-0318118P
PR	12-SEP-2001	2001US-0318740P
PR	18-OCT-2001	2001US-0323379P
PR	18-OCT-2001	2001US-0330245P
PR	14-NOV-2001	2001US-0330388P
PR	18-NOV-2001	2001US-0332701P

Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune disorders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy and epilepsy. Accordingly, these molecules have many activities including cytostatic, cardiac, antiinflammatory, immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, antiasthmatic, nephrotropic, anti-arthritis, hepatotropic, neuroprotective, neurotropic, antibacterial, virucide, antiparasitic, relaxant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a homologue of a human NOVX protein of the invention.

Sequence 2444 AA;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:24:17 ; Search time 30.5 Seconds
(without alignments)
66.083 Million cell updates/sec

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Perfect score: 120
Sequence: 1 CXINQXCXQLDCCSXKCNXXNXCVCV 27

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	81	67.5	26	1	US-08-496-847-19
5	81	67.5	26	2	US-08-742-774-19
6	81	67.5	26	2	US-08-675-354-19
7	81	67.5	26	2	US-08-965-918-19
8	81	67.5	26	2	US-08-138-439-19
9	81	67.5	26	3	US-08-613-400A-19
10	81	67.5	26	3	US-08-298-017-19
11	81	67.5	26	3	US-09-392-979A-19
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15	77	64.2	26	2	US-08-742-774-8
16	77	64.2	26	2	US-08-675-354-8
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45	68	56.7	2556	1	US-08-083-590A-20	Sequence 20, Appl
46	68	56.7	2556	3	US-08-532-384-20	Sequence 20, Appl
47	68	56.7	2556	4	US-08-899-232-2	Sequence 2, Appl
48	68	56.7	2556	4	US-09-121-457-2	Sequence 2, Appl
49	66	55.0	321	4	US-09-270-767-33762	Sequence 33762, A
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51	66	55.0	721	3	US-08-872-855-7	Sequence 7, Appl
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64	65.5	54.6	73	4	US-09-894-882-167	Sequence 167, App
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67	65	54.2	735	3	US-09-540-153-9	Sequence 9, Appl
68	65	54.2	1964	3	US-09-467-997-1	Sequence 1, Appl
69	65	54.2	2321	4	US-09-230-652-2	Sequence 2, Appl
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73	64	53.3	3623	4	US-09-341-461-2	Sequence 2, Appl
74	63.5	52.9	36	4	US-09-894-882-324	Sequence 324, App
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76	63.5	52.9	36	4	US-09-894-882-441	Sequence 441, App
77	63.5	52.9	36	4	US-09-894-882-443	Sequence 443, App
78	63.5	52.9	72	4	US-09-894-882-323	Sequence 323, App
79	63.5	52.9	72	4	US-09-894-882-338	Sequence 338, App
80	63	52.5	76	4	US-09-749-637A-207	Sequence 207, App
81	63	52.5	583	4	US-09-641-612-2	Sequence 2, Appl
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83	63	52.5	1055	3	US-09-214-278-2	Sequence 2, Appl
84	63	52.5	1055	2	US-09-855-722-2	Sequence 2, Appl
85	63	52.5	1055	2	US-08-400-159-8	Sequence 8, Appl
86	63	52.5	1148	3	US-08-882-046-4	Sequence 4, Appl
87	63	52.5	1148	3	US-09-566-047-4	Sequence 4, Appl
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92	63	52.5	1248	3	US-08-882-046-6	Sequence 6, Appl
93	63	52.5	1248	4	US-09-566-047-6	Sequence 6, Appl
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95	63	52.5	1257	4	US-09-195-524-8	Sequence 8, Appl
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99	62.5	52.1	70	4	US-09-894-882-209	Sequence 209, App
100	62.5	52.1	71	4	US-09-894-882-74	Sequence 74, Appl


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RESULT 4
US-08-496-847-19
; Sequence 19, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Ametutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; APPLICATION NUMBER: US/08/496,847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
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US-08-496-847-19
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Best Local Similarity 34.6%; Pred. NO. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels
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; |::|::|::|::|::|::|::|::|::|
DB 1 CKLKGQCSRLMYDCCSGCGRSKC 26
;
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US-08-742-774-19
; Sequence 19, Application US/08742774
; Patent No. 5824645
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,774
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,354
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444

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; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
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Query Match 67.5%; Score 81; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

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; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,354
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
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; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
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Query Match 67.5%; Score 81; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

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Db 1 CKLKGQSCSRLMYDCCSGCSGRSGKC 26

RESULT 7
US-08-965-918-19
; Sequence 19, Application US/08965918
; Patent No. 5891849
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,918
; FILING DATE: 07-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohr, Judy M.
; REGISTRATION NUMBER: 38,563
; REFERENCE/DOCKET NUMBER: 5865-0009.34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-965-918-19

Query Match 67.5%; Score 81; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXOXLDCCSXXCNXXNC 26
Db 1 CKLKGQSCSRLMYDCCSGCSGRSGKC 26

RESULT 8
US-09-138-439-19
; Sequence 19, Application US/09138439
; Patent No. 5954305
; GENERAL INFORMATION:
```



```

; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138.439
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
; US-09-138-439-19

Query Match 67.5%; Score 81; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CXIXNQXCXQXLDCCSXCNXXNC 26
|:::|:::|:::|:::|:::|:::|
Db 1 CKLKGQCSRLMYDCCSGCGSGKC 26

RESULT 9
US-08-613-400A-19
; Sequence 19, Application US/08613400A
; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pettus, Mark, R.
; APPLICANT: Luther, Robert, R.
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA

```

```

; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
; US-08-613-400A-19

Query Match 67.5%; Score 81; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CXIXNQXCXQXLDCCSXCNXXNC 26
|:::|:::|:::|:::|:::|:::|
Db 1 CKLKGQCSRLMYDCCSGCGSGKC 26

RESULT 10
US-09-298-017-19
; Sequence 19, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:

```



```
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-298-017-19

Query Match 67.5%; Score 81; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCQXLDCCSCXXCNXXNC 26
Db 1 CKLKGQSCSRLMYDCCSGSGRSGKC 26

RESULT 11
US-09-392-979A-19
; Sequence 19, Application US/0932979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US/07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-392-979A-19

Query Match 67.5%; Score 81; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCQXLDCCSCXXCNXXNC 26
Db 1 CKLKGQSCSRLMYDCCSGSGRSGKC 26

RESULT 12
US-07-789-913-8
; Sequence 8, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,913
; FILING DATE: 19911112
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0005.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-183
US-07-789-913-8

Query Match 64.2%; Score 77; DB 1; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
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CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/742.774
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/675,354
 FILING DATE: 03-JUL-1996
 APPLICATION NUMBER: US/08/049,794
 FILING DATE: 1993-APR-15
 APPLICATION NUMBER: US 07/814,759
 FILING DATE: 30-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Stratford, Carol A.
 REGISTRATION NUMBER: 34,444
 REFERENCE/DOCKET NUMBER: 5865-0009.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: SVIE/SNX-183, FIGURE 1
 US-08-742-774-8

```

Query Match      64.2%; Score 77; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels

QY 1 CXIXNQXCXOXLDCCSXXCNXXNXC 26
Db 1 CLKLGOSCRKTSYDCSGSGCGRSGKC 26

```

RESULT 16

```

US-08-675-354-8
; Sequence 8, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Deklinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; Zip: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,354
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:

```

NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-675,154-8.

Query Match 64.2%; Score 77; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXXCNXXXNC 26

Db
1 CKLKGOSCRKTSYDCCSGSCGRSGKC 26

RESULT 17

US-08-965-918-8
 / Sequence 8, Application US/08965918
 / Patent No. 5891849
 / GENERAL INFORMATION:
 / APPLICANT: Amstutz, Gary A.
 / APPLICANT: Bowersox, Stephen S.
 / APPLICANT: Gohil, Kishorchandra
 / APPLICANT: Adriaenssens, Peter I.
 / APPLICANT: Kristipati, Ramasharma
 / TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
 / TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
 / NUMBER OF SEQUENCES: 36
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Dehlinger & Associates
 / STREET: 350 Cambridge Avenue, Suite 250
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: US
 / ZIP: 94306-1546
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: Fast-SEQ for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/965,918
 / FILING DATE: 07-NOV-1997
 / CLASSIFICATION: 514
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Mohr, Judy M.
 / REGISTRATION NUMBER: 38,563
 / REFERENCE/DOCKET NUMBER: 5865-0009.34
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 650-324-0880
 / TELEFAX: 650-324-0960
 / INFORMATION FOR SEQ ID NO: 8:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 26 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / HYPOTHETICAL: NO
 / ORIGINAL SOURCE:
 / INDIVIDUAL ISOLATE: SVIB/SNK-183, FIGURE 1
 / US-08-965-918-8


```

; Patent No. 6054423
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pettus, Mark, R.
; APPLICANT: Luther, Robert, R.
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGIN:
; INDIVIDUAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-08-613-400A-8

Query Match 64.2%; Score 77; DB 3; Length 26;
Best Local Similarity 34.1%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXIXNQXCXOXLDDCCSXCNXNC 26
Db 1 CLKKGQSCRKTSYDCCSGSGRSGKC 26
|:::|:::|:::|:::|:::|:::|
|:::|:::|:::|:::|:::|:::|

RESULT 20
US-09-298-017-8
; Sequence 8, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA

```



```
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-09-298-017-8

Query Match 64.2%; Score 77; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXGXNXXNC 25
   |::|::|::|::|::|::|::|::|
Db 1 CKLKGQSCRKTSYDCCSGSGRSGKC 25

RESULT 21
US-09-392-979A-8
; Sequence 8, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
```

```
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-09-392-979A-8

Query Match 64.2%; Score 77; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXGXNXXNC 26
   |::|::|::|::|::|::|::|::|
Db 1 CKLKGQSCRKTSYDCCSGSGRSGKC 26

RESULT 22
US-08-185-432-18
; Sequence 18, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Buseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2523 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-185-432-18
```



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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-496-847-29

Query Match      57.5%; Score 69; DB 1; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches      8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY      1 CXIXNQXCXOXLDCCSXCNXXNC 26
       | : : : : : | | | : : : |
Db      1 CKKGAPCRKWTYDCCSGCGRGKC 26

RESULT 29
US-08-742-774-21
; Sequence 21, Application US/08742774
; Patent No. 5824645
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,774
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,354
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-742-774-21
```

```
Query Match      57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 34.8%; Pred. No. 3.4;
Matches      9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY      1 CXIXNQXCXOXLDCCSXCNXXNC 26
       | : : : : : | | | : : : |
Db      1 CKKGAPCRKWTYDCCSGCGRGKC 26

RESULT 30
US-08-742-774-29
; Sequence 29, Application US/08742774
; Patent No. 5824645
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,774
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,354
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
; US-08-742-774-29

Query Match      57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches      8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY      1 CXIXNQXCXOXLDCCSXCNXXNC 26
       | : : : : : | | | : : : |
Db      1 CKKGAPCRKWTYDCCSGCGRGKC 26

RESULT 31
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US-08-675-354-21
; Sequence 21, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,354
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-675-354-21

```

```

Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 3.4;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNC 26
| : : |::: |::: |::: |::: |
Db 1 CKKGAPCRKTMWDCSGSGRRGKC 26

```

```

RESULT 32
US-08-675-354-29
; Sequence 29, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L

```

```

; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,354
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-675-354-29

Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNC 26
| : : |::: |::: |::: |::: |
Db 1 CKKGAPCRKTMWDCSGSGRRGKC 26

RESULT 33
US-08-965-918-21
; Sequence 21, Application US/08965918
; Patent No. 5891849
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaense, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-965-918-21

Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 3.4;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDCCSCXCNXKNC 26
Db 1 CKRGAXCRKTMYYDCCSGCGRRGKC 26

RESULT 34
US-08-965-918-29
Sequence 29, Application US/08965918
Patent No. 5891849
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-965-918-29

Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDCCSCXCNXKNC 26
Db 1 CKRGAPCRKTMYYDCCSGCGRRGKC 26

RESULT 35
US-09-138-439-21
Sequence 21, Application US/09138439
Patent No. 5994305
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANTICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
FEATURE:


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; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
; US-08-613-400A-29

Query Match 57.5%; Score 69; DB 3; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNOXCXOXLDCCSXXCNXXNC 26
Db 1 CKGKGCXCRKTYDYCCSGCGRGKC 26

RESULT 39
US-09-298-017-21
; Sequence 21, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-09-298-017-21

Query Match 57.5%; Score 69; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 3.4;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNOXCXOXLDCCSXXCNXXNC 26
Db 1 CKGKGCXCRKTYDYCCSGCGRGKC 26

RESULT 40
US-09-298-017-29
; Sequence 29, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
```


REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-09-298-017-29

Query Match 57.5%; Score 69; DB 3; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNOXCXOXLDCCSXNCXNXC 26
| : : : : :
Db 1 CKKGAPCRKWTYDCCSGCGRGKC 26

RESULT 41

US-09-392-979A-21
Sequence 21, Application US/09392979A
Patent No. 6136786
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRES:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO

ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
US-09-392-979A-21

Query Match 57.5%; Score 69; DB 3; Length 26;
Best Local Similarity 34.8%; Pred. No. 3.4;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNOXCXOXLDCCSXNCXNXC 26
| : : : : :
Db 1 CKKGAPCRKWTYDCCSGCGRGKC 26

RESULT 42

US-09-392-979A-29
Sequence 29, Application US/09392979A
Patent No. 6136786
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-09-392-979A-29

Query Match 57.5%; Score 69; DB 3; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNOXCXOXLDCCSXNCXNXC 26
| : : : : :
Db 1 CKKGAPCRKWTYDCCSGCGRGKC 26

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

```

; INFORMATION FOR SEQ ID NO: 20:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 2556 amino acids

```



```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-20

Query Match      56.7%; Score 68; DB 1; Length 2556;
Best Local Similarity 30.8%; Pred. No. 2.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY      2 XIXNQXCXQXLDCCSXKXCNXKXCV 27
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      248 GFTGQNCENIDDCPGNCKNGGACV 273

RESULT 46
US-08-532-384-20
; Sequence 20, Application US/08532384
; Patent No. 6083904
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532.384
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,590
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2556 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-532-384-20

Query Match      56.7%; Score 68; DB 3; Length 2556;
Best Local Similarity 30.8%; Pred. No. 2.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY      2 XIXNQXCXQXLDCCSXKXCNXKXCV 27
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      248 GFTGQNCENIDDCPGNCKNGGACV 273

RESULT 47
US-08-899-232-2
; Sequence 2, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-899-232-2

Query Match      56.7%; Score 68; DB 4; Length 2556;
Best Local Similarity 30.8%; Pred. No. 2.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY      2 XIXNQXCXQXLDCCSXKXCNXKXCV 27
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      248 GFTGQNCENIDDCPGNCKNGGACV 273

RESULT 48
US-09-121-457-2
; Sequence 2, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-457-2

Query Match      56.7%; Score 68; DB 4; Length 2556;
Best Local Similarity 30.8%; Pred. No. 2.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY      2 XIXNQXCXQXLDCCSXKXCNXKXCV 27
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      248 GFTGQNCENIDDCPGNCKNGGACV 273

RESULT 49
US-09-270-767-33762
; Sequence 33762, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33762
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33762
```


Query Match 55.0%; Score 66; DB 4; Length 321;
Best Local Similarity 33.3%; Pred. No. 58;
Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNQCXQXLDCCSXCNXXNXC 27
DB 165 TGNQCQTIDDCA SNPCQHGATCV 188

RESULT 50

US-09-270-767-48979
; Sequence 48979, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 48979
; LENGTH: 321
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-48979

Query Match 55.0%; Score 66; DB 4; Length 321;
Best Local Similarity 33.3%; Pred. No. 58;
Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNQCXQXLDCCSXCNXXNXC 27
DB 165 TGNQCQTIDDCA SNPCQHGATCV 188

RESULT 51

US-08-872-855-7
; Sequence 7, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-855-7

Query Match 55.0%; Score 66; DB 3; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXQXLDCCSXCNXXNXC 26
DB 436 GFSGRNCDNLDCTSFPCQNGGTC 460

RESULT 52

US-08-981-392-5
; Sequence 5, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-981-392-5

Query Match 55.0%; Score 66; DB 3; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXQXLDCCSXCNXXNXC 26
DB 436 GFSGRNCDNLDCTSFPCQNGGTC 460

RESULT 53

US-09-908-322-5
; Sequence 5, Application US/09908322

; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5
Query Match 55.0%; Score 66; DB 4; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
QY 2 XIXNQXCXQXLDCCSXCNXNXC 26
Db 436 GFGGRNCDNLDCTSPFCQNGGTC 460
RESULT 54
US-08-185-432-16
; Sequence 16, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsumo, Kenji
; TITLE OF INVENTION: DELTEx PROTEINS, NUCLEIC ACIDS, AND
; ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York

; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-185-432-16
Query Match 55.0%; Score 66; DB 1; Length 2471;
Best Local Similarity 25.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;
QY 1 CXIXN---QXCXQXLDCCSXCNXNXC 27
Db 324 CVCVNGSGDDCSENIDDCAFASCTPGSTCI 354
RESULT 55
US-08-083-590A-19
; Sequence 19, Application US/08083590A
; Patent No. 5786158
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; AND COMPOSITIONS BASED ON NO. 5786158ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,590A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:

US-08-899-232-1

; PATENT NO. 8832919
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Artavanis-Tsakonas, S.
 ; APPLICANT: Qi, H.

Qy 1 CXIXNQXCQXLDDCCSXXCNXXNXCv 27


```
Db      2 CLSLGQRCXRH-SDCCGXLCFFYDKCV 27

RESULT 63
US-09-894-882-369
; Sequence 369, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Marten
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 369
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-369

Query Match      54.6%; Score 65.5; DB 4; Length 36;
Best Local Similarity 33.3%; Pred. No. 9.2;
Matches 9; Conservative 12; Mismatches 5; Indels 1; Gaps 1;

Qy      1 CXIXNQXCXQXLDCCSXGXCNXXNKCXV 27
; : : : : : : : : : : : : : : : : : : : : : :
Db      2 CLSLGQRCXRH-SDCCGXLCFFYDKCV 27

RESULT 64
US-09-894-882-167
; Sequence 167, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Marten
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 369
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167

Query Match      54.6%; Score 65.5; DB 4; Length 36;
Best Local Similarity 33.3%; Pred. No. 9.2;
Matches 9; Conservative 12; Mismatches 5; Indels 1; Gaps 1;

Qy      1 CXIXNQXCXQXLDCCSXGXCNXXNKCXV 27
; : : : : : : : : : : : : : : : : : : : : : :
Db      2 CLSLGQRCXRH-SDCCGXLCFFYDKCV 27

RESULT 65
US-09-191-647-9
; Sequence 9, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-191-647-9

Query Match      54.2%; Score 65; DB 3; Length 735;
Best Local Similarity 26.9%; Pred. No. 1.5e+02;
Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy      2 XIXNQXCXQXLDCCSXGXCNXXNKCXV 27
; : : : : : : : : : : : : : : : : : : : : : :
Db      248 GFEGDYCEKNIDCVNSKENGKCV 273

RESULT 66
US-09-540-245A-9
; Sequence 9, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; CURRENT APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
```

```
Db      2 CLSLGQRCXRH-SDCCGXLCFFYDKCV 27

RESULT 63
US-09-894-882-369
; Sequence 369, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Marten
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 369
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-369

Query Match      54.6%; Score 65.5; DB 4; Length 36;
Best Local Similarity 33.3%; Pred. No. 9.2;
Matches 9; Conservative 12; Mismatches 5; Indels 1; Gaps 1;

Qy      1 CXIXNQXCXQXLDCCSXGXCNXXNKCXV 27
; : : : : : : : : : : : : : : : : : : : : : :
Db      2 CLSLGQRCXRH-SDCCGXLCFFYDKCV 27

RESULT 64
US-09-894-882-167
; Sequence 167, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Marten
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 369
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167

Query Match      54.6%; Score 65.5; DB 4; Length 36;
Best Local Similarity 33.3%; Pred. No. 9.2;
Matches 9; Conservative 12; Mismatches 5; Indels 1; Gaps 1;

Qy      1 CXIXNQXCXQXLDCCSXGXCNXXNKCXV 27
; : : : : : : : : : : : : : : : : : : : : : :
Db      2 CLSLGQRCXRH-SDCCGXLCFFYDKCV 27

RESULT 65
US-09-191-647-9
; Sequence 9, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-191-647-9

Query Match      54.2%; Score 65; DB 3; Length 735;
Best Local Similarity 26.9%; Pred. No. 1.5e+02;
Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy      2 XIXNQXCXQXLDCCSXGXCNXXNKCXV 27
; : : : : : : : : : : : : : : : : : : : : : :
Db      248 GFEGDYCEKNIDCVNSKENGKCV 273

RESULT 66
US-09-540-245A-9
; Sequence 9, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; CURRENT APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
```



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; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-2318
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 119
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Conus magus
; US-09-894-882-119

Query Match          53.8%; Score 64.5; DB 4; Length 71;
Best Local Similarity 33.3%; Pred.No.21;
Matches      9; Conservative 11; Mismatches    6; Indels   1; Gaps   1;

QY      1 CXIXNQXCXQLDDCCSXXCNXXNKCVCV 27
        :|::||::||::||::||::||::||
DB      39 CSILGQRCDGH-SDCCWDMCCASEMVCV 64

RESULT 73
US-09-341-461-2
; Sequence 2, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 2
; LENGTH: 3623
; TYPE: PRT
; ORGANISM: rat
; FEATURE:
; OTHER INFORMATION: amino acid sequence of rat cubilin protein
; US-09-341-461-2

Query Match          53.3%; Score 64; DB 4; Length 3623;
Best Local Similarity 29.2%; Pred.No. 7.5e+02;
Matches      7; Conservative 13; Mismatches    4; Indels   0; Gaps   0;

QY      4 XNOXCXQXLDDCCSXXCNXXNKCVCV 27
        :|::|||||::||::||::||:
DB      425 SQGNCTENINDCSSNPCLNGGTCTI 448

RESULT 74
US-09-894-882-324
; Sequence 324, Application US/09894882
; Patent No. 6767895
```


US-09-894-882-443


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/ GENERAL INFORMATION:
/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ APPLICANT: Walker, Craig S.
/ APPLICANT: Shetty, Reshma
/ APPLICANT: Jimenez, Elsie C.
/ APPLICANT: McIntosh, J. Michael
/ APPLICANT: Olivera, Baldomero M.
/ APPLICANT: Watkins, Maren
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Shen, Greg S.
/ TITLE OF INVENTION: I-Superfamily Conotoxins
/ FILE REFERENCE: 2314-238
/ CURRENT APPLICATION NUMBER: US/09/894,882
/ CURRENT FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 60/243,410
/ PRIOR FILING DATE: 2000-10-27
/ PRIOR APPLICATION NUMBER: US 60/246,591
/ PRIOR FILING DATE: 2000-11-08
/ PRIOR APPLICATION NUMBER: US 60/247,714
/ PRIOR FILING DATE: 2000-11-14
/ PRIOR APPLICATION NUMBER: US 60/264,256
/ PRIOR FILING DATE: 2001-01-29

```

US-09-749-637A-207
; Sequence 207, Application US/09749637A
; Patent No. 6762185
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Baldomero M. Olivera,
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren


```
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard M.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 207
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Conus distans
US-09-749-637A-207

Query Match      52.5%; Score 63; DB 4; Length 76;
Best Local Similarity 35.7%; Pred. No. 30;
Matches 10; Conservative 12; Mismatches 4; Indels 4; Gaps 2;

QY 1 CXIXNQXCXQXLDCCSXKN-XXNXCV 27
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 48 CNEAQEHCTQN-PDCCSESCNKFVGRCL 74

RESULT 81
US-09-641-612-2
; Sequence 2, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-2

Query Match      52.5%; Score 63; DB 4; Length 583;
Best Local Similarity 30.8%; Pred. No. 1.8e+02;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXKNXXNXCV 27
: : : : : | : : : : : | : : : : : | : : : : : |
Db 378 GFAGPRCEHLDLDDCAGACANGTCTV 403

RESULT 82
US-09-641-612-5
; Sequence 5, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5

; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard M.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 207
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-641-612-5

Query Match      52.5%; Score 63; DB 4; Length 585;
Best Local Similarity 30.8%; Pred. No. 1.8e+02;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXKNXXNXCV 27
: : : : : | : : : : : | : : : : : | : : : : : |
Db 380 GFAGPRCEHLDLDDCAGACANGTCTV 405

RESULT 83
US-09-214-278-2
; Sequence 2, Application US/09214278
; Patent No. 6291210
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/214,278
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-278-2

Query Match      52.5%; Score 63; DB 3; Length 1055;
Best Local Similarity 23.1%; Pred. No. 3.1e+02;
Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXKNXXNXCV 27
: : : : : | : : : : : | : : : : : | : : : : : |
Db 601 GFTGTYCHENIDDLCLGQPCRNNGTCTI 626

RESULT 84
US-09-855-722-2
; Sequence 2, Application US/09855722
; Patent No. 6638741
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/855,722
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/214,278
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-722-2

Query Match      52.5%; Score 63; DB 4; Length 1055;
Best Local Similarity 23.1%; Pred. No. 3.1e+02;
Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXKNXXNXCV 27
: : : : : | : : : : : | : : : : : | : : : : : |
```


Db 601 GFTGTYCHENIDDLGQPCRNNGTCTI 626

RESULT 85

US-08-400-159-8

Sequence 8, Application US/08400159

Patent No. 5869282

GENERAL INFORMATION:

APPLICANT: Ish-Horowitz, David

APPLICANT: Henrique, Domingos M.P.

APPLICANT: Lewis, Julian H.

APPLICANT: Myat, Anna M.

APPLICANT: Fleming, Robert J.

APPLICANT: Artavanis-Tsakonas, Spyridon

APPLICANT: Mann, Robert S.

APPLICANT: Gray, Grace E.

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE

TITLE OF INVENTION: SRRATE GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/400,159

FILING DATE: 07-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-029

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1065 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-400-159-8

Query Match 52.5%; Score 63; DB 2; Length 1065;

Best Local Similarity 23.1%; Pred. No. 3.1e+02;

Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXCQXLDCCSXCNXNXCVCV 27

Db 457 GFTGTYCHENIDDLGQPCRNNGTCTI 482

RESULT 86

US-08-882-046-4

Sequence 4, Application US/08882046

Patent No. 6136952

GENERAL INFORMATION:

APPLICANT: Li, Linheng

APPLICANT: Hood, Leroy

APPLICANT: Krantz, Ian D.

APPLICANT: Spinner, Nancy B.

TITLE OF INVENTION: Human Jugged Polypeptide, Encoding

TITLE OF INVENTION: Nucleic Acids and Methods of Use

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/566,047

FILING DATE: 05-May-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/882,046

FILING DATE: 25-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

Query Match 52.5%; Score 63; DB 3; Length 1148;

Best Local Similarity 23.1%; Pred. No. 3.3e+02;

Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXCQXLDCCSXCNXNXCVCV 27

Db 538 GFTGTYCHENIDDLGQPCRNNGTCTI 563

RESULT 87

US-09-566-047-4

Sequence 4, Application US/09566047

Patent No. 6703198

GENERAL INFORMATION:

APPLICANT: Li, Linheng

APPLICANT: Hood, Leroy

APPLICANT: Krantz, Ian D.

APPLICANT: Spinner, Nancy B.

TITLE OF INVENTION: Methods of Diagnosing Alagille Syndrome

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/566,047

FILING DATE: 05-May-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/882,046

FILING DATE: 25-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

Matches	6;	Conservative	13;	Mismatches	7;	Indels	0;	Gaps	0;
Qy	2	XIXNQXCQXQLDDCCSXXCNXXNXC	27						
Db	601	GFTGTYCHENIDDCGQPCRNNGTCT	626						
<p>RESULT 90</p> <p>US-09-214-278-5</p> <p>Sequence 5, Application US/09214278</p> <p>Patent No. 6291210</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Sakano, Seiji</p> <p>APPLICANT: Itoh, Akira</p> <p>TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE</p> <p>FILE REFERENCE: KP-8576</p> <p>CURRENT APPLICATION NUMBER: US/09/214,278</p> <p>CURRENT FILING DATE: 1999-01-26</p> <p>NUMBER OF SEQ ID NOS: 32</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 5</p> <p>LENGTH: 1238</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo sapiens</p> <p>US-09-214-278-5</p>									
<p>Query Match 52.5%; Score 63; DB 3; Length 1238;</p> <p>Best Local Similarity 23.1%; Pred. No. 3.5e+02;</p> <p>Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;</p>									
Qy	2	XIXNQXCQXQLDDCCSXXCNXXNXC	27						
Db	627	GFTGTYCHENIDDCGQPCRNNGTCT	652						
<p>RESULT 91</p> <p>US-09-855-722-5</p> <p>Sequence 5, Application US/09855722</p> <p>Patent No. 6638741</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Sakano, Seiji</p> <p>APPLICANT: Itoh, Akira</p> <p>TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE</p> <p>FILE REFERENCE: KP-8576</p> <p>CURRENT APPLICATION NUMBER: US/09/855,722</p> <p>CURRENT FILING DATE: 2001-05-16</p> <p>PRIOR APPLICATION NUMBER: 09/214,278</p> <p>PRIOR FILING DATE: 1999-01-26</p> <p>NUMBER OF SEQ ID NOS: 32</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 5</p> <p>LENGTH: 1238</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo sapiens</p> <p>US-09-855-722-5</p>									
<p>Query Match 52.5%; Score 63; DB 4; Length 1238;</p> <p>Best Local Similarity 23.1%; Pred. No. 3.5e+02;</p> <p>Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;</p>									
Qy	2	XIXNQXCQXQLDDCCSXXCNXXNXC	27						
Db	627	GFTGTYCHENIDDCGQPCRNNGTCT	652						
<p>RESULT 92</p> <p>US-08-882-046-6</p> <p>Sequence 6, Application US/08882046</p> <p>Patent No. 6136952</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Li, Linheng</p> <p>APPLICANT: Hood, Leroy</p> <p>APPLICANT: Krantz, Ian D.</p>									
<p>Query Match 52.5%; Score 63; DB 4; Length 1238;</p> <p>Best Local Similarity 23.1%; Pred. No. 3.5e+02;</p> <p>Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;</p>									

Matches	6;	Conservative	13;	Mismatches	7;	Indels	0;	Gaps	0;
Qy	2	XIXNQXCQXQLDDCCSXXCNXXNXC	27						
Db	601	GFTGTYCHENIDDCGQPCRNNGTCT	626						
<p>RESULT 90</p> <p>US-09-214-278-5</p> <p>Sequence 5, Application US/09214278</p> <p>Patent No. 6291210</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Sakano, Seiji</p> <p>APPLICANT: Itoh, Akira</p> <p>TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE</p> <p>FILE REFERENCE: KP-8576</p> <p>CURRENT APPLICATION NUMBER: US/09/214,278</p> <p>CURRENT FILING DATE: 1999-01-26</p> <p>NUMBER OF SEQ ID NOS: 32</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 5</p> <p>LENGTH: 1238</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo sapiens</p> <p>US-09-214-278-5</p>									
<p>Query Match 52.5%; Score 63; DB 3; Length 1238;</p> <p>Best Local Similarity 23.1%; Pred. No. 3.5e+02;</p> <p>Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;</p>									
Qy	2	XIXNQXCQXQLDDCCSXXCNXXNXC	27						
Db	627	GFTGTYCHENIDDCGQPCRNNGTCT	652						
<p>RESULT 91</p> <p>US-09-855-722-5</p> <p>Sequence 5, Application US/09855722</p> <p>Patent No. 6638741</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Sakano, Seiji</p> <p>APPLICANT: Itoh, Akira</p> <p>TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE</p> <p>FILE REFERENCE: KP-8576</p> <p>CURRENT APPLICATION NUMBER: US/09/855,722</p> <p>CURRENT FILING DATE: 2001-05-16</p> <p>PRIOR APPLICATION NUMBER: 09/214,278</p> <p>PRIOR FILING DATE: 1999-01-26</p> <p>NUMBER OF SEQ ID NOS: 32</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 5</p> <p>LENGTH: 1238</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo sapiens</p> <p>US-09-855-722-5</p>									
<p>Query Match 52.5%; Score 63; DB 4; Length 1238;</p> <p>Best Local Similarity 23.1%; Pred. No. 3.5e+02;</p> <p>Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;</p>									
Qy	2	XIXNQXCQXQLDDCCSXXCNXXNXC	27						
Db	627	GFTGTYCHENIDDCGQPCRNNGTCT	652						
<p>RESULT 92</p> <p>US-08-882-046-6</p> <p>Sequence 6, Application US/08882046</p> <p>Patent No. 6136952</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Li, Linheng</p> <p>APPLICANT: Hood, Leroy</p> <p>APPLICANT: Krantz, Ian D.</p>									
<p>Query Match 52.5%; Score 63; DB 4; Length 1238;</p> <p>Best Local Similarity 23.1%; Pred. No. 3.5e+02;</p> <p>Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;</p>									

APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Nucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 2637
TELEPHONE: (619) 535-9901
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-882-046-6

Query Match 52.5%; Score 63; DB 3; Length 1248;
Best Local Similarity 23.1%; Pred. No. 3.6e+02;
Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 2 XIXNOXCXOXLDCCSXXCNXKXCV 27
Db 628 GFTGTYCHENIDDCMGQPCRNGGTCTI 653

RESULT 93
US-09-566-047-6
Sequence 6, Application US/09566047
Patent No. 6703198
GENERAL INFORMATION:
APPLICANT: Li, Linheng
Hood, Leroy
Krantz, Ian D.
Spinner, Nancy B.
TITLE OF INVENTION: Methods of Diagnosing Alegillie Syndrome
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/566,047
FILING DATE: 05-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/882,046

FILING DATE: 25-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 4164
TELEPHONE: (858) 535-9901
TELEFAX: (858) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-566-047-6

Query Match 52.5%; Score 63; DB 4; Length 1248;
Best Local Similarity 23.1%; Pred. No. 3.6e+02;
Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 2 XIXNOXCXOXLDCCSXXCNXKXCV 27
Db 628 GFTGTYCHENIDDCMGQPCRNGGTCTI 653

RESULT 94
US-08-611-729A-8
Sequence 8, Application US/08611729A
Patent No. 6004924
GENERAL INFORMATION:
APPLICANT: Ish-Horowitz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-611-729A-8


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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 210
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus lynceus
; FEATURE: PEPTIDE
; NAME/KEY: (1)..(36)
; LOCATION: (1)..(36)
; OTHER INFORMATION: Xaa at residues 2 and 4 is Trp or bromo-Trp; Xaa at residue 25 is
; OTHER INFORMATION: Tyr, 125i-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
; OTHER INFORMATION: spho-Ty
US-09-894-882-210

Query Match          52.1%; Score 62.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 17;
Matches 10; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

QY 1 CXIXNQXCXQXLDCCSXCNXXNKCVCV 27
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Db 5 CFNAGVKCDNH-SDCCADTCCYDNTCV 30

RESULT 98
US-09-894-882-404
; Sequence 404, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 404
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus lynceus
US-09-894-882-404

Query Match          52.1%; Score 62.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 17;
Matches 10; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

QY 1 CXIXNQXCXQXLDCCSXCNXXNKCVCV 27
| : : : : | : : : : | : : : : | : : : : |
Db 5 CFNAGVKCDNH-SDCCADTCCYDNTCV 30

RESULT 99
US-09-894-882-209
; Sequence 209, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
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; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 209
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus lynceus
US-09-894-882-209

Query Match          52.1%; Score 62.5; DB 4; Length 70;
Best Local Similarity 33.3%; Pred. No. 31;
Matches 9; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

QY 1 CXIXNQXCXQXLDCCSXCNXXNKCVCV 27
| : : : : | : : : : | : : : : | : : : : |
Db 39 CFNAGVKCDNH-SDCCADTCCYDNTCV 64

RESULT 100
US-09-894-882-74
; Sequence 74, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
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; LENGTH: 71
; TYPE: PRT
; ORGANISM: Conus striatus
US-09-894-882-74

Query Match 52.1%; Score 62.5; DB 4; Length 71;
Best Local Similarity 33.3%; Pred. No. 31;
Matches 9; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

Qy 1 CXIXNXXCXQLDDCCSXXCNXXNXXCV 27
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Db 39 CSFLGQCGDH-SDCCWNMCCASEMCV 64

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:29:42 ; Search time 91.5 Seconds
(without alignments)
98.077 Million cell updates/sec

Title: US-10-627-685A-1
Perfect score: 120
Sequence: 1 CXIXNQXQXLDCCSXCNXXNCV 27

Scoring table: BLOSUM62DX
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Searched: 1421835 seqs, 332370683 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	120	100.0	27	15	US-10-352-254-2 Sequence 2, Appli
3	120	100.0	27	15	US-10-352-254-3 Sequence 3, Appli
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13	120	100.0	27	15	US-10-352-254-13 Sequence 14, Appli

14	120	100.0	27	15	US-10-352-254-24 Sequence 24, Appli
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19	120	100.0	27	15	US-10-627-685-6 Sequence 6, Appli
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21	120	100.0	27	15	US-10-627-685-8 Sequence 8, Appli
22	120	100.0	27	15	US-10-627-685-9 Sequence 9, Appli
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25	120	100.0	27	15	US-10-627-685-12 Sequence 12, Appli
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32	116	96.7	27	15	US-10-627-685-23 Sequence 23, Appli
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36	115	95.8	27	15	US-10-627-685-20 Sequence 20, Appli
37	114	95.0	27	15	US-10-352-254-16 Sequence 16, Appli
38	114	95.0	27	15	US-10-352-254-22 Sequence 22, Appli
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44	112	93.3	27	15	US-10-352-254-21 Sequence 21, Appli
45	112	93.3	27	15	US-10-352-254-25 Sequence 25, Appli
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52	81	67.5	26	16	US-10-765-926-395 Sequence 395, App
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54	81	67.5	30	16	US-10-765-926-257 Sequence 257, App
55	74	61.7	26	16	US-09-910-082A-258 Sequence 258, App
56	74	61.7	26	16	US-10-765-926-258 Sequence 258, App
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58	72	60.0	2524	15	US-10-369-072-25 Sequence 25, Appli
59	70	58.3	26	10	US-09-910-082A-268 Sequence 268, App
60	70	58.3	26	16	US-10-765-926-268 Sequence 268, App
61	68	56.7	2444	9	US-09-944-849-2 Sequence 2, Appli
62	68	56.7	2444	15	US-10-072-012-469 Sequence 469, App
63	68	56.7	2555	15	US-10-072-012-468 Sequence 468, App
64	68	56.7	2555	15	US-10-294-006-12 Sequence 12, Appli
65	68	56.7	2556	15	US-10-072-012-134 Sequence 134, App
66	68	56.7	2556	15	US-10-072-012-467 Sequence 467, App
67	68	56.7	2556	17	US-10-765-727-22 Sequence 22, Appli
68	68	56.7	2556	17	US-10-846-989-56 Sequence 56, Appli
69	68	56.7	2556	17	US-10-764-415B-39 Sequence 39, Appli
70	67	55.8	2531	15	US-10-190-115-29 Sequence 29, Appli
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72	67	55.8	2531	15	US-10-072-012-470 Sequence 470, App
73	67	55.8	2531	15	US-10-072-012-471 Sequence 471, App
74	66	55.0	29	10	US-09-910-082A-149 Sequence 149, App
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81	66	55.0	1473	15	US-10-190-115-4 Sequence 4, Appli
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Db 1 CRIXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 4

US-10-352-254-5
; Sequence 5, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRP
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-5

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNOXCXQXLDCCSXCNXXNKCVCV 27
Db 1 CRIXNQKCFQHLDDCCSRACNRFNKCVCV 27

RESULT 5

US-10-352-254-6
; Sequence 6, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRP
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-6

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNOXCXQXLDCCSXCNXXNKCVCV 27
Db 1 CRIXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 6

US-10-352-254-7
; Sequence 7, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRP
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-7

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNOXCXQXLDCCSXCNXXNKCVCV 27
Db 1 CRIXNQKCAQHLDDCCSRKCNRFNKCVCV 27

RESULT 7

US-10-352-254-8
; Sequence 8, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 27
; TYPE: PRP
; ORGANISM: Conus purpurascens
US-10-352-254-8


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; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(27)  
; OTHER INFORMATION: Xaa is Hyp  
US-10-352-254-8  
  
Query Match      100.0%; Score 120; DB 15; Length 27;  
Best Local Similarity 66.7%; Pred. No. 4.7e-05;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CXIXNQXQXQLDDCCSXKCNXXNKCVCV 27  
|:||||:|:||||:|:||||:|:||||:|:||||  
Db 1 CRIXNQKCFQHLLDCCSRKCNRFNKVCV 27  
|-|||:-|-|||:-|-|||:-|-|||:-|-|||:-|-|||  
  
RESULT 8  
US-10-352-254-9  
; Sequence 9, Application US/10352254  
; Publication No. US20030224343A1  
; GENERAL INFORMATION:  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Pemberton-Goodman, Karen  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Temple, Davis  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants  
; FILE REFERENCE: 2314-254  
; CURRENT APPLICATION NUMBER: US/10/352,254  
; PRIOR FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: US 60/352,219  
; PRIOR FILING DATE: 2002-01-29  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Conus purpurascens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(27)  
; OTHER INFORMATION: Xaa is Hyp  
US-10-352-254-9  
  
Query Match      100.0%; Score 120; DB 15; Length 27;  
Best Local Similarity 66.7%; Pred. No. 4.7e-05;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CXIXNQXQXQLDDCCSXKCNXXNKCVCV 27  
|:||||:|:||||:|:||||:|:||||:|:||||  
Db 1 CRIXNQKCFQHLLDCCSRKCNRFNKVCV 27  
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RESULT 9  
US-10-352-254-10  
; Sequence 10, Application US/10352254  
; Publication No. US20030224343A1  
; GENERAL INFORMATION:  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Pemberton-Goodman, Karen  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Temple, Davis  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants  
; FILE REFERENCE: 2314-254  
; CURRENT APPLICATION NUMBER: US/10/352,254  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: US 60/352,219  
; PRIOR FILING DATE: 2002-01-29  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Conus purpurascens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(27)  
; OTHER INFORMATION: Xaa is Hyp  
US-10-352-254-10  
  
Query Match      100.0%; Score 120; DB 15; Length 27;  
Best Local Similarity 66.7%; Pred. No. 4.7e-05;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CXIXNQXQXQLDDCCSXKCNXXNKCVCV 27  
|:||||:~::~|||:-|-|||:-|-|||:-|-|||:-|-|||:-|-|||  
Db 1 CRIXNQKCFQHLLDCCSRKCNRFNKVCV 27  
|-|||:-|-|||:-|-|||:-|-|||:-|-|||:-|-|||:-|-|||  
  
RESULT 10  
US-10-352-254-11  
; Sequence 11, Application US/10352254  
; Publication No. US20030224343A1  
; GENERAL INFORMATION:  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Pemberton-Goodman, Karen  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Temple, Davis  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants  
; FILE REFERENCE: 2314-254  
; CURRENT APPLICATION NUMBER: US/10/352,254  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: US 60/352,219  
; PRIOR FILING DATE: 2002-01-29  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Conus purpurascens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(27)  
; OTHER INFORMATION: Xaa is Hyp  
US-10-352-254-11  
  
Query Match      100.0%; Score 120; DB 15; Length 27;  
Best Local Similarity 66.7%; Pred. No. 4.7e-05;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CXIXNQXQXQLDDCCSXKCNXXNKCVCV 27  
|:||||:~::~|||:-|-|||:-|-|||:-|-|||:-|-|||:-|-|||  
Db 1 CRIXNQKCFQHLLDCCSRKCNRFNKVCV 27  
|-|||:-|-|||:-|-|||:-|-|||:-|-|||:-|-|||:-|-|||  
  
RESULT 11  
US-10-352-254-12  
; Sequence 12, Application US/10352254  
; Publication No. US20030224343A1  
; GENERAL INFORMATION:  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Pemberton-Goodman, Karen  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Temple, Davis  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants  
; FILE REFERENCE: 2314-254  
; CURRENT APPLICATION NUMBER: US/10/352,254  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: US 60/352,219  
; PRIOR FILING DATE: 2002-01-29  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Conus purpurascens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(27)  
; OTHER INFORMATION: Xaa is Hyp  
US-10-352-254-12
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<p>; FEATURE: ; NAME/KEY: PEPTIDE ; LOCATION: (1)..(27) ; OTHER INFORMATION: Xaa is Hyp</p>	<p>US-10-352-254-8</p>	Query Match Best Local Similarity 100.0%; Score 120; DB 15; Matches 66.7%; Pred. No. 4.7e-05;	<p>Mismatches 9; Indels 0; Gaps 0;</p>
QY 1 CXIXNQXCKFQHLLDDCCSRKCNRFNKCVCV 27 :: :: :: :: :: Db 1 CRINXQACFOHLLDDCCSRKCNRFNKCVCV 27		RESULT 8 US-10-352-254-9 Sequence 9, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION: APPLICANT: Cognetix, Inc. APPLICANT: University of Utah Research Foundation APPLICANT: Pemberton-Goodman, Karen APPLICANT: Jones, Robert M. APPLICANT: Temple, Davis APPLICANT: McIntosh, J. Michael APPLICANT: Olivera, Baldomero M. TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants FILE REFERENCE: 2314-254 CURRENT APPLICATION NUMBER: US/10/352,254 PRIOR FILING DATE: 2003-01-28 PRIORITY APPLICATION NUMBER: US 60/352,219 NUMBER OF SEQ ID NOS: 29 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 9 LENGTH: 27 TYPE: PRT ORGANISM: Conus purpurascens FEATURE: NAME/KEY: PEPTIDE LOCATION: (1)..(27) OTHER INFORMATION: Xaa is Hyp	US-10-352-254-9
<p>; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 10 ; LENGTH: 27 ; TYPE: PRT ; ORGANISM: Conus purpurascens ; FEATURE: ; NAME/KEY: PEPTIDE ; LOCATION: (1)..(27) ; OTHER INFORMATION: Xaa is Hyp</p>	<p>US-10-352-254-10</p>	Query Match Best Local Similarity 100.0%; Score 120; DB 15; Matches 66.7%; Pred. No. 4.7e-05;	<p>Mismatches 9; Indels 0; Gaps 0;</p>
QY 1 CXIXNQXCKFQHLLDDCCSRKCNRFNKCVCV 27 :: :: :: :: :: Db 1 CRINXQACFOHLLDDCCSRKCNRFNKCVCV 27		RESULT 10 US-10-352-254-11 Sequence 11, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION: APPLICANT: Cognetix, Inc. APPLICANT: University of Utah Research Foundation APPLICANT: Pemberton-Goodman, Karen APPLICANT: Jones, Robert M. APPLICANT: Temple, Davis APPLICANT: McIntosh, J. Michael APPLICANT: Olivera, Baldomero M. TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants FILE REFERENCE: 2314-254 CURRENT APPLICATION NUMBER: US/10/352,254 PRIOR FILING DATE: 2003-01-28 PRIORITY APPLICATION NUMBER: US 60/352,219 NUMBER OF SEQ ID NOS: 29 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 11 LENGTH: 27 TYPE: PRT ORGANISM: Conus purpurascens FEATURE: NAME/KEY: PEPTIDE LOCATION: (1)..(27) OTHER INFORMATION: Xaa is Hyp	US-10-352-254-11
<p>; FEATURE: ; NAME/KEY: PEPTIDE ; LOCATION: (1)..(27) ; OTHER INFORMATION: Xaa is Hyp</p>	<p>US-10-352-254-8</p>	Query Match Best Local Similarity 100.0%; Score 120; DB 15; Matches 66.7%; Pred. No. 4.7e-05;	<p>Mismatches 9; Indels 0; Gaps 0;</p>
QY 1 CXIXNQXCKFQHLLDDCCSRKCNRFNKCVCV 27 :: :: :: :: :: Db 1 CRINXQACFOHLLDDCCSRKCNRFNKCVCV 27		RESULT 8 US-10-352-254-9 Sequence 9, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION: APPLICANT: Cognetix, Inc. APPLICANT: University of Utah Research Foundation APPLICANT: Pemberton-Goodman, Karen APPLICANT: Jones, Robert M. APPLICANT: Temple, Davis APPLICANT: McIntosh, J. Michael APPLICANT: Olivera, Baldomero M. TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants FILE REFERENCE: 2314-254 CURRENT APPLICATION NUMBER: US/10/352,254 PRIOR FILING DATE: 2003-01-28 PRIORITY APPLICATION NUMBER: US 60/352,219 NUMBER OF SEQ ID NOS: 29 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 9 LENGTH: 27 TYPE: PRT ORGANISM: Conus purpurascens FEATURE: NAME/KEY: PEPTIDE LOCATION: (1)..(27) OTHER INFORMATION: Xaa is Hyp	US-10-352-254-9
<p>; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 10 ; LENGTH: 27 ; TYPE: PRT ; ORGANISM: Conus purpurascens ; FEATURE: ; NAME/KEY: PEPTIDE ; LOCATION: (1)..(27) ; OTHER INFORMATION: Xaa is Hyp</p>	<p>US-10-352-254-10</p>	Query Match Best Local Similarity 100.0%; Score 120; DB 15; Matches 66.7%; Pred. No. 4.7e-05;	<p>Mismatches 9; Indels 0; Gaps 0;</p>
QY 1 CXIXNQXCKFQHLLDDCCSRKCNRFNKCVCV 27 :: :: :: :: :: Db 1 CRINXQACFOHLLDDCCSRKCNRFNKCVCV 27		RESULT 10 US-10-352-254-11 Sequence 11, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION: APPLICANT: Cognetix, Inc. APPLICANT: University of Utah Research Foundation APPLICANT: Pemberton-Goodman, Karen APPLICANT: Jones, Robert M. APPLICANT: Temple, Davis APPLICANT: McIntosh, J. Michael APPLICANT: Olivera, Baldomero M. TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants FILE REFERENCE: 2314-254 CURRENT APPLICATION NUMBER: US/10/352,254 PRIOR FILING DATE: 2003-01-28 PRIORITY APPLICATION NUMBER: US 60/352,219 NUMBER OF SEQ ID NOS: 29 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 11 LENGTH: 27 TYPE: PRT ORGANISM: Conus purpurascens FEATURE: NAME/KEY: PEPTIDE LOCATION: (1)..(27) OTHER INFORMATION: Xaa is Hyp	US-10-352-254-11


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; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: xaa is Hyp
US-10-352-254-12

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Query Match	Score	DB	Length
Best Local Similarity	100.0%	120	27
Matches	66.7%		
Conservative	Pred. No. 4.7e-05		
Mismatches	9		
Indels	0		
Gaps	0		

Qy 1 CXIXNQXCXQLDDCCSXXCNXXXCV 27
| : | : | : | : | : | : | : | : |
Db 1 CRIXNOKCYOHLDDCCSRKCRNFKCVCV 27

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RESULT 12
US-10-352-254-13
; Sequence 13, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVITA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-13

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Query Match	100.0%	Score 120;	DB 15;	Length 27;
Best Local Similarity	66.7%	Pred. NO. 4.7e-05;		
Matches 18;	Conservative	9;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy 1 CXIXNQXCXQLD DCCSXXCNXXNCV 27
| : | | | : | : | | | : | : | : |
Dp 1 COIXNOKCFOHL DDCSRKCNRENKCVC 27

RESULT 13
US-10-352-254-14
; Sequence 14, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.

APPLICANT: Temple, Davis
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Olivera, Baldomero M.
 TITLE OF INVENTION: Kappa-PVITA-Related Conotoxins as Organ Protectants
 FILE REFERENCE: 2314-254
 CURRENT APPLICATION NUMBER: US/10/352,254
 CURRENT FILING DATE: 2003-01-28
 PRIOR APPLICATION NUMBER: US 60/352,219
 PRIOR FILING DATE: 2002-01-29
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 14
 LENGTH: 27
 TYPE: PRT
 ORGANISM: Conus purpurascens
 FEATURE:
 NAME/KEY: PEPTIDE
 LOCATION: (1)..(27)
 OTHER INFORMATION: Xaa is Hyp
 US-10-352-254-14

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels

Qy 1 CXIXNQXCXQLDDCCSXXCNXXXCV 27
| : | | | : | : | | | : | : | |
Dd 1 CRIXNQCFOALDDCCSRKCNRFNKCV 27

RESULT 14
US-10-352-254-24
Sequence 24, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
US-10-352-254-24

Query Match	100.0%	Score 120;	DB 15;	Length 27;
Best Local Similarity	63.0%;	Pred. No. 4.7e-05;		
Matches 17;	Conservative 10;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	CXIXNQXCXQLDCCSXXCNXXNCV	27
		: : : : : : : :	
Db	1	CRIANQKCFQHLDDCCSRKCNRFNCV	27

RESULT 15
US-10-627-685-1 -
; Sequence 1, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.


```

/ GENERAL INFORMATION:
/ APPLICANT: Cornell-Bell, Ann H.
/ APPLICANT: Pemberton, Karen E.
/ APPLICANT: Temple Jr., Davis L.
/ APPLICANT: Layer, Richard T.
/ APPLICANT: McCabe, R. Tyler
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Cognatix, Inc.
/ TITLE OF INVENTION: Uses of Kappa-Conot
/ FILE REFERENCE: Kappa-PVIA
/ CURRENT APPLICATION NUMBER: US/10/627,6
/ CURRENT FILING DATE: 2003-07-28
/ PRIOR APPLICATION NUMBER: US/09/666,837
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US/02/19,438
/ PRIOR FILING DATE: 2000-07-20
/ PRIOR APPLICATION NUMBER: US/60/155,135
/ PRIOR FILING DATE: 1999-09-22
/ NUMBER OF SEQ ID NOS: 25

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; NUMBER OF SEQ ID NOS

APPLICANT: McCabe, R. Tyler

APPLICANT: McCabe, R. Tyler

RESULT 25


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; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-13

Query Match      100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQLDDCCSXXCNXXNKCVCV 27
   |:|::||:||||:||||:||||:|:|
DB 1 CQIXNQKCFQHLDDCCSRKCNRFNKVCV 27

RESULT 27
US-10-627-685-14
; Sequence 14, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-12

Query Match      100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQLDDCCSXXCNXXNKCVCV 27
   |:|::||:||||:||||:||||:|:|
DB 1 CRIXNQKYQHLLDDCCSRKCNRFNKVCV 27

RESULT 26
US-10-627-685-13
; Sequence 13, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-12
```


GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-23

Query Match 96.7%; Score 116; DB 15; Length 27;
Best Local Similarity 65.4%; Pred. No. 0.00011;
Matches 17; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNC 26
|:||||:|:||||:|:||||:|:||||:|
Db 1 CRXNQKCFQHLDDCCSRKCNRFNC 26

RESULT 33
US-10-352-254-4
; Sequence 4, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-4

Query Match 95.8%; Score 115; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00014;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNCV 27
|:||||:|:||||:|:||||:|:||||:|
Db 1 CRXNQKCFQHLDDCCSRKCNRFNCV 27

RESULT 34
US-10-352-254-20
; Sequence 20, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-20

Query Match 95.8%; Score 115; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00014;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNCV 27
|:||||:|:||||:|:||||:|:||||:|
Db 1 CRXNQKCFQHLDDCCSRKCNRFNCV 27

RESULT 35
US-10-627-685-4
; Sequence 4, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:


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; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-16

Query Match          95.0%; Score 114; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00018;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps

Qy      1 CXIXNQXCXQLDDCCSXXCNXXNKCVCV 27
         ||||| :||:|||||:||:||||:||||:
Db      1 CRIXNAKCFOHLDDCCSRKCNRFNKCV 27

RESULT 38
US-10-352-254-22
; Sequence 22, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-22

Query Match          95.0%; Score 114; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00018;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps

Qy      1 CXIXNQXCXQLDDCCSXXCNXXNKCVCV 27
         ||||| :||:|||||:||:||||:||||:
Db      1 CRIXNQCFAPHLDDCCSRKCNRFNKCV 27

RESULT 39
US-10-627-685-16
; Sequence 16, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.

```


Qy 1 CXIXNQXCXQLDCCSXXCNXXXCV 27
| : | | | : : | | | | : | |
Dd 1 CRIXNOKCEAHLDDCSKCNRENKCV 27

Query Match 93.3%; Score 112; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00028;


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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-15

Query Match          93.3%; Score 112; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00028;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQLDDCCSXCNXXNKCVCV 27
|:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
DB 1 CRIXNQKCFQHLDACCCKRKNFNCVCV 27

RESULT 47
US-10-627-685-17
; Sequence 17, Application US/10627685
; Publication No. US2004009247A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-17

Query Match          93.3%; Score 112; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00028;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQLDDCCSXCNXXNKCVCV 27
|:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
DB 1 CRIXNQKCFQHLDACCCKRKNFNCVCV 27

RESULT 48
US-10-627-685-19
; Sequence 19, Application US/10627685
; Publication No. US2004009247A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
```


	: :: : :~::~	
Dd	1 CRXNQKCFQHLDDCCSRKNRNFNCV	27
RESULT 50 US-10-627-685-25 ; Sequence 25, Application US/10627685 ; Publication No. US20040092447A1 ; GENERAL INFORMATION: ; APPLICANT: Cornell-Bell, Ann H. ; APPLICANT: Pemberton, Karen E. ; APPLICANT: Temple Jr., Davis L. ; APPLICANT: Layer, Richard T. ; APPLICANT: McCabe, R. Tyler ; APPLICANT: Jones, Robert M. ; APPLICANT: Cognetix, Inc. ; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIIA ; FILE REFERENCE: Kappa-PVIIA ; CURRENT APPLICATION NUMBER: US/10/627,685 ; PRIOR FILING DATE: 2003-07-28 ; PRIOR FILING DATE: 2000-09-21 ; PRIOR APPLICATION NUMBER: US 60/219,438 ; PRIOR FILING DATE: 2000-07-20 ; PRIOR APPLICATION NUMBER: US 60/155,135 ; PRIOR FILING DATE: 1999-09-22 ; NUMBER OF SEQ ID NOS: 25 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 25 ; LENGTH: 27 ; TYPE: PRT ; ORGANISM: Conus purpurascens ; FEATURE: ; NAME/KEY: PEPTIDE ; LOCATION: (1)..(27) ; OTHER INFORMATION: xaa is Hyp US-10-627-685-25 Query Match 93.3%; Score 112; DB 15; Length 27; Best Local Similarity 63.0%; Pred. No. 0.00028; Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;		
OY	1 CXIXNQCXXQLDCCSXCNXNNXCVCV	27
Dd	1 CHXAQQCFOHLDCCSRKNRNFNCV	27
RESULT 51 US-09-910-082A-395 ; Sequence 395, Application US/09910082A ; Publication No. US20030119731A1 ; GENERAL INFORMATION: ; APPLICANT: University of Utah Research Foundation ; APPLICANT: Cognetix, Inc. ; APPLICANT: Olivera, Baldomero M. ; APPLICANT: McIntosh, J. Michael ; APPLICANT: Watkins, James E. ; APPLICANT: Shon, Ki-Joon ; APPLICANT: Jacobsen, Richard ; APPLICANT: Jones, Robert M. ; APPLICANT: Cartier, G. Edward ; TITLE OF INVENTION: Omega-Conopeptides ; FILE REFERENCE: 2314-241 ; CURRENT APPLICATION NUMBER: US/09/910,082A ; CURRENT FILING DATE: 2001-07-23 ; PRIOR APPLICATION NUMBER: US 60/219,616 ; PRIOR FILING DATE: 2000-07-21 ; PRIOR APPLICATION NUMBER: US 60/265,888 ; PRIOR FILING DATE: 2001-02-05 ; NUMBER OF SEQ ID NOS: 413 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 395 ; LENGTH: 26 ; TYPE: PRT ; ORGANISM: Conus striatus US-10-627-685-25		
OY	1 CXIXNQCXXQLDCCSXCNXNNXCVCV	26
Dd	1 CKLKGQSCRTPWDCSGCGRRGKC	26
RESULT 53 US-09-910-082A-257 ; Sequence 257, Application US/09910082A ; Publication No. US20030119731A1 ; GENERAL INFORMATION: ; APPLICANT: University of Utah Research Foundation ; APPLICANT: Cognetix, Inc. ; APPLICANT: Olivera, Baldomero M. ; APPLICANT: McIntosh, J. Michael ; APPLICANT: Watkins, James E. ; APPLICANT: Garrett, James E. ; APPLICANT: Shon, Ki-Joon ; APPLICANT: Jacobsen, Richard ; APPLICANT: Jones, Robert M. ; APPLICANT: Cartier, G. Edward ; TITLE OF INVENTION: Omega-Conopeptides ; FILE REFERENCE: 2314-241 ; CURRENT APPLICATION NUMBER: US/09/910,082A ; CURRENT FILING DATE: 2001-07-23 ; PRIOR APPLICATION NUMBER: US 60/219,616 ; PRIOR FILING DATE: 2000-07-21 ; PRIOR APPLICATION NUMBER: US 60/265,888 ; PRIOR FILING DATE: 2001-02-05 ; NUMBER OF SEQ ID NOS: 413 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 395		

; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 257
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus striatus
US-09-910-082A-257

Query Match 67.5%; Score 81; DB 10; Length 30;

Best Local Similarity 34.6%; Pred. No. 0.31;

Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXXCNXXNXC 26

Db 4 CKLGGSCRRMTYDCSGSGCGRRGKC 29

RESULT 54

US-10-765-926-257

; Sequence 257, Application US/10765926

; Publication No. US20040132663A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J. Michael

; APPLICANT: Watkins, Maren

; APPLICANT: Garrett, James E.

; APPLICANT: Shon, Ki-Joon

; APPLICANT: Jacobsen, Richard

; APPLICANT: Jones, Robert M.

; APPLICANT: Cartier, G. Edward

; TITLE OF INVENTION: Omega-Conopeptides

; FILE REFERENCE: 2314-241

; CURRENT APPLICATION NUMBER: US/10/765,926

; CURRENT FILING DATE: 2004-01-29

; PRIOR APPLICATION NUMBER: US 09/910,082

; PRIOR FILING DATE: 2001-07-23

; PRIOR APPLICATION NUMBER: US 60/219,616

; PRIOR FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: US 60/265,888

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 413

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 257

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Conus striatus

US-10-765-926-257

Query Match

Best Local Similarity 67.5%; Score 81; DB 16; Length 30;

Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXXCNXXNXC 26

Db 4 CKLGGSCRRMTYDCSGSGCGRRGKC 29

RESULT 55

US-09-910-082A-258

; Sequence 258, Application US/09910082A

; Publication No. US20030119731A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 258
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Conus striatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(26)
; OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
US-09-910-082A-258

Query Match 61.7%; Score 74; DB 10; Length 26;

Best Local Similarity 34.6%; Pred. No. 1.3;

Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXXCNXXNXC 26

Db 1 CKLGGSCRRMTYDCSGSGCGRRGKC 26

RESULT 56

US-10-765-926-258

; Sequence 258, Application US/10765926

; Publication No. US20040132663A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J. Michael

; APPLICANT: Watkins, Maren

; APPLICANT: Garrett, James E.

; APPLICANT: Shon, Ki-Joon

; APPLICANT: Jacobsen, Richard

; APPLICANT: Jones, Robert M.

; APPLICANT: Cartier, G. Edward

; TITLE OF INVENTION: Omega-Conopeptides

; FILE REFERENCE: 2314-241

; CURRENT APPLICATION NUMBER: US/10/765,926

; CURRENT FILING DATE: 2004-01-29

; PRIOR APPLICATION NUMBER: US 09/910,082

; PRIOR FILING DATE: 2001-07-23

; PRIOR APPLICATION NUMBER: US 60/219,616

; PRIOR FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: US 60/265,888

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 413

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 258

; LENGTH: 26

; TYPE: PRT

; ORGANISM: Conus striatus

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (1)-(26)

; OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,

; OTHER INFORMATION: di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.


```

; TYPE: PRT
; ORGANISM: Conus striatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(26)
; OTHER INFORMATION: Xaa at residue 13 is Tyr, 12SI-Tyr, mono-iodo-Tyr,
; OTHER INFORMATION: di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
US-10-765-926-268

Query Match      58.3%; Score 70; DB 16; Length 26;
Best Local Similarity 34.6%; Pred No. 3.2; Mismatches 5; Indels 0; Gaps 0;
Matches 9; Conservative 12;

Qy   1 CXIXNOXCXOXLDCCSCXXCNXXXNC 26
     |:|::|::|||::|::|
Db   1 CKLKGQSCRKTSXDCCSGCGRSKC 26


RESULT 61
US-09-944-849-2
; Sequence 2, Application US/09944849
; Patent No. US20020151487A1
; GENERAL INFORMATION:
; APPLICANT: Nickoloff, Brian
; APPLICANT: Mele, Lucio
; TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREATMENT OF SKIN DISORDERS BY MODULATING THE NOTCH SIGNALING PATHWAY
; FILE REFERENCE: 212583
; CURRENT APPLICATION NUMBER: US/09/944,849
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,614
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (891)..(891)
; OTHER INFORMATION: The 'Xaa' at location 891 stands for Gly, or Ala.
; NAME/KEY: misc feature
; LOCATION: (1763)..(1763)
; OTHER INFORMATION: The 'Xaa' at location 1763 stands for Glu, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (1787)..(1787)
; OTHER INFORMATION: The 'Xaa' at location 1787 stands for Thr, Ala, Pro, or Ser.
; OTHER INFORMATION: Constitutively Active No. US20020151487Alch-1
US-09-944-849-2

Query Match      56.7%; Score 68; DB 9; Length 2444;
Best Local Similarity 30.8%; Pred. No. 3.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy   2 XIXNOCXOXLDDCCSXCNXXXNCV 27
     |:|::|::|||::|::|
Db   248 GTGQCENIIDCFGNCKNGACV 273


RESULT 62
US-10-072-012-469
; Sequence 469, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muraidhara
```


Qy 2 XIXNQXCXQLDDCCSXXCNXXNKCXV 27
Db 248 GFTGQNCENIDDCPGNNCKNGGACV 273

RESULT 64

US-10-294-006-12
; Sequence 12, Application US/10294006
; Publication No. US20040013657A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Yang, Yonghong
; APPLICANT: Zhang, Jie
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040013657A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 21272-029CIP2H-PCT
; CURRENT APPLICATION NUMBER: US/10/294,006
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/815,925
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 12
; LENGTH: 2556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-006-12

Query Match 56.7%; Score 68; DB 15; Length 2556;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQLDDCCSXXCNXXNKCXV 27
Db 248 GFTGQNCENIDDCPGNNCKNGGACV 273

RESULT 65

US-10-072-012-134
; Sequence 134, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Wolenc, Steven D.
; APPLICANT: Colman, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012

; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 134
; LENGTH: 2556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-134

Query Match 56.7%; Score 68; DB 15; Length 2556;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQLDDCCSXXCNXXNKCXV 27
Db 248 GFTGQNCENIDDCPGNNCKNGGACV 273

RESULT 66

US-10-072-012-467
; Sequence 467, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30


```

RESULT 69
US-10-764-415B-39
; Sequence 39, Application US/10764415B
; Publication NO. US2005005903A1
; GENERAL INFORMATION:
; APPLICANT: Loralantis Ltd.
; TITLE OF INVENTION: Modulations of Notch signalling for use in Immunotherapy
; FILE REFERENCE: P011073US
; CURRENT APPLICATION NUMBER: US/10/764,415B
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: GB0118153.6
; PRIOR FILING DATE: 2001-07-01
; PRIOR APPLICATION NUMBER: GB0207930.9
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0212283.6
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: GB0212282.8
; PRIOR FILING DATE: 2002-05-28
;

```


Db 248 GFAGQCNCEENVDDCPGNCKNGGACV 273

RESULT 74

US-09-910-082A-149
; Sequence 149, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910.082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 149
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Conus geographus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(29)
; OTHER INFORMATION: Xaa at residue 4, and 7 is Pro or Hyp; Xaa at residue 22 and 29 is
; OTHER INFORMATION: Tyr, 125i-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
US-09-910-082A-149

Query Match 55.0%; Score 66; DB 10; Length 29;

Best Local Similarity 38.5%; Pred. No. 8.7;
Matches 10; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXIXNOXCXQXLDCCSXCNXXNXC 26
|:| |:::| |:::| |:::| |:::|
Db 1 CKSXGTXCGRMRDCCCTCLSLXSNKC 26

RESULT 75

US-10-765-926-149
; Sequence 149, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888

; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 149
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Conus geographus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(29)
; OTHER INFORMATION: Xaa at residue 4 and 7 is Pro or Hyp; Xaa at
; OTHER INFORMATION: residue 22 and 29 is Tyr, 125i-Tyr, mono-iodo-Tyr,
; OTHER INFORMATION: di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
US-10-765-926-149

Query Match 55.0%; Score 66; DB 16; Length 29;

Best Local Similarity 38.5%; Pred. No. 8.7;
Matches 10; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXIXNOXCXQXLDCCSXCNXXNXC 26
|:| |:::| |:::| |:::| |:::|
Db 1 CKSXGTXCGRMRDCCCTCLSLXSNKC 26

RESULT 76

US-10-024-599-4
; Sequence 4, Application US/10024599
; Publication No. US20020165352A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Cimborra, Daniel M.
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions
; FILE REFERENCE: 2318-278-II
; CURRENT APPLICATION NUMBER: US/10/024,599
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/256,986
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: 1..176
; OTHER INFORMATION: Xaa is Gly or Cys
US-10-024-599-4

Query Match 55.0%; Score 66; DB 13; Length 176;

Best Local Similarity 25.8%; Pred. No. 46;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

Qy 1 CXIXN----QXCXQXLDCCSXCNXXNXC 27
|:| |:::| |:::| |:::| |:::|
Db 9 CVCVNGWSGDCCSENIDDCAFASCTPGSTCI 39

RESULT 77

US-09-908-322-5
; Sequence 5, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94


```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mirostock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5

Query Match 55.0%; Score 66; DB 9; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNXC 26
Db 436 GFSGRNCDNLDCTSPFCQNGGTC 460

RESULT 78
US-09-783-931-5
Sequence 5, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-783-931-5

Query Match 55.0%; Score 66; DB 10; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNXC 26
Db 436 GFSGRNCDNLDCTSPFCQNGGTC 460

RESULT 79
US-10-417-719-7
Sequence 7, Application US/10417719
Publication No. US20030180784A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
FILE REFERENCE: MBIO1997-002CP2M
CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US/09/568,218
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: 08/872,855
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 08/832,633
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 721
TYPE: PRT
ORGANISM: Xenopus Laevis
US-10-417-719-7

Query Match 55.0%; Score 66; DB 14; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNXC 26
Db 436 GFSGRNCDNLDCTSPFCQNGGTC 460

RESULT 80
US-10-042-865-109
Sequence 109, Application US/10042865
Publication No. US20040029216A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
```



```
; APPLICANT: Li, Li
; APPLICANT: Zerkhusen, Bryan D
; APPLICANT: Caeman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Payman, John
; APPLICANT: Smithson, Glennnda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 109
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-042-865-109

Query Match 55.0%; Score 66; DB 15; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSXXCNXNXC 26
Db 436 GFSGRNCDNLDCTSPFCQNGTC 460

RESULT 81
US-10-190-115-4
; Sequence 4, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Caeman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
```

```
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerkhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 1473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-4

Query Match 55.0%; Score 66; DB 15; Length 1473;
Best Local Similarity 25.8%; Pred. No. 3.3e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

Qy 1 CXIXN---QXCXQXLDCCSXXCNXNXC 27
Db 324 CVCVNGSGDCSENIDDCAFASCTPGSTCI 354

RESULT 82
US-10-369-072-4
; Sequence 4, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
```


RESULT 85

US-10-369-072-28
; Sequence 28, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
; APPLICANT: Szekeeres, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 2447
; TYPE: PRT
; ORGANISM: Takifugu rubripes

US-10-369-072-28

Query Match 55.0%; Score 66; DB 15; Length 2447;
Best Local Similarity 29.0%; Pred. No. 5.3e+02;
Matches 9; Conservative 15; Mismatches 3; Indels 4; Gaps 1;

QY 1 CXIXN---QXCXQXLDCCSXCNXXNXCVCV 27

Db 279 CVCVNGWSGLDCSENIDDCDTAACSPGTCV 309

RESULT 86

US-10-190-115-2
; Sequence 2, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.

; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 2469
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-190-115-2

Query Match 55.0%; Score 66; DB 15; Length 2469;
Best Local Similarity 25.8%; Pred. No. 5.3e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 CXIXN---QXCXQXLDCCSXCNXXNXCVCV 27

Db 323 CVCVNGWSGDDCSENIDDCAFGACTPGSTCI 353

RESULT 87

US-10-369-072-2
; Sequence 2, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan


```
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
; APPLICANT: Szerkerez, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed. - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-072-2
```

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Query Match 55.0%; Score 66; DB 15; Length 2469;
Best Local Similarity 25.8%; Pred. No. 5.3e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 CXIXN-----QXCXQXLDCCSXXCNXXNCV 27
Db 323 CVCVNGWSGDDCSENIDDCAFGACTPGSTCI 353
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RESULT 88
US-10-190-115-27
; Sequence 27, Application US/10190115
; Publication No. US2003020734A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
```

```
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szerkerez, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 27
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-27
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Query Match 55.0%; Score 66; DB 15; Length 2471;
Best Local Similarity 25.8%; Pred. No. 5.3e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 CXIXN-----QXCXQXLDCCSXXCNXXNCV 27
Db 324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
```

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RESULT 89
US-10-369-072-27
; Sequence 27, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
; APPLICANT: Szerkerez, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 369
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-369

Query Match          54.6%; Score 65.5; DB 9; Length 36;
Best Local Similarity 33.3%; Pred. No. 12;
Matches 9; Conservative 12; Mismatches 5; Indels 1; Gaps 1;

QY      1 CXINQXCXQXLDGCCSXXCNXKXCV 27
      | : | : : | | | : | : : |
Db      2 CLSLQRCERH-SDCCGYLCCFYDKCV 27

RESULT 96
US-09-894-882-167
; Sequence 167, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael

```



```
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 26
; LENGTH: 2317
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (440)..(440)
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-10-190-115-26
```

```
Query Match 54.2%; Score 65; DB 15; Length 2317;
Best Local Similarity 30.0%; Pred. No. 6.2e+02;
Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;

Qy 1 CXIXN---OXCXQLDCCSXCNXXNKC 26
Db 301 CVCVNGWTGSCSQNIDDCATAVCFHGATC 330
```

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RESULT 100
US-10-369-072-26
; Sequence 26, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
; APPLICANT: Szerkeres, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
```

```
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (440)
; OTHER INFORMATION: Wherein Xaa represents O.
US-10-369-072-26
```

```
Query Match 54.2%; Score 65; DB 15; Length 2317;
Best Local Similarity 30.0%; Pred. No. 6.2e+02;
Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;
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Qy 1 CXIXN---OXCXQLDCCSXCNXXNKC 26
Db 301 CVCVNGWTGSCSQNIDDCATAVCFHGATC 330
```

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Search completed: April 18, 2005, 20:43:00
Job time : 93.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 20:23:04 ; Search time 26.5 Seconds
(without alignments)
98.032 Million cell updates/sec

Title: US-10-627-685A-1

Perfect score: 120

Sequence: 1 CXIXNQXCQXLDDCCSXXCNXXNVCV 27

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	27	2	A58997
2	77	64.2	26	2	C44379
3	72	60.0	2524	2	A58844
4	69	57.5	29	2	JH0699
5	68	56.7	2555	2	A40043
6	67	55.8	293	2	B26637
7	67	55.8	2139	2	A35672
8	67	55.8	2437	2	S42612
9	67	55.8	2531	2	S18188
10	67	55.8	2531	2	A46019
11	66	55.0	29	2	B43620
12	66	55.0	1203	2	A49175
13	66	55.0	2471	2	A49128
14	66	55.0	2703	1	A24420
15	65	54.2	601	2	T22025
16	65	54.2	601	2	D89711
17	65	54.2	1964	2	T09059
18	65	54.2	2318	2	S45306
19	65	54.2	2321	2	S78549
20	65	54.2	2531	2	T31070
21	64	53.3	1372	2	T25933
22	64	53.3	2352	2	T30201
23	64	53.3	3623	2	T08618
24	63	52.5	43	2	S18174
25	63	52.5	570	2	A48836
26	63	52.5	1687	2	T30176
27	62	51.7	29	2	A43620
28	62	51.7	722	2	I48324
29	62	51.7	1064	2	A40136

30	61.5	51.2	36	1	A32038	mu-agatoxin I - fu
31	61	50.8	29	2	A58537	omega-conotoxin MV
32	61	50.8	728	2	I50719	C-Delta-1 - chicke
33	61	50.8	1025	2	T42626	secreted leucine-r
34	61	50.8	1408	2	S16148	gene serrate prote
35	61	50.8	1469	2	B36655	slit protein 2 pre
36	61	50.8	1480	2	A36685	slit protein 1 pre
37	60	50.0	354	2	T22274	hypothetical prote
38	60	50.0	832	2	A31246	neurogenic protein
39	60	50.0	833	2	S19087	gene Delta protein
40	60	50.0	880	2	S00670	neurogenic repetit
41	60	50.0	1295	2	A32901	glp1 protein precu
42	60	50.0	1722	2	B89753	protein FltC7.4 li
43	59	49.2	25	2	JH0701	omega-conotoxin MV
44	59	49.2	43	2	S33382	metallothionein -
45	59	49.2	43	2	S18173	metallothionein -
46	59	49.2	53	2	T10405	conotoxin-like pro
47	59	49.2	53	2	C72850	conotoxin homolog
48	59	49.2	53	2	T30499	conotoxin-like pro
49	59	49.2	63	2	A34958	metallothionein -
50	59	49.2	63	2	S33381	metallothionein -
51	59	49.2	63	2	A34620	metallothionein -
52	59	49.2	63	2	C34620	metallothionein -
53	59	49.2	419	2	T04215	hypothetical prote
54	59	49.2	1257	2	S28764	neurocan precursor
55	59	49.2	1268	2	S52781	neurocan - mouse
56	58.5	48.8	250	2	T16342	hypothetical prote
57	58.5	48.8	559	1	C9HU	complement C9 prec
58	58	48.3	63	2	S08191	metallothionein 2
59	58	48.3	387	2	B49175	Notch A protein -
60	58	48.3	861	2	A48825	Notch homolog Motc
61	58	48.3	3562	2	A47171	chondroitin sulfat
62	57	47.5	25	2	JH0700	omega-conotoxin MV
63	57	47.5	60	2	S31723	metallothionein -
64	57	47.5	1220	2	A56136	jagged protein pre
65	57	47.5	1531	2	T42218	slit-1 protein hom
66	56.5	47.1	217	2	S23244	hypothetical prote
67	56.5	47.1	1810	1	A32230	tenascin precursor
68	56	46.7	60	2	S38335	metallothionein -
69	56	46.7	68	2	S25775	testis-specific pr
70	56	46.7	164	2	T24272	hypothetical prote
71	56	46.7	188	2	H82933	hypothetical prote
72	56	46.7	188	2	T15651	hypothetical prote
73	56	46.7	198	2	T24476	hypothetical prote
74	56	46.7	385	2	S53718	homeotic protein d
75	56	46.7	385	2	A54785	preadipocyte facto
76	56	46.7	491	2	T21421	hypothetical prote
77	56	46.7	971	2	S23408	prematurely termin
78	56	46.7	1429	2	S06434	homeotic protein 1
79	56	46.7	1523	2	T13953	MEGF5 protein - ra
80	56	46.7	2610	2	T20968	hypothetical prote
81	55.5	46.2	121	1	PSSNAM	phospholipase A2 h
82	55.5	46.2	137	2	S68429	myotoxin precursor
83	55.5	46.2	571	2	T40956	conserved hypothet
84	55.5	46.2	613	2	S15468	complement C3b/C4b
85	55	45.8	118	2	T49515	hypothetical prote
86	55	45.8	152	2	S00332	alpha-amylase inhi
87	55	45.8	197	2	T46413	keratin KAP5.5 - s
88	55	45.8	383	2	S53716	delta-like homeoti
89	55	45.8	3623	2	T09456	intrinsic factor-B
90	54.5	45.4	42	1	NTIIRF	robustoxin - funne
91	54.5	45.4	42	1	NTIIV	versutoxin - funne
92	54.5	45.4	398	2	T39631	hypothetical prote
93	54.5	45.4	736	2	E71414	hypothetical prote
94	54.5	45.4	1046	2	A26838	praetalk protein p
95	54.5	45.4	1208	2	T27822	hypothetical prote
96	54.5	45.4	1766	2	A42125	trophozoite cystei
97	54.5	45.4	1959	1	AGRT	agrin - rat
98	54.5	45.4	2643	2	T29149	hypothetical prote
99	54	45.0	62	2	I51538	metallothionein -
100	54	45.0	67	2	T11547	metallothionein -

RESULT 3

RESULT 3

A35844

Xotch protein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004

C:Accession: A35844

R:Coifman, C.; Harris, W.; Kintner, C.

Science 249, 1438-1441, 1990

A:Title: Xotch, the Xenopus homolog of Drosophila notch.

A:Reference number: A35844; MUID:90385285; PMID:2402639

A:Accession: A35844

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-2524 <COF>

C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology

C:Keywords: transmembrane protein

F:146-177/Domain: EGF homology <EGX1>

F:184-215/Domain: EGF homology <EGF1>

F:222-254/Domain: EGF homology <EGF>

F:456-487/Domain: EGF homology <EGX2>

F:757-788/Domain: EGF homology <EGF3>

F:1025-1056/Domain: EGF homology <EGX3>

F:1924-1956/Domain: ankyrin repeat homology <AN1>

F:1957-1989/Domain: ankyrin repeat homology <AN2>

F:1991-2023/Domain: ankyrin repeat homology <AN3>

F:2024-2056/Domain: ankyrin repeat homology <AN4>

F:2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match 60.0%; Score 72; DB 2; Length 2524;

Best Local Similarity 34.6%; Pred. No. 27;

Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSXKXNXXNXCXV 27

Db 248 GFSSQNCENIDDCPSNCRNGTGV 273

RESULT 4

JH0699

omega-conotoxin MVIIIC precursor [validated] - cone shell (Conus magus) (fragment)

C:Species: Conus magus (magus cone)

C>Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004

C:Accession: JH0699; PC2380

R:Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; M

Neuron 9, 69-77, 1992

A:Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.

A:Reference number: JH0699; MUID:92337922; PMID:1352986

A:Accession: JH0699

A:Molecule type: mRNA

A:Residues: 1-29 <HL>

A:Cross-references: UNIPROT:P37300; GB:S40826; NID:9252126; PIDN:AAB22674.1; PID:9252127

R:Nemoto, N.; Kubo, S.; Yoshida, T.; Chino, N.; Kimura, T.; Sakakibara, S.; Kyogoku, Y.;

Biochem. Biophys. Res. Commun. 207, 695-700, 1995

A:Title: Solution structure of omega-conotoxin MVIIIC determined by NMR.

A:Reference number: PC2380; MUID:95169113; PMID:7864862

A:Accession: PC2380

A:Molecule type: protein

A:Residues: 3-28 <NEM>

R:Rarr-Jones, S.; Basus, V.J.

submitted to the Brookhaven Protein Data Bank, December 1994

A:Reference number: A66297; PDB:1OWN

A:Contents: annotation; conformation by (1)H-NMR, residues 3-28

R:Rarr-Jones, S.; Miljanich, G.P.; Nadasdi, L.; Ramachandran, J.; Basus, V.J.

J. Mol. Biol. 248, 106-124, 1995

A:Title: Solution structure of omega-conotoxin MVIIIC, a high affinity of P-type calcium c

A:Reference number: A58582; MUID:95248539; PMID:7731037

A:Contents: annotation; conformation by (1)H-NMR

C:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh

F:3-18/28/Product: omega-conotoxin MVIIIC #status experimental <WAT>

F:3-18,10-22,17-28/Disulfide bonds: #status experimental

F:28/Modified site: amidated carboxyl end (Cys) (amide in mature form from following glyco


```

Query Match          57.5%; Score 69; DB 2; Length 29;
Best Local Similarity 30.8%; Pred. No. 2.5;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXKCNXNKC 26
    : : : : : : : : : : : : : : : : : : : : : :
Db 3 CKGKGFCKRTMYDCCSGCGRRGKC 28

RESULT 5
A40043
notch protein homolog TAN-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 16-Aug-2004
C:Accession: A40043
R:Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar,
Cell 66, 649-661, 1991
A:Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal
A:Reference number: A40043; MUID:91347367; PMID:1831692
A:Accession: A40043
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-2555 <ELL>
A:Cross-references: GB:W73980
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F:261-292/Domain: EGF homology <EGX1>
F:494-525/Domain: EGF homology <EGF1>
F:987-1018/Domain: EGF homology <EGX2>
F:1149-1180/Domain: EGF homology <EGF>
F:1187-1218/Domain: EGF homology <EGF3>
F:1233-1264/Domain: EGF homology <EGX3>
F:1327-1359/Domain: ankyrin repeat homology <AN1>
F:1960-1992/Domain: ankyrin repeat homology <AN2>
F:1994-2026/Domain: ankyrin repeat homology <AN3>
F:2027-2059/Domain: ankyrin repeat homology <AN4>
F:2060-2092/Domain: ankyrin repeat homology <AN5>

Query Match          56.7%; Score 68; DB 2; Length 2555;
Best Local Similarity 30.8%; Pred. No. 64;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSXKCNXNKC 27
    : : : : : : : : : : : : : : : : : : : : : :
Db 248 GFTGQNCENIDCPGNCKNGGACV 273

RESULT 6
B26637
neurogenic repetitive locus 95F protein - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C:Accession: B26637
R:Knuist, E.; Dietrich, U.; Tepas, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-ort
EMBO J. 6, 761-766, 1987
A:Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and
A:Reference number: A91081; MUID:87218537; PMID:3107986
A:Accession: B26637
A:Molecule type: mRNA
A:Residues: 1-293 <XNU>
A:Cross-references: UNIPROT:P10040; GB:X05144; NID:g7519; PIDN:CAA28793.1; PID:g929536
C:Genetics:
A:Gene: FlyBase:crb
A:Cross-references: FlyBase:FBgn0000368
C:Keywords: transmembrane protein
F:139-170/Domain: EGF homology <EGX1>
F:177-208/Domain: EGF homology <EGF1>
F:216-252/Domain: EGF homology <EGF>

Query Match          55.8%; Score 67; DB 2; Length 293;
Best Local Similarity 28.0%; Pred. No. 18;
Matches 7; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSXKCNXNKC 26

```


RESULT 9

S18188
Notch protein homolog - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C:Accession: S18188
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991.
A>Title: A homolog of Drosophila Notch expressed during mammalian development.
A:Reference number: S18188; MUID:92111383; PMID:1764995
A:Accession: S18188
A:Molecule type: mRNA
A:Residues: 1-2531 <WEI>
A:Cross-references: EMBL:X57405; NID:g57634; PID:g57635
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:987-1018/Domain: EGF homology <EGF1>
F:1025-1056/Domain: EGF homology <EGF2>
F:1233-1264/Domain: EGF homology <EGF3>
F:1917-1949/Domain: ankyrin repeat homology <AN1>
F:1950-1982/Domain: ankyrin repeat homology <AN2>
F:1984-2016/Domain: ankyrin repeat homology <AN3>
F:2017-2049/Domain: ankyrin repeat homology <AN4>
F:2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match 55.8%; Score 67; DB 2; Length 2531;

Best Local Similarity 30.8%; Pred. No. 78;

Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXQXQLDDCCSXCNXXNCV 27

DB 248 GFAGQNCENVDPCFNNCKNGACV 273

RESULT 10

A46019
Notch-1 protein - mouse
N:Alternate names: notch protein
C:Species: Mus musculus (house mouse)
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C:Accession: A46019; S25144; G49175; B46438; P1569; S32109
R:del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid
Genomics 15, 259-264, 1993
A>Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of
A:Reference number: A46019; MUID:93194170; PMID:8449489
A:Accession: A46019
A>Status: not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-2531
A:Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1;
A>Note: sequence extracted from NCBI backbone (NCBI:127318)
R:Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;
submitted to the EMBL Data Library, April 1992
A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggest
A:Reference number: S25144
A:Accession: S25144

A:Molecule type: mRNA

A:Residues: 1351-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <PRA>

A:Cross-references: EMBL:Z11886

R:Lardelli, M.; Lendahl, U.

Exp. Cell Res. 204, 364-372, 1993

A>Title: Notch A and Notch B-two mouse Notch homologues coexpressed in a wide variety of
A:Reference number: A49175; MUID:93178563; PMID:8440332

A:Accession: A49175

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1161-1547 <LAR>

A:Cross-references: EMBL:X68278; NID:g287987; PIDN:CAA48339.1; PID:g287988

A:Experimental source: embryo

A>Note: sequence extracted from NCBI backbone (NCBI:126159)

R:Kopan, R.; Weintraub, H.

J. Cell Biol. 121, 631-641, 1993

A>Title: Mouse notch: expression in hair follicles correlates with cell fate determinati
A:Reference number: A46438; MUID:93252998; PMID:8486742

A:Accession: B46438

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054-

A:Experimental source: embryo

A>Note: sequence extracted from NCBI backbone (NCBI:131246, NCBI:131247)

C:Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.

C:Genetics: This protein is one of the neurogenic proteins controlling the decision between

A:Gene: notch-1

A:Map position: 2

A>Note: proximal region of chromosome 2

C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology

F:106-138/Domain: EGF homology <EGF1>

F:144-175/Domain: EGF homology <EGF1>

F:222-254/Domain: EGF homology <EGF2>

F:261-292/Domain: EGF homology <EGF2>

F:339-370/Domain: EGF homology <EGF3>

F:416-449/Domain: EGF homology <EGF3>

F:456-487/Domain: EGF homology <EGF3>

F:494-525/Domain: EGF homology <EGF3>

F:532-563/Domain: EGF homology <EGF3>

F:607-638/Domain: EGF homology <EGF3>

F:682-713/Domain: EGF homology <EGF3>

F:757-788/Domain: EGF homology <EGF3>

F:795-826/Domain: EGF homology <EGF3>

F:873-904/Domain: EGF homology <EGF3>

F:911-942/Domain: EGF homology <EGF3>

F:949-980/Domain: EGF homology <EGF3>

F:987-1018/Domain: EGF homology <EGF3>

F:1025-1056/Domain: EGF homology <EGF3>

F:1063-1094/Domain: EGF homology <EGF3>

F:1149-1180/Domain: EGF homology <EGF3>

F:1187-1218/Domain: EGF homology <EGF3>

F:1233-1264/Domain: EGF homology <EGF3>

F:1352-1383/Domain: EGF homology <EGF3>

F:1391-1425/Domain: EGF homology <EGF3>

F:1917-1948/Domain: ankyrin repeat homology <AN1>

F:1949-1981/Domain: ankyrin repeat homology <AN2>

F:1983-2015/Domain: ankyrin repeat homology <AN3>

F:2016-2048/Domain: ankyrin repeat homology <AN4>

F:2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 55.8%; Score 67; DB 2; Length 2531;

Best Local Similarity 30.8%; Pred. No. 78;

Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXQXQLDDCCSXCNXXNCV 27

DB 248 GFAGQNCENVDPCFNNCKNGACV 273

RESULT 11

B43620

omega-conotoxin GVIIIB - cone shell (Conus geographus)

N:Alternate names: shaker peptide GVIIIB

C:Species: Conus geographus (geography cone)

C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004

C:Accession: B43620

R:Oliviera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santos

Science 230, 1338-1343, 1985

A>Title: Peptide neurotoxins from fish-hunting cone snails.

A:Reference number: A43620; MUID:86070213; PMID:4071055

A:Accession: B43620

A:Molecule type: protein

A:Residues: 1-29 <OLI>

A:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;

F:1-16, 8-19, 15-26/Disulfide bonds: #status predicted

F:4, 7/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 55.0%; Score 66; DB 2; Length 29;


```
Matches 7; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
QY 4 XNQCXQXLDCCSXCNXNXCVCV 27
Db 822 TGQKCTNIDCVTPNGCGGTCTI 845
RESULT 15
T22025
hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22025
R:Smyle, R.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z19503
A:Accession: T22025
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-601 <WIL>
A:Cross-references: UNIPROT:Q20204; EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10
A:Experimental source: clone F40E10
C:Genetics:
A:Gene: CESP:F40E10.4
A:Map position: X
Query Match 54.2%; Score 65; DB 2; Length 601;
Best Local Similarity 26.9%; Pred. No. 46;
Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
QY 2 XIXNQXQXLDCCSXCNXNXCVCV 27
Db 114 GFEGDYCEKNIDCVNSKCGNGKVCV 139
RESULT 16
D89711
Protein F40E10.4 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89711
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 287, 122, 2001
A:Accession: D89711
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-601 <STO>
A:Cross-references: UNIPROT:Q20204; GB:chr_X; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4
C:Genetics:
A:Gene: F40E10.4
A:Map position: X
Query Match 54.2%; Score 65; DB 2; Length 601;
Best Local Similarity 26.9%; Pred. No. 46;
Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
QY 2 XIXNQXQXLDCCSXCNXNXCVCV 27
Db 114 GFEGDYCEKNIDCVNSKCGNGKVCV 139
RESULT 17
T09059
notch4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09059
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; and others
submitted to the EMBL Data Library, October 1997
```

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A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09059
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1964 <ROW>
A:Cross-references: UNIPROT:P31695; EMBL:AF030001; NID:G2564945; PID:G2564947
C:Genetics:
A:Gene: notch4
A:Map position: 17
A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 671/1; 1679/3; 1729/1; 1761/3
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: receptor; signal transduction
F:514-545/Domain: EGF homology <EGF>
Query Match 54.2%; Score 65; DB 2; Length 1964;
Best Local Similarity 33.3%; Pred. No. 1e+02;
Matches 7; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
QY 7 XCXQXLDCCSXCNXNXCVCV 27
Db 348 GCEENLDDCAATCAPGSTCI 368
RESULT 18
S45306
notch3 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S45306
R:Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 46, 123-136, 1994
A>Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-like repeats
A:Reference number: S45306; MUID:95001556; PMID:7918097
A:Accession: S45306
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2318 <LAR>
A:Cross-references: UNIPROT:Q61982; EMBL:X74760; NID:G483580; PIDN:CAA52776.1; PID:G483580
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:163-195/Domain: EGF homology <EGF1>
F:474-505/Domain: EGF homology <EGF2>
F:854-885/Domain: EGF homology <EGF2>
F:1839-1871/Domain: ankyrin repeat homology <AN1>
F:1872-1904/Domain: ankyrin repeat homology <AN2>
F:1906-1938/Domain: ankyrin repeat homology <AN3>
F:1939-1971/Domain: ankyrin repeat homology <AN4>
F:1972-2004/Domain: ankyrin repeat homology <AN5>
Query Match 54.2%; Score 65; DB 2; Length 2318;
Best Local Similarity 30.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;
QY 1 CXIXN-----QXCXQXLDCCSXCNXNXCVCV 26
Db 301 CVCVNGWTGSCSQNIDCATAVCFHGATC 330
RESULT 19
S78549
notch3 protein - human
C:Species: Homo sapiens (man)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: S78549; S71825
R:Joutel, A.; Tournier-Lasserre, E.
submitted to the EMBL Data Library, April 1997
A:Reference number: S78549
A:Accession: S78549
A:Molecule type: mRNA
A:Residues: 1-2321 <JOUT1>
A:Cross-references: UNIPROT:Q9UM47; EMBL:U97669; NID:G2668591; PIDN:AA891371.1; PID:G2668591
R:Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, P.; Alamowitch
```


x, M.M.; Weisenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserre, E.
Nature 383, 707-710, 1996
A>Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke
A:Reference number: S71825; MUID:97032728; PMID:8878478
A:Accession: S71825
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 67-113;138-194;268-333,'G','G';335-346;536-613;716-765;1240-1279;1815-1888 <JOUZ
A:CROSS-references: EMBL:U97669
C:Genetics:
A:Gene: notch3
A:Map position: 19p13.1
C:Function:
C>Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: tandem repeat; transmembrane protein
F:123-155/Domain: EGF homology <EGX1>
F:162-194/Domain: EGF homology <EGF1>
F:240-271/Domain: EGF homology <EGX2>
F:318-349/Domain: EGF homology <EGF>
F:473-504/Domain: EGF homology <EGX3>
F:853-884/Domain: EGF homology <EGF3>
F:928-959/Domain: EGF homology <EGX4>
F:1838-1870/Domain: ankyrin repeat homology <AN1>
F:1871-1903/Domain: ankyrin repeat homology <AN2>
F:1905-1937/Domain: ankyrin repeat homology <AN3>
F:1938-1970/Domain: ankyrin repeat homology <AN4>
F:1971-2003/Domain: ankyrin repeat homology <AN5>

Query Match 54.2%; Score 65; DB 2; Length 2321;
Best Local Similarity 30.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;

QY 1 CXIXN----OXCKQLDCCSXCNXXNC 26
 |:| :||:||::||| ::||::||
Db 300 CVCVNGWTGESCSQNIDDCATACVFHGATC 329

RESULT 20
T31070
Notch homolog - sea urchin (Lytechinus variegatus)
C:Species: Lytechinus variegatus (variegated urchin)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C:Accession: T31070
R:Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 1997
A>Title: Identification and localization of a sea urchin Notch homologue: insights into
A:Reference number: Z20966; MUID:97454256; PMID:9310331
A:Accession: T31070
A>Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: mRNA
A:Residues: 1-2531 <SHE>
A:CROSS-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 54.2%; Score 65; DB 2; Length 2531;
Best Local Similarity 38.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 7 KCXOXLDDCCSXCNXXNCV 27
 |::::||| ||::|||
Db 661 NCBEDIDDCESPCHNGTCV 681

RESULT 21
T25933
hypothetical protein W02C12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25933
R:Murray, J.; Wohlmann, P.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of C. elegans cosmid W02C12.

DB 205 GFTGDCNCETDIDBCASAPCRNGGACV 230

RESULT 26

T30176

ECF repeat transmembrane protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30176

R:Sell, C.; Hoff III, H.B.

submitted to the EMBL Data Library, May 1996

A:Description: Cloning of a novel mRNA regulated by the insulin like growth

A:Reference number: Z20762

A:Accession: T30176

A:Status: preliminary; translated from GB/EMBL/DBDJB

A:Molecule type: mRNA

A:Residues: 1-1687 <SEP>

A:Cross-references: UNIPROT:G61204; EMBL:U57368; NID:gl336627; PID:gl336628

A:Experimental source: strain C57BL/6J; clone DBI-1; whole embryo

Query Match 52.5%; Score 63; DB 2; Length 1687;

Best Local Similarity 26.9%; Pred No. 1.4e+02;

Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps

QY 2 XIXNQXCXQXLDCCSXCNXXNXCVCV 27

DB 480 GFEGSTCERNIDDCPNHRCQNGVCV 505

RESULT 27

A43620

omega-conotoxin GVIIA - cone shell (Conus geographus)

N:Alternate names: shaker peptide GVIIA

C:Species: Conus geographus (geography cone)

C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004

C:Accession: A43620

R:Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, Science 230, 1338-1343, 1985

A:Title: Peptide neurotoxins from fish-hunting cone snails.

A:Reference number: A43620; MUID:86070213; PMID:4071055

A:Accession: A43620

A:Molecule type: protein

A:Residues: 1-29 <OLI>

A:Cross-references: UNIPROT:P05483

C:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; calcium channel inhibitor; hyo

F;1-16,18,19,15-26/disulfide bonds: #status predicted

F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 51.7%; Score 62; DB 2; Length 29;

Best Local Similarity 26.9%; Pred. No. 11;

Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps

QY 1 CXIXNQXCXQXLDCCSXCNXXNXC 26

DB 1 CKSPGTCGRMRDCTCSLLYSNKC 26

RESULT 28

I48324

DETA-like 1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I48324

R:Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A. Development 121, 2407-2418, 1995

A:Title: Transient and restricted expression during mouse embryogenesis of D

A:Reference number: I48324; MUID:95401858; PMID:7671806

A:Accession: I48324

A:Status: preliminary; translated from GB/EMBL/DBDJB

A:Molecule type: mRNA

A:Residues: 1-722 <RES>

A:Cross-references: UNIPROT:O61483; EMBL:Y80903; NID:G906559; PID:G906559

C:Genetics:
 A:Gene: Dll1
 C:Superfamily: delta-4 protein; EGF homology
 F:331-362/Domain: EGF homology <EGF2>
 F:446-477/Domain: EGF homology <EGF>
 F:484-515/Domain: EGF homology <EGF1>

Query Match 51.7%; Score 62; DB 2; Length 722;
 Best Local Similarity 28.0%; Pred. No. 99;
 Matches 7; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSXXCNXXNC 26

Db 433 GFSRGYCEDNVDDCASSPCANGGTC 457

RESULT 29

A40136
 fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
 N:Alternate names: epidermal growth factor homolog precursor
 C:Contains: alternatively spliced fibropellin Ib (EGFI)
 C:Species: Strongylocentrotus purpuratus (purple urchin)
 C:Date: 13-May-1992 #sequence revision 17-Sep-1997 #text_change 09-Jul-2004
 C:Accession: A40136; B40136; A29316; A43131
 R:Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
 J. Mol. Evol. 29, 314-327, 1989
 A:Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpuratus
 A:Reference number: A40136; MUID:90112459; PMID:2514273
 A:Accession: A40136
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-114
 A:Cross-references: UNIPROT:P10079; GB:X17530; NID:g10225; PID:g667061
 A:Accession: B40136
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>
 A:Accession: C40136
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 'K',747-821,898-978 <DE3>
 R:Hursh, D.A.; Andrews, M.E.; Raff, R.A.
 Science 237, 1487-1490, 1987
 A:Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
 A:Reference number: A29316; MUID:87319677; PMID:3498216
 A:Accession: A29316
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 'S',280-481,786-1064 <HUR>
 A:Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260
 R:Hunt, L.T.; Barker, W.C.
 FASEB J. 3, 1760-1764, 1989
 A:Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.
 A:Reference number: A4331; MUID:89198606; PMID:2784773
 A:Contents: annotation
 C:Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-1064/Product: fibropellin I #status predicted <FIB>
 F:23-54/Domain: EGF homology <EG01>
 F:57-175/Domain: C1r/C1s repeat homology <C1R>
 F:180-211/Domain: EGF homology <EG02>
 F:218-249/Domain: EGF homology <EG03>
 F:256-287/Domain: EGF homology <EG04>
 F:294-325/Domain: EGF homology <EG05>
 F:332-363/Domain: EGF homology <EG06>
 F:370-401/Domain: EGF homology <EG07>
 F:408-439/Domain: EGF homology <EG08>
 F:446-477/Domain: EGF homology <EG09>
 F:484-515/Domain: EGF homology <EG10>
 F:522-553/Domain: EGF homology <EG11>
 F:560-591/Domain: EGF homology <EG12>
 F:598-629/Domain: EGF homology <EG13>
 F:636-667/Domain: EGF homology <EG14>

F:674-705/Domain: EGF homology <EG15>
 F:712-743/Domain: EGF homology <EG16>
 F:750-781/Domain: EGF homology <EG17>
 F:788-819/Domain: EGF homology <EG18>
 F:826-857/Domain: EGF homology <EG19>
 F:864-895/Domain: EGF homology <EG20>
 F:902-933/Domain: EGF homology <EG21>
 F:936-1064/Region: avidin-like
 F:23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-272,275-284,288-297,300-311,314-327,330-341,344-355,358-369,372-383,386-397,400-411,414-425,428-439,442-453,456-467,470-481,484-495/Disulfide bonds: #status predicted
 F:489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-627,630-641,644-655,658-669,672-683,686-697,700-711,714-725,728-739,742-753,756-767,770-781,784-795,798-809,812-823,826-837,839-850,853-864,867-878,881-892,895-906,909-920,923-934,937-948,951-962,965-976,979-990,993-1004,1007-1018,1021-1032,1035-1046,1049-1060,1063-1074,1077-1088,1091-1102,1105-1116,1119-1130,1133-1144,1147-1158,1161-1172,1175-1186,1189-1200,1203-1214,1217-1228,1231-1242,1245-1256,1259-1270,1273-1284,1287-1298,1301-1312,1315-1326,1329-1340,1343-1354,1357-1368,1371-1382,1385-1396,1399-1410,1413-1424,1427-1438,1441-1452,1455-1466,1469-1480,1483-1494,1497-1508,1511-1522,1525-1536,1539-1550,1553-1564,1567-1578,1581-1592,1595-1606,1609-1620,1623-1634,1637-1648,1651-1662,1665-1676,1679-1690,1693-1704,1707-1718,1721-1732,1735-1746,1749-1760,1763-1774,1777-1788,1791-1802,1805-1816,1819-1830,1833-1844,1847-1858,1861-1872,1875-1886,1889-1900,1903-1914,1917-1928,1931-1942,1945-1956,1959-1970,1973-1984,1987-1998,2001-2012,2015-2026,2029-2040,2043-2054,2057-2068,2071-2082,2085-2096,2099-2110,2113-2124,2127-2138,2141-2152,2155-2166,2169-2180,2183-2194,2197-2208,2211-2222,2225-2236,2239-2250,2253-2264,2267-2278,2281-2292,2295-2306,2309-2320,2323-2334,2337-2348,2351-2362,2365-2376,2379-2390,2393-2404,2407-2418,2421-2432,2435-2446,2449-2460,2463-2474,2477-2488,2491-2502,2505-2516,2519-2530,2533-2544,2547-2558,2561-2572,2575-2586,2589-2600,2603-2614,2617-2628,2631-2642,2645-2656,2659-2670,2673-2684,2687-2698,2701-2712,2715-2726,2729-2740,2743-2754,2757-2768,2771-2782,2785-2796,2799-2810,2813-2824,2827-2838,2841-2852,2855-2866,2869-2880,2883-2894,2897-2908,2911-2922,2925-2936,2939-2950,2953-2964,2967-2978,2981-2992,2995-3006,3009-3020,3023-3034,3037-3048,3051-3062,3065-3076,3079-3090,3093-3104,3107-3118,3121-3132,3135-3146,3149-3160,3163-3174,3177-3188,3191-3202,3205-3216,3219-3230,3233-3244,3247-3258,3261-3272,3275-3286,3289-3300,3303-3314,3317-3328,3331-3342,3345-3356,3359-3370,3373-3384,3387-3398,3401-3412,3415-3426,3429-3440,3443-3454,3457-3468,3471-3482,3485-3496,3499-3510,3513-3524,3527-3538,3541-3552,3555-3566,3569-3580,3583-3594,3597-3608,3611-3622,3625-3636,3639-3650,3653-3664,3667-3678,3681-3692,3695-3706,3709-3720,3723-3734,3737-3748,3751-3762,3765-3776,3779-3790,3793-3804,3807-3818,3821-3832,3835-3846,3849-3860,3863-3874,3877-3888,3891-3902,3905-3916,3919-3930,3933-3944,3947-3958,3961-3972,3975-3986,3989-4000,4003-4014,4017-4028,4031-4042,4045-4056,4059-4070,4073-4084,4087-4098,4101-4112,4115-4126,4129-4140,4143-4154,4157-4168,4171-4182,4185-4196,4199-4210,4213-4224,4227-4238,4241-4252,4255-4266,4269-4280,4283-4294,4297-4308,4311-4322,4325-4336,4339-4350,4353-4364,4367-4378,4381-4392,4395-4406,4409-4420,4423-4434,4437-4448,4451-4462,4465-4476,4479-4490,4493-4504,4507-4518,4521-4532,4535-4546,4549-4560,4563-4574,4577-4588,4591-4602,4605-4616,4619-4630,4633-4644,4647-4658,4661-4672,4675-4686,4689-4700,4703-4714,4717-4728,4731-4742,4745-4756,4759-4770,4773-4784,4787-4798,4801-4812,4815-4826,4829-4840,4843-4854,4857-4868,4871-4882,4885-4896,4899-4910,4913-4924,4927-4938,4941-4952,4955-4966,4969-4980,4983-4994,4997-5008,5011-5022,5025-5036,5039-5050,5053-5064,5067-5078,5081-5092,5095-5106,5109-5120,5123-5134,5137-5148,5151-5162,5165-5176,5179-5190,5193-5204,5207-5218,5221-5232,5235-5246,5249-5260,5263-5274,5277-5288,5291-5302,5305-5316,5319-5330,5333-5344,5347-5358,5361-5372,5375-5386,5389-5400,5403-5414,5417-5428,5431-5442,5445-5456,5459-5470,5473-5484,5487-5498,5501-5512,5515-5526,5529-5540,5543-5554,5557-5568,5571-5582,5585-5596,5599-5610,5613-5624,5627-5638,5641-5652,5655-5666,5669-5680,5683-5694,5697-5708,5711-5722,5725-5736,5739-5750,5753-5764,5767-5778,5781-5792,5795-5806,5809-5820,5823-5834,5837-5848,5851-5862,5865-5876,5879-5890,5893-5904,5907-5918,5921-5932,5935-5946,5949-5960,5963-5974,5977-5988,5991-6002,6005-6016,6019-6030,6033-6044,6047-6058,6061-6072,6075-6086,6089-6100,6103-6114,6117-6128,6131-6142,6145-6156,6159-6170,6173-6184,6187-6198,6201-6212,6215-6226,6229-6240,6243-6254,6257-6268,6271-6282,6285-6296,6299-6310,6313-6324,6327-6338,6341-6352,6355-6366,6369-6380,6383-6394,6397-6408,6411-6422,6425-6436,6439-6450,6453-6464,6467-6478,6481-6492,6495-6506,6509-6520,6523-6534,6537-6548,6551-6562,6565-6576,6579-6590,6593-6604,6607-6618,6621-6632,6635-6646,6649-6660,6663-6674,6677-6688,6691-6702,6705-6716,6719-6730,6733-6744,6747-6758,6761-6772,6775-6786,6789-6800,6803-6814,6817-6828,6831-6842,6845-6856,6859-6870,6873-6884,6887-6898,6901-6912,6915-6926,6929-6940,6943-6954,6957-6968,6971-6982,6985-6996,6999-7010,7013-7024,7027-7038,7041-7052,7055-7066,7069-7080,7083-7094,7097-7108,7111-7122,7125-7136,7139-7150,7153-7164,7167-7178,7181-7192,7195-7206,7209-7220,7223-7234,7237-7248,7251-7262,7265-7276,7279-7290,7293-7304,7307-7318,7321-7332,7335-7346,7349-7360,7363-7374,7377-7388,7391-7402,7405-7416,7419-7430,7433-7444,7447-7458,7461-7472,7475-7486,7489-7500,7503-7514,7517-7528,7531-7542,7545-7556,7559-7570,75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[illegible]

Genes Dev. 2, 1723-1735, 1988
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes a
A;Reference number: A31246; MUID:89196890; PMID:3149249
A;Accession: A31246
A;Molecule type: mRNA
A;Residues: 1-832 <KOP>
A;Cross-references: GB:Y00222
C;Genetics:
A;Gene: FlyBase:D1
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
F;295-328/Domain: EGF homology <EGX1>
F;422-450/Domain: EGF homology <EGF1>
F;457-488/Domain: EGF homology <EGF>
F;533-564/Domain: EGF homology <EGF3>
Query Match 50.0%; Score 60; DB 2; Length 832;
Best Local Similarity 23.1%; Pred. No. 1.7e+02;
Matches 6; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 2 XIXNQXCXQXLDCCSXCNXXNXCVCV 27
Db 444 GFSGTRCETNIDDLGHQCENGGTCTI 469
RESULT 39
S19087
gene Delta protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S19087
R;Muskavitch, M.A.T.
submitted to the EMBL Data Library, June 1991
A;Reference number: S19087
A;Accession: S19087
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-833 <MUS>
A;Cross-references: UNIPROT:P10041; EMBL:Y00222
C;Genetics:
A;Gene: FlyBase:D1
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
F;335-371/Domain: EGF homology <EGF1>
F;378-415/Domain: EGF homology <EGX1>
F;457-488/Domain: EGF homology <EGF>
F;533-564/Domain: EGF homology <EGF3>
Query Match 50.0%; Score 60; DB 2; Length 833;
Best Local Similarity 23.1%; Pred. No. 1.7e+02;
Matches 6; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 2 XIXNQXCXQXLDCCSXCNXXNXCVCV 27
Db 444 GFSGTRCETNIDDLGHQCENGGTCTI 469
RESULT 40
S00670
neurogenic repetitive locus delta protein precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: gene D1 protein
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: S00670; A26637
R;Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.
EMBO J. 6, 3431-3440, 1987
A;Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic
A;Reference number: S00670
A;Accession: S00670
A;Molecule type: mRNA
A;Residues: 1-880 <VAE>
A;Cross-references: UNIPROT:P10041; EMBL:X06289; NID:g7852; PID:g7853
R;Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ortega

EMBO J. 6, 761-766, 1987
A;Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and
A;Reference number: A91081; MUID:87218537; PMID:3107986
A;Accession: A26637
A;Molecule type: mRNA
A;Residues: 422-436, 'ET', 439-458, 'A', 460-489, 'T', 491-621 <KNU>
A;Cross-references: GB:X05140; NID:g7851; PIDN:CAA28786.1; PID:g929563
C;Genetics:
A;Gene: Delta; D1
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
C;Keywords: transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
F;457-488/Domain: EGF homology <EGF1>
F;533-564/Domain: EGF homology <EGF2>
Query Match 50.0%; Score 60; DB 2; Length 880;
Best Local Similarity 23.1%; Pred. No. 1.7e+02;
Matches 6; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 2 XIXNQXCXQXLDCCSXCNXXNXCVCV 27
Db 444 GFSGTRCETNIDDLGHQCENGGTCTI 469
RESULT 41
A32901
glp1 protein precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Dec-1989 #sequence_revision 04-Sep-1992 #text_change 09-Jul-2004
C;Accession: A32901
R;Jochem, J.; Greenwald, I.
Cell 58, 553-563, 1989
A;Title: glp-1 and lin-12, genes implicated in distinct cell-cell interactions in Caenorhabditis
A;Reference number: A32901; MUID:89336787; PMID:2758466
A;Accession: A32901
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1295 <YOC>
A;Cross-references: UNIPROT:P13508; GB:M25580; NID:g156316; PIDN:AAA28058.1; PID:g156317
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
F;121-151/Domain: EGF homology <EGF1>
F;125-307/Domain: EGF homology <EGX1>
F;275-307/Domain: EGF homology <EGF1>
F;373-405/Domain: EGF homology <EGF>
F;411-442/Domain: EGF homology <EGF3>
F;450-478/Domain: EGF homology <EGF2>
F;961-993/Domain: ankyrin repeat homology <AN1>
F;1074-1106/Domain: ankyrin repeat homology <AN2>
F;1107-1139/Domain: ankyrin repeat homology <AN3>
Query Match 50.0%; Score 60; DB 2; Length 1295;
Best Local Similarity 25.8%; Pred. No. 2.2e+02;
Matches 8; Conservative 13; Mismatches 6; Indels 4; Gaps 1;
QY 1 CXIXN----QXCXQXLDCCSXCNXXNXCVCV 27
Db 140 CXCNGYGGSYCEGIDHCAQNECAEGSTCV 170
RESULT 42
E89753
protein Fl1C7.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89753
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXIXNQXCKQLDDCCSXCNXXNC 26
| : | : | : ||| : : |
Db 6 CKKNCRCRSCRKSCCSCPAGCNC 31

RESULT 45
S18173
metallothionein - common bobwhite (fragment)
C/Species: Colinus virginianus (Common bobwhite)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S33378; S18173
F./Shartzel, K.L.; Kage, K.; Sobieski, R.J.; Andrews, G.K.
J. Mol. Evol. 36, 255-262, 1993
A/Title: Evolution of avian metallothionein: DNA sequence analyses of the turkey metallo-
A/Reference number: S33378; MUID:93247066; PMID:8483164
A/Accession: S33378
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-43 <SHA>
A/Cross-references: UNIPROT:P27086; EMBL:X62511; NID:g62749; PIDN:CAA44370.1; PID:g62750
C/Superfamily: metallothionein

Query Match 49.2%; Score 59; DB 2; Length 43;
Best Local Similarity 30.8%; Pred. No. 28;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXIXNQXCKQLDDCCSXCNXXNC 26
| : | : | : ||| : : |
Db 6 CKKNCRCRSCRKSCCSCPAGCNC 31

RESULT 46
T10405
conotoxin-like protein 1 - Orgyia pseudotsugata nuclear polyhedrosis virus
C/Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNVP
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C/Accession: T10405
R./Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A/Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis vi-
A/Reference number: Z17011; MUID:97271300; PMID:9126251
A/Accession: T10405
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-53 <NR>
A/Cross-references: EMBL:U75930; NID:g2934903; PID:g1911382

Query Match 49.2%; Score 59; DB 2; Length 53;
Best Local Similarity 32.1%; Pred. No. 32;
Matches 9; Conservative 13; Mismatches 4; Indels 2; Gaps 2;

Qy 1 CXIXNQXCKQLDDCCSXCN-XXNXCV 27
| : | : | : ||| : : |
Db 25 CAETGAVCVHS-DECCSGACSPVFNYCL 51

RESULT 47
C72850
conotoxin homolog - Autographa californica nuclear polyhedrosis virus
C/Species: Autographa californica nuclear polyhedrosis virus, ACMNPV
A/Note: dsDNA virus
C/Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C/Accession: C72850; A44003
R./Ayres, M.D.; Howard, S.C.; Kusio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A/Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A/Reference number: A72850; MUID:94303173; PMID:8030224
A/Accession: C72850
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-53 <AYR>

A>Title: Cloning and expression of an avian metallothionein-encoding gene.
A:Reference number: JQ0030; MUID:90034180; PMID:2806910
A:Accession: JQ0030
A:Molecule type: DNA
A:Residues: 1-63 <FE2>
R:McCormick, C.C.; Fullmer, C.S.; Garvey, J.S.
Proc. Natl. Acad. Sci. U.S.A. 85, 309-313, 1988
A>Title: Amino acid sequence and comparative antigenicity of chicken metal.
A:Reference number: A28113; MUID:88124831; PMID:2448773
A:Accession: A28113
A:Molecule type: protein
A:Residues: 1-63 <MCC>
A:Experimental source: liver
C:Comment: Metallothioneins are a class of cysteine-rich, heavy-metal-binding proteins.
C:Genetics:
A:Gene: cmt
A:Introns: 11/1; 33/1
C:Superfamily: metallothionein
F:1-63/Product: metallothionein #status experimental <MAT>

Query Match 49.2%; Score 59; DB 2; Length 63;
Best Local Similarity 30.8%; Pred. No. 36;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps

QY 1 CXIXNQXCXOXLDCCSCXXCNXXNC 26
| : | : | : | : | : | : | :
DB 20 CKCKNCRCSRKSCSCCPAGCNC 45

RESULT 50
S33381
metallothionein - turkey
C:Species: Meleagris gallopavo (common turkey)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33381; S33380; SI8180
R:Shartzer, K.L.; Kage, K.; Sobieski, R.J.; Andrews, G.K.
J. Mol. Evol. 36, 255-262, 1993
A>Title: Evolution of avian metallothionein: DNA sequence analyses of the
A:Reference number: S33378; MUID:93247066; PMID:8483164
A:Accession: S33381
A:Molecule type: DNA
A:Residues: 1-63 <SHA>
A:Cross-references: UNIPROT:P09576; EMBL:X62513
A:Accession: S33380
A:Molecule type: mRNA
A:Residues: 15-57 <SH2>
A:Cross-references: EMBL:X62514; NID:964090; PIDN:CAA44372.1; PID:964091
C:Genetics:
A:Introns: 11/1; 33/1
C:Superfamily: metallothionein

Query Match 49.2%; Score 59; DB 2; Length 63;
Best Local Similarity 30.8%; Pred. No. 36;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps

QY 1 CXIXNQXCXOXLDCCSCXXCNXXNC 26
| : | : | : | : | : | : | :
DB 20 CKCKNCRCSRKSCSCCPAGCNC 45

RESULT 51
A34620
metallothionein - duck
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C:Accession: A34620; B34620; SI3154; JC5095
R:Liu, L.Y.; Huang, P.C.
Biochem. Biophys. Res. Commun. 168, 182-187, 1990
A>Title: Complete homology in metallothionein from two genera of ducks and
A:Reference number: A34620; MUID:90226357; PMID:2327997
A:Accession: A34620
A>Status: preliminary
A:Molecule type: protein

RESULT 55
S52781
neurocan - mouse

C:Species: Mus musculus (house mouse)
C>Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S52781
R:Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, February 1995
A:Description: Amino acid sequence of mouse neurocan and brevican and their different ex
A:Reference number: S52781
A:Accession: S52781
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1268 <RAU>
A:CROSS-references: UNIPROT:P55066; EMBL:X84727; NID:G758629; PIDN:CAA59216.1; PID:G7586
C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
F:176-253/Domain: link protein repeat homology <LNK1>
F:274-355/Domain: link protein repeat homology <LNK2>
F:964-995/Domain: EGF homology <EGF>
F:1040-1160/Domain: C-type lectin homology <LCH>
F:1167-1223/Domain: complement factor H repeat homology <FHD>
Query Match 49.2%; Score 59; DB 2; Length 1268;
Best Local Similarity 25.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
Qy 4 XNQXCXQXLDCCSXKCNXXKCV 27
Db 991 AGENCEIDDCLCPCPCNGGTCT 1014
RESULT 56
T16342
Hypothetical protein F42C5.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16342
R:Du, Z.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F42C5.
A:Reference number: Z18497
A:Accession: T16342
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-250 <DUZ>
A:CROSS-references: UNIPROT:Q20327; EMBL:U40799; NID:G1065935; PID:G1065941; PIDN:AAA814
C:Genetics:
A:Gene: CESP:F42C5.7
A:Introns: 15/2; 40/3; 167/3; 191/3
Query Match 48.8%; Score 58.5; DB 2; Length 250;
Best Local Similarity 32.0%; Pred. No. 1e+02;
Matches 8; Conservative 11; Mismatches 3; Indels 3; Gaps 1;
Qy 2 XIXNQXCXQXLDCCSXKCNXXKVC 26
Db 134 PVFNQYAMQANDCC---CRCGSPC 155
RESULT 57
C9HU
complement C9 precursor [validated] - human
C:Species: Homo sapiens (man)
C>Date: 27-Nov-1985 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C:Accession: A59363; I52400; A91029; S68647; A59364; A03208
R:Maraziti, D.; Eggertsen, G.; Fey, G.H.; Stanley, K.K.
unpublished results, 1988, cited by GenBank
A:Description: Relationships between the gene and protein structure in human complement
A:Reference number: A59363
A:Accession: A59363
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-559 <MAR2>
A:CROSS-references: UNIPROT:P02748; GB:X02176; NID:G29580; PIDN:CAA26117.1; PID:G29581
R:Maraziti, D.; Eggertsen, G.; Fey, G.H.; Stanley, K.K.
Biochemistry 27, 6529-6534, 1988

A:Title: Relationships between the gene and protein structure in human complement compone
A:Reference number: I52400; MUID:89118250; PMID:3219351
A:Accession: I52400
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 62-159 <MAR2>
A:CROSS-references: GB:J02833; NID:G179727; PIDN:AAA51890.1; PID:G179728
R:Stanley, K.K.; Kocher, H.P.; Luzio, J.P.; Jackson, P.; Tschopp, J.
EMBO J. 4, 375-382, 1985
A:Title: The sequence and topology of human complement component C9.
A:Reference number: A91029; MUID:85257464; PMID:4018030
A:Accession: A91029
A:Molecule type: mRNA
A:Residues: S'1-313,315-559 <STA>
R:DiScipio, R.G.; Gehring, M.R.; Podack, E.R.; Kan, C.C.; Hugli, T.E.; Fey, G.H.
Proc. Natl. Acad. Sci. U.S.A. 81, 7298-7302, 1984
A:Title: Nucleotide sequence of cDNA and derived amino acid sequence of human complement
A:Reference number: A94019; MUID:85063778; PMID:6095282
A:Accession: A94019
A:Molecule type: mRNA
A:Residues: 2-12,'X',14-16,'X',18-42,'R',44-313,315-416,'P',418-559 <DIS>
A:CROSS-references: GB:K02766; NID:G179725; PIDN:AAA51889.1; PID:G179726
R:Lengweiller, S.; Schaller, J.; Rickli, E.E.
FEBS Lett. 380, 8-12, 1995
A:Title: Identification of disulfide bonds in the ninth component (C9) of human complement
A:Reference number: S68647; MUID:96181657; PMID:8603752
A:Accession: S68647
A:Molecule type: protein
A:Residues: 34-47;52-59;69-87,'X',89-93,'T',94-98;106-113;118-131;136-145;180-181,'X',182
R:Witze.Schlomp, K.; Hobart, M.J.; Fernie, B.A.; Orren, A.; Wurzman, R.; Rittner, C.; Kau
Immunogenetics 48, 144-147, 1998
A:Title: Heterogeneity in the genetic basis of human complement C9 deficiency.
A:Reference number: A59364; MUID:98298010; PMID:9634479
A:Note: submitted to GenBank, September 1996
A:Accession: A59364
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 27-559 <WIT>
A:CROSS-references: GB:Y08545; NID:G1834472; PIDN:CAA69849.1; PID:G2258128
A:Experimental source: macronuclear; tissue type blood; cell type lymphocyte
R:Hofsteenge, J.; Blommestein, M.; Hess, D.; Furmanek, A.; Miroshnichenko, O.
J. Biol. Chem. 274, 32786-32794, 1999
A:Title: The four terminal components of the complement system are C-mannosylated on mult
A:Reference number: A59362; MUID:20020247; PMID:10551839
A:Contents: annotation
A:Note: identification and location of C-mannosylation sites by mass-spectroscopy and (1)
C:Genetics:
A:Gene: GDB:C9
A:CROSS-references: GDB:I19738; OMIM:120940
A:Map position: 5p13-5p13
C:Complex: monomer in plasma; 10 to 16 chain multimer in transmembrane form
C:Function:
A:Description: in association with complement C5b-8 complex polymerizes to form a transme
C:Pathway: complement pathway
C:Superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat homology;
C:Keywords: complement pathway; cytolysis; glycoprotein; inflammation; membrane attack c
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-265,266-559/Product: complement C9 #status predicted <MAT>
F:22-265/Domain: complement C9a #status predicted <C9A>
F:41-95/Domain: thrombospondin type 1 repeat homology <THR>
F:101-134/Domain: LDL receptor ligand-binding repeat homology <LDL>
F:166-559/Domain: complement C9b #status predicted <C9B>
F:510-539/Domain: EGF homology <EGF>
F:43-78,54-57,88-94,142-181,254-255,380-405,510-526,513-528,530-539/Disulfide bonds: #ste
F:48/Modified site: 2'-mannosyl-tryptophan (Trp) #status experimental
F:51/Modified site: 2'-mannosyl-tryptophan (Trp) (partial) #status experimental
F:265-266/Cleavage site: His-Gly (thrombin) #status predicted
F:1277,415/Binding site: carbohydrate (Asn) #status predicted
Query Match 48.8%; Score 58.5; DB 1; Length 559;
Best Local Similarity 26.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 12; Mismatches 3; Indels 13; Gaps 2;

A;Residues: 1-25 <HIL>
 A;Cross-references: UNIPROT:P05484
 R;Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santis, Science 230, 1338-1343, 1985
 A;Title: Peptide neurotoxins from fish-hunting cone snails.
 A;Reference number: A43620; MUID:86070213; PMID:4071055
 A;Accession: C60133
 A;Molecule type: protein
 A;Residues: 1-25 <OLI>
 R;Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.; Biochemistry 26, 2086-2090, 1987
 A;Title: Neuronal calcium channel antagonists. Discrimination between calcium channel subtypes.
 A;Reference number: A34115; MUID:87299637; PMID:2441741
 A;Contents: annotation
 R;Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A;Reference number: A67648; PDB:1MWI
 A;Contents: annotation; conformation by (1)H-NMR, residues 1-25
 R;Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
 J. Mol. Biol. 263, 297-310, 1996
 A;Title: A consensus structure for omega-conotoxins with different selectivities for voltage-gated calcium channels.
 A;Reference number: A58619; MUID:97070382; PMID:8913308
 A;Contents: annotation; conformation by (1)H-NMR
 R;Kohn, T.; Kim, J.I.; Kobayashi, K.; Koder, Y.; Maeda, T.; Sato, K.
 submitted to the Brookhaven Protein Data Bank, April 1995
 A;Reference number: A66296; PDB:1OMG
 A;Contents: annotation; conformation by (1)H-NMR, residues 1-25
 R;Kohn, T.; Kim, J.I.; Kobayashi, K.; Koder, Y.; Maeda, T.; Sato, K.
 Biochemistry 34, 10256-10265, 1995
 A;Title: Three-dimensional structure in solution of the calcium channel blocker omega-conotoxin MVIIIC.
 A;Reference number: A58627; MUID:95367555; PMID:7640281
 A;Contents: annotation; conformation by (1)H-NMR
 C;Superfamily: omega-conotoxin
 C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inhibitor
 F;1-16,8-20,15-25/Disulfide bonds: #status predicted
 F;25/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 47.5%; Score 57; DB 2; Length 25;
 Best Local Similarity 24.0%; Pred. No. 30;
 Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCQXLDCCSXCNXXNXX 25
 DB 1 CKGKAKSKMLVDCYTCGSCSGKC 25

RESULT 63
 S31723
 Metallothionein - northern pike
 C;Species: Esox lucius (northern pike)
 C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S38334; S17175; S15503; S31723
 R;Kille, P.; Kay, J.; Sweeney, G.E.
 Biochim. Biophys. Acta 1216, 55-64, 1993
 A;Title: Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant fish.
 A;Reference number: S38334; MUID:94032489; PMID:8218416
 A;Accession: S38334
 A;Molecule type: DNA
 A;Residues: 1-60 <KIT>
 A;Cross-references: UNIPROT:P25127; EMBL:X70042; NID:G62782; PIDN:CAA49636.1; PID:G62782
 A;Note: the authors translated the codon ACT for residue 9 as Ser
 R;Kille, P.; Stephens, P.E.; Kay, J.
 Biochim. Biophys. Acta 1089, 407-410, 1991
 A;Title: Elucidation of cDNA sequences for metallothioneins from rainbow trout, stone loach, and goldfish.
 A;Reference number: S16996; MUID:91316146; PMID:1859844
 A;Accession: S17175
 A;Molecule type: mRNA
 A;Residues: 1-60 <KIT>
 A;Cross-references: EMBL:X59392; NID:G62780; PIDN:CAA42035.1; PID:G62781
 C;Genetics:
 A;Introns: 9/1; 31/1
 C;Superfamily: metallothionein
 C;Keywords: Chelation; metal binding; metal-thiolate cluster

Query Match 47.5%; Score 57; DB 2; Length 60;
 Best Local Similarity 26.9%; Pred. No. 54;
 Matches 7; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 CXIXNQXCQXLDCCSXCNXXNXX 26
 DB 18 CKSCNCACTCKKSCSCGCPGCGSKC 43

RESULT 64
 A56136
 Jagged protein precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003
 C;Accession: A56136
 R;Lindseil, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.
 Cell 80, 909-917, 1995
 A;Title: Jagged: a mammalian ligand that activates Notch1.
 A;Reference number: A56136; MUID:95211842; PMID:7697721
 A;Accession: A56136
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1220 <LIN>
 A;Cross-references: GB:L38483
 F;379-410/Domain: EGF homology <EGF1>
 F;492-523/Domain: EGF homology <EGF>
 F;634-665/Domain: EGF homology <EGF2>

Query Match 47.5%; Score 57; DB 2; Length 1220;
 Best Local Similarity 26.1%; Pred. No. 4,1e+02;
 Matches 6; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNQXCQXLDCCSXCNXXNXX 26
 DB 481 AGDHCEKIDICASNPCNLGCGHC 503

RESULT 65
 T42218
 Slit-1 protein homolog - rat
 N;Alternate names: MEGF4 protein
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T42218
 R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs in the rat slit-1 protein.
 A;Reference number: Z14126; MUID:98360089; PMID:9693030
 A;Accession: T42218
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1531 <NAK>
 A;Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:G3449289; PIDN:BAA32460.1; PID:G3449289
 A;Experimental source: strain Sprague-Dawley; brain
 C;Genetics:
 A;Gene: MEGF4
 C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein repeat

Query Match 47.5%; Score 57; DB 2; Length 1531;
 Best Local Similarity 30.4%; Pred. No. 4.8e+02;
 Matches 7; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 4 XNQXCQXLDCCSXCNXXNXX 26
 DB 957 KGRNCEVSLDSCSNPCNGGTC 979

RESULT 66
 S23244
 Hypothetical protein ZK643.6 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004


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F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-33/Domain: propeptide #status predicted <PRO>
F;34-1810/Product: tenascin 230K #status predicted <MAT>
F;223-249/Domain: EGF homology <EGF>
F;316-342/Domain: EGF homology <EGF>
F;552-673/Domain: fibronectin type III repeat homology <FN3A>
F;681-765/Domain: fibronectin type III repeat homology <FN3B>
F;773-857/Domain: fibronectin type III repeat homology <FN3C>
F;865-949/Domain: fibronectin type III repeat homology <FN3D>
F;957-1037/Domain: fibronectin type III repeat homology <FN3E>
F;1046-1128/Domain: fibronectin type III repeat homology <FN3F>
F;1137-1219/Domain: fibronectin type III repeat homology <FN3G>
F;1228-1310/Domain: fibronectin type III repeat homology <FN3H>
F;1318-1399/Domain: fibronectin type III repeat homology <FN3I>
F;1407-1487/Domain: fibronectin type III repeat homology <FN3J>
F;1495-1575/Domain: fibronectin type III repeat homology <FN3K>
F;1590-1798/Domain: fibrinogen beta/gamma homology <FBG>
F;1734-1747/Domain: calcium binding #status predicted <CAB>

Query Match 47.1%; Score 56.5; DB 1; Length 1810;
Best Local Similarity 29.7%; Pred. No. 5.9e+02;
Matches 11; Conservative 9; Mismatches 4; Indels 13; Gaps 2;

Qy 4 XNQCXQXHL-----DDC-----CSXXCNXXNXC 27
Db 353 GNGRCENGLCVCHRGFGVGDGCSQRKCPKTCNNRGCV 389
: : : : : ||| | : : : : :
: : : : : ||| | : : : : :

RESULT 68
S8335
metallothionein - stone loach
C;Species: Noemacheilus barbatulus (stone loach)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S18335; S17176; S15505
R;Kille, P.; Kay, J.; Sweeney, G.E.
Biochim. Biophys. Acta 1216, 55-64, 1993
A;Title: Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant
A;Reference number: S38334; MUID:94032489; PMID:8218416
A;Accession: S38335
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 <KIL>
A;Cross-references: UNIPROT:P25128; EMBL:X70043
R;Kille, P.; Stephens, P.E.; Kay, J.
Biochim. Biophys. Acta 1089, 407-410, 1991
A;Title: Elucidation of cDNA sequences for metallothioneins from rainbow trout, stone loach
A;Reference number: S16996; MUID:91316146; PMID:1859844
A;Accession: S17176
A;Molecule type: mRNA
A;Residues: 1-4,'E',6-60 <KIL2>
A;Cross-references: EMBL:X59393
C;Genetics:
A;Introns: 9/1, 31/1
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 46.7%; Score 56; DB 2; Length 60;
Best Local Similarity 26.9%; Pred. No. 67;
Matches 7; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDPCCSXXCNXXNXC 26
: : : : : ||| : : : : :
Db 18 CKTNQCCTTCKSCCSCCPGCSKC 43

RESULT 69
S25775
testis-specific protein Mst84D - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S25775; D56565
R;Kuhn, R.; Kuhn, C.; Boerssch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991

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A:Title: A cluster of four genes selectively expressed in the male germ line of Drosophila
 A:Reference number: A56565; PMID:92102953; PMID:1684716
 A:Accession: S25775
 A:Molecule type: DNA
 A:Residues: 1-68 <KUH>
 A:Cross-references: UNIPROT:Q01645; EMBL:X57703; NID:G11072; PIDN:CAA47940.1; PID:G11076
 A:Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBIP:74223)
 C:Genetics:
 A:Gene: Mst84Dd
 A:Cross-references: FlyBase:FBgn00041175
 A:Map position: 3
 C:Superfamily: fruit fly testis-specific protein
 C:Keywords: spermatogenesis; tandem repeat

Query Match 46.7%; Score 56; DB 2; Length 68;
 Best Local Similarity 23.1%; Pred. No. 73;
 Matches 6; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQXLDCCSXCNXXNKC 26
 DB 10 CGPCGCGCGCCGCGCGCGCGPC 35

RESULT 70
 T24272
 hypothetical protein T01B7.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T24272
 R:Sims, M.
 submitted to the EMBL Data Library, October 1995
 A:Reference number: Z19867
 A:Accession: T24272
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-164 <WIL>
 A:Cross-references: UNIPROT:Q22048; EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:T01B7.8
 A:Experimental source: clone T01B7
 C:Genetics:
 A:Gene: CESP:T01B7.8
 A:Map position: 2
 A:Introns: 20/3; 90/2

Query Match 46.7%; Score 56; DB 2; Length 164;
 Best Local Similarity 23.1%; Pred. No. 1.3e+02;
 Matches 6; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQXLDCCSXCNXXNKC 26
 DB 92 CCCRCCTCCTCCTCCTCCTCCTCCTC 117

RESULT 71
 H82933
 hypothetical protein UU101 [imported] - Ureaplasma urealyticum
 C:Species: Ureaplasma urealyticum
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: H82933
 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseil, G.H.
 submitted to GenBank, February 2000
 A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
 A:Reference number: A82870
 A:Accession: H82933
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-188 <GLA>
 A:Cross-references: GB:AE002110; GB:AF222894; NID:G6899051; PIDN:AAF30507.1; GSPDB:GN001
 A:Experimental source: serovar 3; biovar 1
 C:Genetics:
 A:Gene: UU101
 A:Genetic code: SGC3

Query Match 46.7%; Score 56; DB 2; Length 188;

Best Local Similarity 24.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
 QY 2 XIXNQXCXQXLDCCSXCNXXNKC 26
 DB 126 KVEECGCGAKDDCCGHEHEVC 150

RESULT 72
 T15651
 hypothetical protein C27A2.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T15651
 R:Nhan, M.
 submitted to the EMBL Data Library, May 1996
 A:Description: The sequence of C. elegans cosmid C27A2.
 A:Reference number: Z18382
 A:Accession: T15651
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-188 <NHA>
 A:Cross-references: UNIPROT:Q18238; EMBL:US8760; NID:G1330384; PID:G1330389; PIDN:AAB0071
 A:Experimental source: strain Bristol N2; clone C27A2
 C:Genetics:
 A:Gene: CESP:C27A2.5
 A:Map position: 2
 A:Introns: 19/3; 91/2

Query Match 46.7%; Score 56; DB 2; Length 188;
 Best Local Similarity 23.1%; Pred. No. 1.4e+02;
 Matches 6; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQXLDCCSXCNXXNKC 26
 DB 93 CCCRCCTCCTCCTCCTCCTCCTCCTC 118

RESULT 73
 T24476
 hypothetical protein T04H1.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T24476
 R:Harris, B.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19896
 A:Accession: T24476
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-198 <WIL>
 A:Cross-references: UNIPROT:Q22179; EMBL:Z78200; PIDN:CAB01583.1; GSPDB:GN00023; CESP:T04
 A:Experimental source: clone T04H1
 C:Genetics:
 A:Gene: CESP:T04H1.6
 A:Map position: 5
 A:Introns: 33/1; 75/1; 120/1; 159/1
 F:38-74/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:77-115/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:121-158/Domain: LDL receptor ligand-binding repeat homology <LDL3>
 F:162-197/Domain: LDL receptor ligand-binding repeat homology <LDL4>

Query Match 46.7%; Score 56; DB 2; Length 198;
 Best Local Similarity 24.2%; Pred. No. 1.5e+02;
 Matches 8; Conservative 13; Mismatches 6; Indels 6; Gaps 1;
 QY 1 CXIXNQXCXQXLDCC-----CSXXCNXXNKC 27
 DB 90 CIPANKRCGVDCCEDGNSLDEIGCSKNVTCI 122

RESULT 74
 S53718

homeotic protein dlk - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S53718
R:Lee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.
Biochim. Biophys. Acta 1261, 223-232, 1995
A:Title: dlk, PG2 and Pref-1 mRNAs encode similar proteins belonging to the EGF-like superfamily
A:Reference number: S53716; MUID:95226449; PMID:7711066
A:Accession: S53718
A:Molecule type: mRNA
A:Residues: 1-385 <LEE>
A:Cross-references: UNIPROT:Q09163; EMBL:U15980; NID:g562107; PIDN:AA60495.1; PID:g562107
C:Superfamily: preadipocyte factor 1; EGF homology
C:Keywords: transmembrane protein
F:54-85/Domain: EGF homology <EGF1>
F:92-124/Domain: EGF homology <EGF>
F:131-167/Domain: EGF homology <EGF3>
F:214-246/Domain: EGF homology <EGX1>
F:303-332/Domain: transmembrane #status predicted <TM1>

Query Match 46.7%; Score 56; DB 2; Length:385;
Best Local Similarity 19.2%; Pred.No. 2.3e+02;
Matches 5; Conservative 16; Mismatches 5; Indels 0; Gaps 0;

QY 2 XIXNQXQXQLDDCCSXCNXXNXCVCV 27
DB 201 GFVDKTCRPNVSCASGPGCQNGGTCL 226

RESULT 75
A54785
preadipocyte factor 1 precursor, long form - mouse
N:Alternate names: delta-like dlk homeotic protein; pref-1
C:Species: Mus musculus (house mouse)
C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C:Accession: A54785; A45484; A40746; S21585
R:Smad, C.M.; Green, D.; Sul, H.S.
Biochemistry 33, 9257-9265, 1994
A:Title: Structural characterization and alternate splicing of the gene encoding the preadipocyte factor 1 precursor
A:Reference number: A54785; MUID:94325292; PMID:7519443
A:Accession: A54785
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-385 <SMA>
A:Cross-references: UNIPROT:Q09163; GB:S71340
R:Laborda, J.; Sauvillie, E.A.; Hoffman, T.; Notario, V.
J. Biol. Chem. 268, 3817-3820, 1993
A:Title: dlk, a putative mammalian homeotic gene differentially expressed in small cell carcinoma
A:Reference number: A45484; MUID:93179372; PMID:8095043
A:Accession: A45484
A:Molecule type: mRNA
A:Residues: 1-78, 'G', '80-343, 'TF', '346-385 <LAB>
A:Cross-references: EMBL:212171; NID:g50716; PIDN:CAA78162.1; PID:g50717
A:Note: sequence extracted from NCBI backbone (NCBIP:125734)
A:Note: species designations for this sequence report and for B45484 originally were transferred from NCBI backbone
R:Smad, C.M.; Sul, H.S.
Cell 73, 725-734, 1993
A:Title: Pref-1, a protein containing EGF-like repeats, inhibits adipocyte differentiation
A:Reference number: A40746; MUID:93272313; PMID:8500166
A:Accession: A40746
A:Molecule type: mRNA
A:Residues: 1-78, 'G', '80-249, 'P', '251-319, 'CWAPWPFSSFTSAKPGCTATTCTCFARRRRTSCSITAARSWRSISSE
A:Cross-references: GB:I12721; NID:g309092; PIDN:AAA37175.1; PID:g309093
A:Experimental source: 3T3-L1 preadipocytes
A:Note: this sequence extracted from NCBI backbone (NCBIN:132685, NCBIP:1132713)
C:Superfamily: preadipocyte factor 1; EGF homology
C:Keywords: alternative splicing; tandem repeat; transmembrane protein
F:1-385/Product: preadipocyte factor 1 precursor splice form A #status predicted <FOA>
F:1-230, 282-385/Product: preadipocyte factor 1 precursor splice form B #status predicted
F:1-230, 304-385/Product: preadipocyte factor 1 precursor splice form C #status predicted
F:1-230, 306-385/Product: preadipocyte factor 1 precursor splice form C2 #status predicted
F:1-230, 304-385/Product: preadipocyte factor 1 precursor splice form D #status predicted
F:1-230, 306-385/Product: preadipocyte factor 1 precursor splice form E #status predicted

F:1-210, 306-385/Product: preadipocyte factor 1 precursor splice form D2 #status predicted
F:92-124/Domain: EGF homology <EGF>
F:214-246/Domain: EGF homology <EGF1>

Query Match 46.7%; Score 56; DB 2; Length 385;
Best Local Similarity 19.2%; Pred.No. 2.3e+02;
Matches 5; Conservative 16; Mismatches 5; Indels 0; Gaps 0;

QY 2 XIXNQXQXQLDDCCSXCNXXNXCVCV 27
DB 201 GFVDKTCRPNVSCASGPGCQNGGTCL 226

RESULT 76
T21421
hypothetical protein F26E4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21421
R:Lightning, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19419
A:Accession: T21421
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-491 <WILP>
A:Cross-references: UNIPROT:P90850; EMBL:Z81070; PIDN:CAB03007.1; GSPDB:GN00019; CESP:F26E4
A:Experimental source: clone F26E4
C:Genetics:
A:Gene: CESP:F26E4.3
A:Map position: 1
A:Introns: 23/3; 67/1; 108/1; 134/1; 149/2; 179/2; 232/2; 261/2; 306/2; 334/2; 419/2; 461/2

Query Match 46.7%; Score 56; DB 2; Length 491;
Best Local Similarity 23.1%; Pred.No. 2.8e+02;
Matches 6; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXQXQLDDCCSXCNXXNXCVCV 26
DB 70 CSVRTHTCENRRDDCTVPILGDHLC 95

RESULT 77
S23408
prematurely terminated mRNA decay factor NAM7 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YN9583.05c; protein YMR080c; UPF1 protein
C:Species: Saccharomyces cerevisiae
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S23408; A44388; S54455
R:Altamura, N.; Groudinsky, O.; Dujardin, G.; Slonimski, P.P.
J. Mol. Biol. 224, 575-587, 1992
A:Title: NAM7 nuclear gene encodes a novel member of a family of helicases with a Zn-ligand
A:Reference number: S23408; MUID:92235815; PMID:1314899
A:Accession: S23408
A:Molecule type: DNA
A:Residues: 1-971 <ALT>
A:Cross-references: UNIPROT:P30771; EMBL:X62394; NID:g4022; PIDN:CAA44266.1; PID:g4023
R:Leeds, P.; Wood, J.M.; Lee, B.S.; Culbertson, M.R.
Mol. Cell. Biol. 12, 2165-2177, 1992
A:Title: Gene products that promote mRNA turnover in Saccharomyces cerevisiae.
A:Reference number: A44388; MUID:92236591; PMID:1569946
A:Accession: A44388
A:Molecule type: DNA
A:Residues: 1-971 <LEE>
A:Cross-references: GB:M76659; NID:gl73141; PIDN:AAA35197.1; PID:gl73142
R:Gentles, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54451
A:Accession: S54455
A:Molecule type: DNA
A:Residues: 1-971 <GEN>
A:Cross-references: EMBL:Z49259; NID:g807956; PID:g807962; MIPS:YMR080C
A:Experimental source: strain AB972

A>Note: the authors confirmed the identity of the purified protein by composition and pI.
R;Holland, D.R.; Clancy, L.L.; Muchmore, S.W.; Rydel, T.J.; Einspahr, H.M.; Finzel, B.C.
submitted to The Brookhaven Protein Data Bank, October 1991
A:Reference number: A51920; PDB:1PPA
A:Contents: annotation: X-ray crystallography, 2.0 angstroms, residues 1-121
R;Holland, D.R.; Clancy, L.L.; Muchmore, S.W.; Ryde, T.J.; Einspahr, H.M.; Finzel, B.C.;
J. Biol. Chem. 265, 17649-17656, 1990
A>Title: The crystal structure of a lysine 49 phospholipase A-2 from the venom of the cc
A:Reference numbers: A39221; MUID:91009222; PMID:2120215
A:Contents: annotation: X-ray crystallography, 2.0 angstroms
C;Comment: This homolog of phospholipase A2 lacks enzymatic activity because a Lys-48 re
C;Superfamily: Phospholipase A2
C;Keywords: venom
F;26-115,28-44,43-95,49-121,50-88,57-81,75-86/Disulfide bonds: #status experimental

Query Match 46.2%; Score 55.5; DB 1; Length 121;
Best Local Similarity 20.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 15; Mismatches 4; Indels 13; Gaps 1;

QY 1 CXIXNQXCXQLDDC-----CSXXCNXXNXCVCV 27
| : ::::: || |
Db 43 CCFVHKCCYKKLTDCNHKTDTRYSYMKNKAIICEKNPCL 82
| : ::::: || |

RESULT 82
S68429
myotoxin precursor - southern copperhead
C;Species: Agkistrodon contortrix contortrix (southern copperhead)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68429; S74296
R;de Araujo, H.S.S.; White, S.P.; Ownby, C.L.
Arch. Biochem. Biophys. 326, 21-30, 1996
A>Title: cDNA cloning and sequence analysis of a lysine-49 phospholipase A(2) myotoxin f
A:Reference number: S68429; MUID:96154243; PMID:8579368
A;Accession: S68429
A:Molecule type: mRNA
A:Residues: 1-137 <DEA>
A;Cross-references: UNIPROT:P49121; EMBL:U21335; NID:g809484; PIDN:AAC59887.1; PID:g8094
A;Accession: S74296
A:Molecule type: protein
A:Residues: 17-36 <DER>
C;Superfamily: phospholipase A2
F;1-16/DNA: signal sequence #status predicted <SIG>
F;17-137/Product: myotoxin #status experimental <MAT>

Query Match 46.2%; Score 55.5; DB 2; Length 137;
Best Local Similarity 20.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 15; Mismatches 4; Indels 13; Gaps 1;

QY 1 CXIXNQXCXQLDDC-----CSXXCNXXNXCVCV 27
| : ::::: || |
Db 59 CCFVHKCCYKKLTDCNHKTDTRYSYMKNKAIICEKNPCL 98
| : ::::: || |

RESULT 83
T40996
conserved hypothetical protein SPCC1450.14c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40996
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21962
A;Accession: T40996
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-571 <LYN>
A;Cross-references: UNIPROT:Q9V7P1; EMBL:AL049559; PIDN:CAB40181.1; GSPDB:GN00068; SPDB:
A;Experimental source: strain 972h-; cosmid c1450
C;Genetics:
A:Gene: SPDB:SPCC1450.14c
A;Map position: 3
A;Introns: 4/3

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characterization.
A;Reference number: Z16677; MUID:98241400; PMID:9572993
A;Accession: T09456
A;Status: preliminary; translated from GB/EMBL/DBDJB
A;Molecule type: mRNA
A;Residues: 1-3623 <KOZ>
A;Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:g329528; PIDN:AAC82612.1; PID:g329528
C;Genetics:
A;Map position: 10p12
C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C;Keywords: receptor; vitamin B12 uptake
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F:436-467/Domain: EGF homology <EGF>

Query Match 45.8%; Score 55; DB 2; Length 3623;
Best Local Similarity 28.6%; Pred. No. 1.3e+03;
Matches 6; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 7 KCXQXLDCCSXKXNXXKCV 27
: : : : : | : : : : :
Db 428 NCTENINECLSNPLNGTGV 448

RESULT 90
NTIIRF
robustoxin - funnel-web spider (Atrax robustus)
C;Species: Atrax robustus
C;Date: 27-Nov-1995 #sequence_revision 27-Nov-1995 #text_change 09-Jul-2004
C;Accession: A01738
R;Sheumack, D.D.; Claasens, R.; Whiteley, N.M.; Howden, M.E.H.
FEBS Lett. 181, 154-156, 1995
A;Title: Complete amino acid sequence of a new type of lethal neurotoxin from the venom
A;Reference number: A01738; MUID:85127480; PMID:3972101
A;Accession: A01738
A;Molecule type: protein
A;Residues: 1-42 <SHE>
A;Cross-references: UNIPROT:P01478
C;Comment: In this species, the venom of the male is lethal rather than that of the female.
C;Comment: Four disulfide bonds are present.
C;Superfamily: robustoxin
C;Keywords: neurotoxin; venom

Query Match 45.4%; Score 54.5; DB 1; Length 42;
Best Local Similarity 25.8%; Pred. No. 73;
Matches 8; Conservative 11; Mismatches 7; Indels 5; Gaps 1;

Qy 1 CXIXNQXQXQLDDCCSXKC-----NXXNXC 26
: : : : : | : : : : :
Db 1 CAKKRNWCKNEIDCCCPMKCIYAWYNQGS 31

RESULT 91
NTIIV
versutoxin - funnel-web spider (Atrax versutus)
C;Species: Atrax versutus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00343
R;Brown, M.R.; Sheumack, D.D.; Tyler, M.I.; Howden, M.E.H.
Biochem. J. 250, 401-405, 1988
A;Title: Amino acid sequence of versutoxin, a lethal neurotoxin from the venom of the funnel-web spider.
A;Reference number: S00343; MUID:88183359; PMID:3355530
A;Accession: S00343
A;Molecule type: protein
A;Residues: 1-42 <BRO>
A;Cross-references: UNIPROT:P13494
C;Comment: All cysteine residues are linked by disulfide bonds.
C;Superfamily: robustoxin

[illegible]

Search completed: April 18, 2005, 20:38:44
Job time : 29.5 secs

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QM protein - protein search, using sw model

Run on: April 18, 2005, 20:00:51 ; Search time 117 Seconds
(without alignments)
118.172 Million cell updates/sec

Title: US-10-627-685a-1
Perfect score: 120
Sequence: 1 CXIXNQXCXQLDDCCSXCNXXNCV 27

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	120	100.0	67	Q71KT2	Q71kt2 conus purpu
2	120	100.0	72	1 CKX7 CONPU	P56633 conus purpu
3	77	64.2	72	1 CXOB CONST	P28881 conus stria
4	73	60.8	26	1 CXOC CONCT	P58919 conus catus
5	72	60.0	2524	1 NOTC_XENLA	P21783 xenopus lae
6	69	57.5	29	1 CXOC_CONMA	P37300 conus magus
7	69	57.5	1820	2 Q6LPM8	Q6lpm8 plasmodium
8	68	56.7	74	2 Q646U5	Q646u5 phytophthor
9	68	56.7	1961	2 Q6MG89	Q6mg89 rattus norv
10	68	56.7	2556	1 NTC1_HUMAN	P46531 homo sapien
11	68	56.7	2556	2 Q8MSX5	Q8mx5 drosophila
12	67	55.8	487	2 Q8MSX5	Q8mx5 drosophila
13	67	55.8	2139	1 CRB_DROME	P10040 drosophila
14	67	55.8	2146	2 Q9VC97	Q9vc97 drosophila
15	67	55.8	2437	1 NTC1_BRARE	P46530 brachydanio
16	67	55.8	2516	2 Q7TQ52	Q7tq52 mus musculu
17	67	55.8	2516	2 Q7TQ51	Q7tq51 mus musculu
18	67	55.8	2531	1 NTC1_MOUSE	Q71705 mus musculu
19	67	55.8	2531	1 NTC1_RAT	Q70008 rattus norv
20	67	55.8	2531	1 NTC1_RAT	Q70008 rattus norv
21	67	55.8	2531	2 Q8K428	Q8k428 mus musculu
22	67	55.8	2531	2 Q7TQ50	Q7tq50 mus musculu
23	66	55.0	664	2 Q91AT6	Q9iat6 brachydanio
24	66	55.0	721	2 Q91902	Q91902 xenopus lae
25	66	55.0	1317	2 Q61Q50	Q6iq50 homo sapien
26	66	55.0	1551	2 Q9NGV4	Q9ngv4 drosophila
27	66	55.0	2447	2 O13149	O13149 fugu rubrip
28	66	55.0	2470	1 NTC2_MOUSE	O35516 mus musculu
29	66	55.0	2471	1 NTC2_HUMAN	Q04721 homo sapien
30	66	55.0	2471	1 NTC2_RAT	Q9q30 rattus norv
31	66	55.0	2528	2 Q8AXP0	Q8axp0 cynops pyrr

32	66	55.0	2703	1	NOTC_DROME
33	66	55.0	3396	2	Q9VM55
34	65	54.2	726	2	Q8AW87
35	65	54.2	752	2	O42374
36	65	54.2	1075	2	Q9NC90
37	65	54.2	1214	2	Q90YD2
38	65	54.2	1290	2	Q9W6E1
39	65	54.2	1410	2	Q20204
40	65	54.2	1964	1	NTC4_MOUSE
41	65	54.2	2318	1	NTC3_MOUSE
42	65	54.2	2319	1	NTC3_RAT
43	65	54.2	2321	1	NTC3_HUMAN
44	65	54.2	2531	2	O16004
45	65	54.2	2531	2	Q25253
46	64.5	53.8	74	2	Q646V4
47	64.5	53.8	74	2	Q646V5
48	64.5	53.8	74	2	Q646W1
49	64	53.3	647	2	Q6P3V5
50	64	53.3	838	2	Q9VQA9
51	64	53.3	1372	2	P91526
52	64	53.3	2003	1	NTC4_HUMAN
53	64	53.3	2352	2	O61240
54	64	53.3	3623	2	O70244
55	63	52.5	43	1	MTB_COLVI
56	63	52.5	570	1	FBP3_STRPU
57	63	52.5	585	2	Q8OW06
58	63	52.5	587	2	Q8NBS4
59	63	52.5	589	1	DLI3_RAT
60	63	52.5	592	1	DLI3_MOUSE
61	63	52.5	618	1	DLI3_HUMAN
62	63	52.5	642	2	P79941
63	63	52.5	642	2	Q7ZXT4
64	63	52.5	1202	1	JAG2_RAT
65	63	52.5	1238	1	JAG2_HUMAN
66	63	52.5	1247	1	JAG2_MOUSE
67	63	52.5	1687	2	O61204
68	63	52.5	3523	2	Q7QCP4
69	62	51.7	29	1	CKO7_CONGE
70	62	51.7	62	2	Q71KS8
71	62	51.7	73	1	CXOD_CONCT
72	62	51.7	74	2	Q646U3
73	62	51.7	74	2	Q646U4
74	62	51.7	74	2	Q646W2
75	62	51.7	74	2	Q646W3
76	62	51.7	74	2	Q646W6
77	62	51.7	153	2	Q9AUD1
78	62	51.7	382	1	EFL9_MOUSE
79	62	51.7	383	1	EFL9_HUMAN
80	62	51.7	638	2	Q7PM27
81	62	51.7	713	2	Q962W9
82	62	51.7	714	1	DLI1_RAT
83	62	51.7	722	1	DLI1_MOUSE
84	62	51.7	722	2	Q6PFV7
85	62	51.7	723	1	DLI1_HUMAN
86	62	51.7	824	2	Q66S04
87	62	51.7	1064	1	FBP1_STRPU
88	62	51.7	1286	2	Q7QCT2
89	62	51.7	1515	2	Q9DE37
90	62	51.7	1685	2	Q9U4A2
91	62	51.7	2037	2	Q7QFS2
92	62	51.7	2428	2	Q816X6
93	62	51.7	2524	2	Q9GPA5
94	61.5	51.2	36	1	TXM1_AGEAP
95	61.5	51.2	81	2	Q9BP77
96	61.5	51.2	471	2	O8LAG1
97	61.5	51.2	471	2	O8VZE5
98	61.5	51.2	481	2	Q9ZV27
99	61.5	51.2	2050	2	Q81X03
100	61	50.8	29	1	CXOD_CONMA

ALIGNMENTS

RESULT 1	Q71KT2	PRELIMINARY;	PRT;	67 AA.
AC	Q71KT2;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DE	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
OS	Four-loop conotoxin preproprotein (Fragment).			
OS	Conus purpurascens (Purple cone).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;			
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;			
OC	Neogastropoda; Conoidea; Conidae; Conus.			
OX	NCBI_TaxID=41690;			
RA	[1]			
RP	SEQUENCE FROM N.A.			
RP	Duda T.F. Jr., Palumbi S.R.;			
RA	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF480312; AAQ05864.1; -			
DR	HSSP; P56633; IAV3.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0008200; F:ion channel inhibitor activity; IEA.			
DR	GO; GO:0009405; P:pathogenesis; IEA.			
DR	InterPro; IPR004214; Conotoxin.			
DR	Pfam; PF02950; Conotoxin; 1.			
FT	NON TER 1			
FT	CHAIN 41 67			
FT	SEQUENCE 67 AA; 7712 MW; E7E77CC61873B1DB CRC64;			
SQ				
Query Match	100.0%;	Score 120;	DB 2;	Length 67;
Best Local Similarity	63.0%;	Pred. No. 6e-05;		
Matches	17;	Conservative 10;	Mismatches 0;	Indels 0;
Gaps	0;			
Qy	1 CXIXNQXKXQXLDCCSXXCNXXNXCXV 27			
Db	41 CRIPNCKFOHLDCCSRKCNRENKCV 67			
RESULT 2				
CXK7_CONPU	STANDARD;	PRT;	72 AA.	
AC	P56633;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Kappa-conotoxin PVIIA precursor (fin-popping peptide).			
OS	Conus purpurascens (Purple cone).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;			
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;			
OC	Neogastropoda; Conoidea; Conidae; Conus.			
OX	NCBI_TaxID=41690;			
RA	[1]			
RP	SEQUENCE FROM N.A., SYNTHESIS, AND MASS SPECTROMETRY.			
RP	MEDLINE=98079023; PubMed=9417043; DOI=10.1074/jbc.273.1.33;			
RA	Shon K.-J., Stocker M., Terlau H., Stuehmer W., Jacobsen R.B.,			
RA	Walker C.S., Grille M.M., Watkins M., Hillyard D.R., Gray W.R.,			
RA	Olivera B.M.;			
RT	"Kappa-conotoxin PVIIA is a peptide inhibiting the shaker K+			
RT	channel.";			
RL	J. Biol. Chem. 273:33-38 (1998).			
RA	[2]			
RP	SEQUENCE OF 46-72, AND SYNTHESIS.			
RP	MEDLINE=22068471; PubMed=12074021; DOI=10.1038/381148a0;			
RA	Terlau H., Shon K.-J., Grille M.M., Stocker M., Stuehmer W.,			
RA	Olivera B.M.;			
RT	"Strategy for rapid immobilization of prey by a fish-hunting marine			
RT	snail.";			
RL	Nature 381:148-151 (1996).			
RA	[3]			
RP	STRUCTURE BY NMR.			
RC	TISSUE=Venom;			
RC	MEDLINE=98104087; PubMed=9438859; DOI=10.1016/S0969-2126(97)00307-9;			
RA	Scanlon M.J., Naranjo D., Thomas L., Alewood P.F., Lewis R.J.,			

RL J. Biol. Chem. 275:35335-35344 (2000).

CC -|- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind

CC and block voltage-sensitive calcium channels (VSCC) (By

CC similarity). This toxin blocks N-, P-, and Q-type calcium

CC channels.

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -|- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type

CC family.

DR HSSP; P05484; 1DW4.

KW Amidation; Calcium channel inhibitor; Direct protein sequencing;

KW Ionic channel inhibitor; Neurotoxin; presynaptic neurotoxin; Toxin.

FT DISULFID 1 16 By similarity.

FT DISULFID 8 20 By similarity.

FT DISULFID 15 26 By similarity.

FT MOD_RES 26 26 Cysteine amide.

FT SEQUENCE 26 AA; 2790 MW; 56EFC382335C4A8B CRC64;

SQ Query Match 60.8%; Score 73; DB 1; Length 26;

Best Local Similarity 30.8%; Pred. No. 1.3;

Matches 8; Conservative 14; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CXIXNXXCXQLDCCSXCNXXWC 26

Db 1 CKRGQSCSKMLYDCCTGCSRRGKC 26

RESULT 5

NOTC_XENLA STANDARD; PRT; 2524 AA.

AC P21783;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Neurogenic locus notch protein homolog precursor (XOTCH protein).

GN Name=XOTCH;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90385285; PubMed=2402639;

RA Coffman C., Harris W., Kintner C.;

RT "Xotch, the Xenopus homolog of Drosophila notch.",

RL Science 249:1438-1441 (1990).

RN [2]

RP REVISIONS TO 1759-1782.

RA Kintner C.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

CC -|- SUBCELLULAR LOCATION: Type I membrane protein.

CC -|- DEVELOPMENTAL STAGE: Expressed almost uniformly in early embryos.

CC -|- SIMILARITY: Belongs to the NOTCH family.

CC -|- SIMILARITY: Contains 6 ANK repeats.

CC -|- SIMILARITY: Contains 36 EGF-like domains.

CC -|- SIMILARITY: Contains 3 Lin/Notch repeats.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; M33874; AAB02039.1; -

DR HSSP; P46531; 1PB5.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR000152; Asx_hydroxyl_S.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001438; EGF_II.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR010660; NOD.

DR InterPro; IPR008297; Notch.

DR InterPro; IPR000800; Notch_region.

DR Pfam; PF00023; Ank; 6.

DR Pfam; PF00008; EGF; 36.

DR Pfam; PF06816; NOD; 1.

DR Pfam; PF00066; Notch; 3.

DR PIRSF; PIRSF002279; Notch; 1.

DR PRINTS; PR01415; ANKYRIN.

DR PRINTS; PR00010; EGFLOOD.

DR PRINTS; PR01452; NOTCH.

DR SMART; SM00248; ANK; 6.

DR SMART; SM00179; EGF_Ca; 24.

DR SMART; SM00004; NL; 3.

DR PROSITE; PS0297; ANK_REPEAT; 4.

DR PROSITE; PS00088; ANK_REPEAT; 4.

DR PROSITE; PS00010; ASX_HYDROXYL; 23.

DR PROSITE; PS00022; EGF_1; 34.

DR PROSITE; PS01186; EGF_2; 29.

DR PROSITE; PS00026; EGF_3; 36.

DR PROSITE; PS01187; EGF_Ca; 21.

KW ANK repeat; Differentiation; EGF-like domain; Glycoprotein;

KW Neurogenesis; Notch signaling pathway; Repeat; Signal; Transmembrane.

FT SIGNAL 1 19 Potential.

FT CHAIN 20 2524 Neurogenic locus notch protein homolog.

FT DOMAIN 20 1728 Extracellular (Potential).

FT TRANSMEM 1729 1750 Potential.

FT DOMAIN 1751 2524 Cytoplasmic (Potential).

FT DOMAIN 20 57 EGF-like 1.

FT DOMAIN 58 99 EGF-like 2.

FT DOMAIN 102 140 EGF-like 3.

FT DOMAIN 141 177 EGF-like 4.

FT DOMAIN 179 215 EGF-like 5.

FT DOMAIN 217 254 EGF-like 6.

FT DOMAIN 256 292 EGF-like 7.

FT DOMAIN 294 332 EGF-like 8.

FT DOMAIN 334 370 EGF-like 9.

FT DOMAIN 371 409 EGF-like 10.

FT DOMAIN 411 449 EGF-like 11.

FT DOMAIN 451 487 EGF-like 12.

FT DOMAIN 489 525 EGF-like 13.

FT DOMAIN 527 563 EGF-like 14.

FT DOMAIN 565 600 EGF-like 15.

FT DOMAIN 602 638 EGF-like 16.

FT DOMAIN 640 675 EGF-like 17.

FT DOMAIN 677 713 EGF-like 18.

FT DOMAIN 715 750 EGF-like 19.

FT DOMAIN 752 788 EGF-like 20.

FT DOMAIN 790 826 EGF-like 21.

FT DOMAIN 828 866 EGF-like 22.

FT DOMAIN 868 904 EGF-like 23.

FT DOMAIN 906 942 EGF-like 24.

FT DOMAIN 944 980 EGF-like 25.

FT DOMAIN 982 1018 EGF-like 26.

FT DOMAIN 1020 1056 EGF-like 27.

FT DOMAIN 1058 1094 EGF-like 28.

FT DOMAIN 1096 1142 EGF-like 29.

FT DOMAIN 1144 1180 EGF-like 30.

FT DOMAIN 1182 1218 EGF-like 31.

FT DOMAIN 1220 1264 EGF-like 32.

FT DOMAIN 1266 1304 EGF-like 33.

FT DOMAIN 1306 1346 EGF-like 34.

FT DOMAIN 1347 1383 EGF-like 35.

FT DOMAIN 1386 1424 EGF-like 36.

FT REPEAT 1441 1478 Lin/Notch 1.

FT REPEAT 1479 1520 Lin/Notch 2.

FT REPEAT 1521 1560 Lin/Notch 3.

FT REPEAT 1876 1919 ANK 1.

FT REPEAT 1924 1953 ANK 2.

FT REPEAT 1957 1987 ANK 3.

FT REPEAT 1991 2020 ANK 4.

FT REPEAT 2024 2053 ANK 5.


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FT REPEAT 2057 2086 ANK 6.
FT DISULFID 22 35 By similarity.
FT DISULFID 29 45 By similarity.
FT DISULFID 47 56 By similarity.
FT DISULFID 62 74 By similarity.
FT DISULFID 68 87 By similarity.
FT DISULFID 89 98 By similarity.
FT DISULFID 106 117 By similarity.
FT DISULFID 111 128 By similarity.
FT DISULFID 130 139 By similarity.
FT DISULFID 145 156 By similarity.
FT DISULFID 150 165 By similarity.
FT DISULFID 167 176 By similarity.
FT DISULFID 183 194 By similarity.
FT DISULFID 188 203 By similarity.
FT DISULFID 205 214 By similarity.
FT DISULFID 221 232 By similarity.
FT DISULFID 226 242 By similarity.
FT DISULFID 244 253 By similarity.
FT DISULFID 260 271 By similarity.
FT DISULFID 265 280 By similarity.
FT DISULFID 282 291 By similarity.
FT DISULFID 298 311 By similarity.
FT DISULFID 305 320 By similarity.
FT DISULFID 322 331 By similarity.
FT DISULFID 338 349 By similarity.
FT DISULFID 343 358 By similarity.
FT DISULFID 360 369 By similarity.
FT DISULFID 375 386 By similarity.
FT DISULFID 380 397 By similarity.
FT DISULFID 399 408 By similarity.
FT DISULFID 415 428 By similarity.
FT DISULFID 422 437 By similarity.
FT DISULFID 439 448 By similarity.
FT DISULFID 455 466 By similarity.
FT DISULFID 460 475 By similarity.
FT DISULFID 477 486 By similarity.
FT DISULFID 493 504 By similarity.
FT DISULFID 498 513 By similarity.
FT DISULFID 515 524 By similarity.
FT DISULFID 531 542 By similarity.
FT DISULFID 536 551 By similarity.
FT DISULFID 553 562 By similarity.
FT DISULFID 569 579 By similarity.
FT DISULFID 574 588 By similarity.
FT DISULFID 590 599 By similarity.
FT DISULFID 606 617 By similarity.
FT DISULFID 611 626 By similarity.
FT DISULFID 628 637 By similarity.
FT DISULFID 644 654 By similarity.
FT DISULFID 649 663 By similarity.
FT DISULFID 665 674 By similarity.
FT DISULFID 681 692 By similarity.
FT DISULFID 686 701 By similarity.
FT DISULFID 703 712 By similarity.
FT DISULFID 719 729 By similarity.
FT DISULFID 724 738 By similarity.
FT DISULFID 740 749 By similarity.
FT DISULFID 756 767 By similarity.
FT DISULFID 761 776 By similarity.
FT DISULFID 778 787 By similarity.
FT DISULFID 794 805 By similarity.
FT DISULFID 799 814 By similarity.
FT DISULFID 816 825 By similarity.
FT DISULFID 832 843 By similarity.
FT DISULFID 837 854 By similarity.
FT DISULFID 856 865 By similarity.
FT DISULFID 872 883 By similarity.
FT DISULFID 877 892 By similarity.
FT DISULFID 894 903 By similarity.
FT DISULFID 910 921 By similarity.
FT DISULFID 915 930 By similarity.
FT DISULFID 932 941 By similarity.

Query Match 60.0%; Score 72; DB 1; Length 2524;
Best Local Similarity 34.6%; Pred. No. 1e+02; Mismatches 5; Indels 0; Gaps 0;
Matches 9; Conservative 12;

QY 2 XIXNQXQXQLDDCGSXCNXXNXCVC 27
DB 247 GFSGQNCENIDDCPSNNCRNGGTVCV 272

RESULT 6
CXOC CONMA STANDARD; PRT; 29 AA.
ID CXOC CONMA STANDARD; PRT; 29 AA.
AC P37300;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Omega-conotoxin MVIIc precursor (SNX-230) (Fragment).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorboconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE FROM N.A., AND SYNTHESIS.
RX MEDLINE=92337922; PubMed=1352986; DOI=10.1016/0896-6273(92)90221-X;
RA Hillyard D.R., Monje V.D., Mintz I.M., Bean B.P., Nadaesi L.,
RA Ramachandran J., Miljanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
RA Cruz L.J., Imperial J.S., Olivera B.M.;
RT "A new Conus peptide ligand for mammalian presynaptic Ca2+ channels.";
RL Neuron 9:69-77(1992).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=95248539; PubMed=7731037;
RA Farr-Jones S., Miljanich G.P., Nadaesi L., Ramachandran J.,
RA Basus V.J.;
RT "Solution structure of omega-conotoxin MVIIc, a high affinity ligand
of P-type calcium channels, using 1H NMR spectroscopy and complete
relaxation matrix analysis.";
RL J. Mol. Biol. 248:106-124(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99303703; PubMed=10733375; DOI=10.1006/jmbi.1999.2817;
RA Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
RA Lewis R.J.;
RT "Structure-activity relationships of omega-conotoxins MVIIA, MVIIc and
14 loop splice hybrids at N and P/Q-type calcium channels.";
RL J. Mol. Biol. 289:1405-1421(1999).
RN [4]
RP MUTAGENESIS OF TYR-15.
RX MEDLINE=95408251; PubMed=7677735;
RA Kim J.I., Takahashi M., Martin-Mouton N., Seagar M.J., Ohtake A.,
RA Sato K.;
RT "Tyr13 is essential for the binding of omega-conotoxin MVIIc to the
P/Q-type calcium channel.";
RL Biochem. Biophys. Res. Commun. 214:305-309(1995).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
and block voltage-sensitive calcium channels (VSCC). This toxin
blocks N-type calcium channels as well as types of high-threshold
voltage-gated calcium channels resistant to both dihydropyridines
and omega-conotoxin GVIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
```


CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; 540826; AAB322674.1; -
 CC PIR; JH0699; JH0699.
 CC PDB; 1CNN; NMR; A=3-29.
 CC PDB; 10MN; NMR; Q=3-29.
 CC 3D-structure; Amidation; Calcium channel inhibitor; Hydroxylation;
 KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
 FT NON_TER 1
 FT PROPEP 1 2
 FT PEPTIDE 3 28
 FT BINDING 15 15
 FT DISULFID 3 18
 FT DISULFID 10 22
 FT DISULFID 17 28
 FT MOD_RES 9 9
 FT MOD_RES 28 28
 FT MUTAGEN 15 15
 FT TURN 6 7
 FT STRAND 9 9
 FT HELIX 12 14
 FT TURN 24 25
 FT STRAND 27 27
 SQ SEQUENCE 29 AA; 3071 MW; AC7A6894E474728A CRC64;
 Query Match 57.5%; Score 69; DB 1; Length 29;
 Best Local Similarity 30.8%; Pred. No. 3.5;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 Y->A: High decrease in binding.
 Hydroxyproline (Probable).
 Cysteine amide (G-29 provides amide group).
 Omega-conotoxin MVIIc.
 Essential for calcium channel binding.
 RESULT 7
 Q6LFM8 PRELIMINARY; PRT; 1820 AA.
 ID Q6LFM8
 AC Q6LFM8
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=MALEP1.41, PFF0185c;
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12368867; DOI=10.1038/nature01035;
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Clark R.,
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corto C.,
 RA Cronin A., Davies R., Davies P., Dear P., Dearden F., Doggett J.,
 RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Horrocks P.,
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
 RA Humphray S., Jagels K., James D., Johnson D., Kerhornou A., Knight A.,
 RA Kontfortov B., Keyes S., Larke N., Lawson D., Lennard N., Line A.,
 RA Maddison M., McLean J., Mooney P., Moule S., Murphy L., Oliver K.,
 RA Ormond D., Price C., Quail M.A., Rabinowitsch E., Rajandream M.A.,
 RA Rutter S., Rutherford K.M., Sanders M., Simmonds M., Seeger K.,
 RA Sharp S., Smith R., Squares R., Stevens K., Taylor K.,
 RA Tivey A., Unwin L., Whitehead S., Woodward J., Sulston J.E., Craig A.,

RA Newbold C., Barrell B.G;
 RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
 RL Nature 419:527-531 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,
 RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
 RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.G;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382398; CAG25208.1; -
 DR InterPro; IPR000875; Cecropin.
 DR InterPro; IPR009077; Prot_act_rega.
 DR PROSITE; PS00286; CECROPIN; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 1820 AA; 218564 MW; 84F330E57FA6150 CRC64;
 Query Match 57.5%; Score 69; DB 2; Length 1820;
 Best Local Similarity 32.1%; Pred. No. 1.5e+02;
 Matches 9; Conservative 12; Mismatches 5; Indels 2; Gaps 1;
 QY 1 CXIXNQXCQXL--DDCCSXKXCNXXNC 26
 Db 1301 CDYNEFCDDCCDDECCDDECCDDEYC 1328
 RESULT 8
 Q646U5 PRELIMINARY; PRT; 74 AA.
 ID Q646U5
 AC Q646U5
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Phytotoxin-like SCR74.
 OS Phytophthora infestans (Potato late blight fungus).
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 OC Phytophthora.
 OX NCBI_TaxID=4787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
 RA Tarto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
 RA Kamoun S.;
 RT "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene
 RT Family of Phytophthora infestans";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY723722; AAU21463.1; -
 DR EMBL; AY723721; AAU21462.1; -
 SQ SEQUENCE 74 AA; 7702 MW; 294DC1A85D1D9FF0 CRC64;
 Query Match 56.7%; Score 68; DB 2; Length 74;
 Best Local Similarity 29.0%; Pred. No. 10;
 Matches 9; Conservative 14; Mismatches 2; Indels 6; Gaps 1;
 QY 2 XIXNQXCQ-----XLDCCSXKXCNXXNC 26
 Db 41 GWSQCKKAINAEFVAFNDCCSCNTGSPC 71
 RESULT 9
 Q646U7 PRELIMINARY; PRT; 74 AA.
 ID Q646U7
 AC Q646U7
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Phytotoxin-like SCR74.
 OS Phytophthora infestans (Potato late blight fungus).
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 OC Phytophthora.
 OX NCBI_TaxID=4787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,

DR PROSITE; PS0297; ANK REP REGION; 1.
DR PROSITE; PS0010; ASX_HYDROXYL; 10.
DR PROSITE; PS0002; EGF_1; 28.
DR PROSITE; PS01186; EGF_2; 21.
DR PROSITE; PS00026; EGF_3; 27.
DR PROSITE; PS01187; EGF_CA; 9.
DR PROSITE; PS00200; RIESKE_2; UNKNOWN_1.
KW ANK repeat; EGF-like domain.
SQ SEQUENCE 1961 AA; 206074 MW; 5B1034E9EE07A3C CRC64;

Query Match 56.7%; Score 68; DB 2; Length 1961;
Best Local Similarity 29.2%; Pred. No. 2e+02;
Matches 7; Conservative 14; Mismatches 3; Indels 0; Gaps

QY 4 XNQXCQXLDDCCSXCNXXNXCVCV 27
: :|::||| :|: :|:
Db 345 GGEGCDENLDCAAATCALGSTCI 368

RESULT 11
NTCL HUMAN
ID NTCL HUMAN STANDARD; PRT; 2556 AA.

AC P46531;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (hnl)
DE (Translocation-associated notch protein TAN-1).
GN Name=NOTCH1; Synonyms=TAN1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Brain;
RA Mann R.S., Blumuellner C.M., Zagouras P.;
RC "Complete human notch 1 (hnl) cDNA sequence.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
[2]
SEQUENCE OF 1-2444 FROM N.A.
RX MEDLINE=91347367; PubMed=1831692; DOI=10.1016/0092-8674(91)90111-B;
RX Ellisen L.W., Bird J., West D.C., Soreng A.L., Reynolds T.C.,
RA Smith S.D., Sklar J.;
RA "TAN-1, the human homolog of the Drosophila notch gene, is broken by
RT chromosomal translocations in T lymphoblastic neoplasms."; Cell
RN Cell 66:649-661(1991).
[3]
IDENTIFICATION OF LIGANDS.
RX MEDLINE=99180765; PubMed=10079256;
RX Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
RT "Human ligands of the Notch receptor."; Ann. J. Pathol. 154:785-794(1999).
[4]
INTERACTION WITH DTG1.
RX MEDLINE=98250176; PubMed=9590294;
RX Matsuno K., Eastman D., Mitsiades T., Quinn A.M., Carcanci M.L.,
RA Ordentlich P., Kadesch T., Artavanis-Tsakonas S.;
RT "Human deltex is a conserved regulator of Notch signalling."; Nat. Genet. 19:74-78(1998).

-!- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta1 to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May be important for normal lymphocyte function. In altered form, may contribute to transformation or progression in some T-cell neoplasms. Involved in the maturation of both CD4+ and CD8+ cells in the thymus (By similarity).
-!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EIC) which are probably linked by disulfide

CC bonds (By similarity). Interacts with DTX1 and DTX2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: In fetal tissues most abundant in spleen,
 CC brain stem and lung. Also present in most adult tissues where it
 CC is found mainly in lymphoid tissues.
 CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(BC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane (By similarity).
 CC -!- PTM: Phosphorylated (By similarity).
 CC -!- DISEASE: NOTCH1 truncation is associated with T-cell acute
 CC lymphoblastic leukemia.
 CC -!- SIMILARITY: Belongs to the NOTCH family.
 CC -!- SIMILARITY: Contains 5 ANK repeats.
 CC -!- SIMILARITY: Contains 36 EGF-like domains.
 CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
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 CC -----
 CC EMBL; AF308602; AAG33848.1; .
 CC EMBL; M73980; AAA60614.1; .
 CC PDB; 1PB5; NMR; A=1447-1481.
 CC Genew; HGNC:7881; NOTCH1.
 CC MIM; 190198; .
 CC GO; GO:0016021; C: integral to membrane; NAS.
 CC GO; GO:0006955; P: immune response; NAS.
 CC InterPro; IPR002110; ANK.
 CC InterPro; IPR00152; Asx_hydroxyl_S.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR001436; EGF_II.
 CC InterPro; IPR006209; EGF_like.
 CC InterPro; IPR010660; NOD.
 CC InterPro; IPR008297; Notch.
 CC InterPro; IPR000800; Notch_region.
 CC Pfam; PF00023; Ank; 6.
 CC Pfam; PF00008; EGF; 35.
 CC Pfam; PF06816; NOD; 1.
 CC Pfam; PF00066; Notch; 3.
 CC PIRSF; PIRSF002279; Notch; 1.
 CC PRINTS; PR01415; ANKYRIN.
 CC PRINTS; PR00010; EGFLOOD.
 CC PRINTS; PR01452; NOTCH.
 CC SMART; SM00248; ANK; 6.
 CC SMART; SM00179; EGF_CA; 23.
 CC SMART; SM00004; NL; 3.
 CC PROSITE; PS00088; ANK_REPEAT; 4.
 CC PROSITE; PS0297; ANK_REPEAT_REGION; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 20.
 CC PROSITE; PS00022; EGF_1; 34.
 CC PROSITE; PS01186; EGF_2; 26.
 CC PROSITE; PS00026; EGF_3; 36.
 CC PROSITE; PS01187; EGF_CA; 18.
 CC 3D-structure; Activator; ANK repeat; Developmental protein;
 CC Differentiation; EGF-like domain; Glycoprotein;
 CC Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal;
 CC Transcription regulation; Transmembrane.
 CC SIGNAL 1 18 Potential.

FT CHAIN	19	2556	Neurogenic locus notch homolog protein 1.
FT CHAIN	1722	2556	Notch extracellular truncation (By
FT			similarity).
FT CHAIN	1755	2556	Notch intracellular domain (By
FT			similarity).
FT DOMAIN	19	1736	Extracellular (Potential).
FT TRANSMEM	1737	1757	Potential.
FT DOMAIN	1758	2556	Cytoplasmic (Potential).
FT DOMAIN	20	58	EGF-like 1.
FT DOMAIN	59	99	EGF-like 2.
FT DOMAIN	102	139	EGF-like 3.
FT DOMAIN	140	176	EGF-like 4.
FT DOMAIN	178	216	EGF-like 5.
FT DOMAIN	218	255	EGF-like 6.
FT DOMAIN	257	293	EGF-like 7.
FT DOMAIN	295	333	EGF-like 8.
FT DOMAIN	335	371	EGF-like 9.
FT DOMAIN	372	410	EGF-like 10.
FT DOMAIN	412	450	EGF-like 11.
FT DOMAIN	450	488	EGF-like 12.
FT DOMAIN	490	526	EGF-like 13.
FT DOMAIN	528	564	EGF-like 14.
FT DOMAIN	565	601	EGF-like 15.
FT DOMAIN	603	639	EGF-like 16.
FT DOMAIN	641	676	EGF-like 17.
FT DOMAIN	678	714	EGF-like 18.
FT DOMAIN	716	751	EGF-like 19.
FT DOMAIN	753	789	EGF-like 20.
FT DOMAIN	791	827	EGF-like 21.
FT DOMAIN	829	868	EGF-like 22.
FT DOMAIN	870	906	EGF-like 23.
FT DOMAIN	908	944	EGF-like 24.
FT DOMAIN	946	982	EGF-like 25.
FT DOMAIN	984	1020	EGF-like 26.
FT DOMAIN	1022	1058	EGF-like 27.
FT DOMAIN	1060	1096	EGF-like 28.
FT DOMAIN	1098	1144	EGF-like 29.
FT DOMAIN	1146	1182	EGF-like 30.
FT DOMAIN	1184	1220	EGF-like 31.
FT DOMAIN	1222	1266	EGF-like 32.
FT DOMAIN	1268	1306	EGF-like 33.
FT DOMAIN	1308	1347	EGF-like 34.
FT DOMAIN	1349	1385	EGF-like 35.
FT DOMAIN	1388	1427	EGF-like 36.
FT REPEAT	1446	1481	Lin/Notch 1.
FT REPEAT	1482	1523	Lin/Notch 2.
FT REPEAT	1524	1563	Lin/Notch 3.
FT REPEAT	1528	1957	ANK 1.
FT REPEAT	1961	1991	ANK 2.
FT REPEAT	1995	2024	ANK 3.
FT REPEAT	2028	2057	ANK 4.
FT REPEAT	2061	2090	ANK 5.
FT DOMAIN	1576	1579	Poly-Val.
FT DOMAIN	1562	1665	Poly-Arg.
FT DOMAIN	1729	1732	Poly-Pro.
FT DOMAIN	1741	1744	Poly-Ala.
FT DOMAIN	1902	1905	Poly-Glu.
FT DOMAIN	2260	2263	Poly-Gly.
FT DOMAIN	2404	2407	Poly-Gln.
FT DOMAIN	2411	2418	Poly-Ser.
FT DOMAIN	2522	2525	Poly-Ser.
FT SITE	1665	1666	Cleavage (by furin-like protease) (By
FT			similarity).
FT DISULFID	24	37	By similarity.
FT DISULFID	31	46	By similarity.
FT DISULFID	48	57	By similarity.
FT DISULFID	63	74	By similarity.
FT DISULFID	68	87	By similarity.
FT DISULFID	89	98	By similarity.
FT DISULFID	106	117	By similarity.
FT DISULFID	111	127	By similarity.
FT DISULFID	129	138	By similarity.
FT DISULFID	144	155	By similarity.

RESULT 14	CRB_DROME	ID	CRB

Receptor; Repeat; Signal; Transcription regulation; Transmembrane.
 FT CHAIN 21 2437 Neurogenic locus notch homolog protein 1.
 FT TRANSMEM 1725 1747 Extracellular (Potential).
 FT DOMAIN 1748 2437 Cytoplasmic (Potential).
 FT DOMAIN 21 57 EGF-like 1.
 FT DOMAIN 58 98 EGF-like 2.
 FT DOMAIN 101 138 EGF-like 3.
 FT DOMAIN 139 175 EGF-like 4.
 FT DOMAIN 177 215 EGF-like 5.
 FT DOMAIN 217 254 EGF-like 6.
 FT DOMAIN 256 292 EGF-like 7.
 FT DOMAIN 294 332 EGF-like 8.
 FT DOMAIN 334 370 EGF-like 9.
 FT DOMAIN 371 409 EGF-like 10.
 FT DOMAIN 411 449 EGF-like 11.
 FT DOMAIN 451 487 EGF-like 12.
 FT DOMAIN 489 524 EGF-like 13.
 FT DOMAIN 526 562 EGF-like 14.
 FT DOMAIN 564 599 EGF-like 15.
 FT DOMAIN 601 637 EGF-like 16.
 FT DOMAIN 639 674 EGF-like 17.
 FT DOMAIN 676 712 EGF-like 18.
 FT DOMAIN 714 749 EGF-like 19.
 FT DOMAIN 751 787 EGF-like 20.
 FT DOMAIN 789 825 EGF-like 21.
 FT DOMAIN 827 865 EGF-like 22.
 FT DOMAIN 867 903 EGF-like 23.
 FT DOMAIN 905 941 EGF-like 24.
 FT DOMAIN 943 979 EGF-like 25.
 FT DOMAIN 981 1017 EGF-like 26.
 FT DOMAIN 1019 1055 EGF-like 27.
 FT DOMAIN 1057 1093 EGF-like 28.
 FT DOMAIN 1095 1141 EGF-like 29.
 FT DOMAIN 1143 1179 EGF-like 30.
 FT DOMAIN 1181 1217 EGF-like 31.
 FT DOMAIN 1219 1263 EGF-like 32.
 FT DOMAIN 1265 1303 EGF-like 33.
 FT DOMAIN 1305 1344 EGF-like 34.
 FT DOMAIN 1346 1382 EGF-like 35.
 FT DOMAIN 1385 1423 EGF-like 36.
 FT REPEAT 1446 1486 Lin/Notch 1.
 FT REPEAT 1487 1520 Lin/Notch 2.
 FT REPEAT 1521 1561 Lin/Notch 3.
 FT REPEAT 1562 1600 ANK 1.
 FT REPEAT 1601 1640 ANK 2.
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 FT REPEAT 11801 11840 ANK 257.
 FT REPEAT 11841 11880 ANK 258.
 FT REPEAT 11881 11920 ANK 259.
 FT REPEAT 11921 11960 ANK 260.
 FT REPEAT 11961 12000 ANK 261.
 FT REPEAT 12001 12040 ANK 262.
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 FT REPEAT 12081 12120 ANK 264.
 FT REPEAT 12121 12160 ANK 265.
 FT REPEAT 12161 12200 ANK 266.
 FT REPEAT 12201 12240 ANK 267.
 FT REPEAT 12241 12280 ANK 268.
 FT REPEAT 12281 12320 ANK 269.
 FT REPEAT 12321 12360 ANK 270.
 FT REPEAT 12361 12400 ANK 271.
 FT REPEAT 12401 12440 ANK 272.
 FT REPEAT 12441 12480 ANK 273.
 FT REPEAT 12481 12520 ANK 274.
 FT REPEAT 12521 12560 ANK 275.
 FT REPEAT 12561 12600 ANK 276.
 FT REPEAT 12601 12640 ANK 277.
 FT REPEAT 12641 12680 ANK 278.
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 FT REPEAT 12841 12880 ANK 283.
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 FT REPEAT 13241 13280 ANK 293.
 FT REPEAT 13281 13320 ANK 294.
 FT REPEAT 13321 13360 ANK 295.
 FT REPEAT 13361 13400 ANK 296.
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 FT REPEAT 13441 13480 ANK 298.
 FT REPEAT 13481 13520 ANK 299.
 FT REPEAT 13521 13560 ANK 300.
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 FT REPEAT 13841 13880 ANK 308.
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 FT REPEAT 14201 14240 ANK 317.
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 FT REPEAT 14361 14400 ANK 321.
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 FT REPEAT 14721 14760 ANK 330.
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 FT REPEAT 16041 16080 ANK 363.
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 FT REPEAT 16481 16520 ANK 374.
 FT REPEAT 16521 16560 ANK 375.
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 FT REPEAT 16641 16680 ANK 378.
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 FT REPEAT 18041 18080 ANK 413.
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 FT REPEAT 18641 18680 ANK 428.
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 FT REPEAT 18921 18960 ANK 435.
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 FT REPEAT 19161 19200 ANK 441.
 FT REPEAT 19201 19240 ANK 442.
 FT REPEAT 19241 19280 ANK 443.
 FT REPEAT 19281 19320 ANK 444.
 FT REPEAT 19321 19360 ANK 445.
 FT REPEAT 19361 19400 ANK 446.
 FT REPEAT 19401 19440 ANK 447.
 FT REPEAT 19441 19480 ANK 448.
 FT REPEAT 19481 19520 ANK 449.
 FT REPEAT 19521 19560 ANK 450.
 FT REPEAT 19561 19600 ANK 451.
 FT REPEAT 19601 19640 ANK 452.
 FT REPEAT 19641 19680 ANK 453.
 FT REPEAT 19681 19720 ANK 454.
 FT REPEAT 19721 19760 ANK 455.


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RC STRAIN=C.B-17; TISSUE=Thymus;
RX MEDLINE=22753192; PubMed=12807718; DOI=10.1093/carcin/bgg071;
RA Tsuji H., Ishii-Obba H., Ukai H., Katsube T., Ogii T.;
RT "Radiation-induced deletions in the 5' end region of Notch1 lead to
RT the formation of truncated proteins and are involved in the
RT development of mouse thymic lymphoma.";
RL Carcinogenesis 24:1257-1268(2003).
DR EMBL; AB100603; BAC77038.1; -.
DR HSSP; P07207; IOT8.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004872; P:cell differentiation; IEA.
DR GO; GO:0030152; P:cell differentiation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR00152; Asx hydroxyl S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 31.
DR Pfam; PF07645; EGF_Ca; 4.
DR Pfam; PF00066; Notch; 3.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_Ca; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS0010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS00026; EGF_3; 35.
DR PROSITE; PS01187; EGF_Ca; 21.
KW ANK repeat; EGF-like domain; Receptor; Transmembrane.
SQ SEQUENCE 2516 AA; 269177 MW; 17FD72740EBD6E35 CRC64;

Query Match 55.8%; Score 67; DB 2; Length 2516;
Best Local Similarity 30.8%; Pred.No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNKCVCV 27
DQ 233 GFAGQNCENVDPCGNNCKNGACV 259

RESULT 18
Q7TQ51
ID Q7TQ51 PRELIMINARY; PRT; 2536 AA.
AC Q7TQ51;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane receptor Notch1 D.
GN Name=Notch1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17; TISSUE=Thymus;
RX MEDLINE=22753192; PubMed=12807718; DOI=10.1093/carcin/bgg071;
RA Tsuji H., Ishii-Obba H., Ukai H., Katsube T., Ogii T.;
RT "Radiation-induced deletions in the 5' end region of Notch1 lead to
RT the formation of truncated proteins and are involved in the
RT development of mouse thymic lymphoma.";
RL Carcinogenesis 24:1257-1268(2003).
DR EMBL; AB100603; BAC77038.1; -.
DR HSSP; P07207; IOT8.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.

us-10-627-685a-1.rup

DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 31.
DR Pfam; PF07645; EGF_Ca; 4.
DR Pfam; PF00066; Notch; 3.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_Ca; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS0010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS00026; EGF_3; 36.
DR PROSITE; PS01187; EGF_Ca; 21.
KW ANK repeat; EGF-like domain; Receptor; Transmembrane.
SQ SEQUENCE 2526 AA; 270583 MW; 017563FCE9703264 CRC64;

Query Match 55.8%; Score 67; DB 2; Length 2526;
Best Local Similarity 30.8%; Pred.No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNKCVCV 27
DQ 243 GFAGQNCENVDPCGNNCKNGACV 268

RESULT 19
NTCL MOUSE
ID NTCL_MOUSE STANDARD; PRT; 2531 AA.
AC Q01705; Q06007; Q61905; Q99JC2; Q9QW58; Q9R0X7;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-JAN-2005 (Rel. 45, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Notch A)
DE (mrl4) (p300).
GN Name=Notch1; Synonyms=Notch;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Embryo;
RX MEDLINE=93194170; PubMed=849489;
RA Franco del Amo F., Gendron-Maguire M., Swiatek P.J., Jenkins N.A.,
RA Copeland N.G., Gridley T.;
RT "Cloning, analysis, and chromosomal localization of Notch-1, a mouse
RT homolog of Drosophila Notch.";
RN Genomics 15:259-264(1993).
RN [2]
RP SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.
RC STRAIN=CD-1; TISSUE=Embryo;
RX MEDLINE=93050801; PubMed=1426644;
RA Reaume A.G., Conlon R.A., Ziringibl R., Yamaguchi T.P., Rossant J.;
RT "Expression analysis of a Notch homologue in the mouse embryo.";
RN Dev. Biol. 154:377-387(1992).
RN [3]
RP SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.
RC TISSUE=Embryo;
RX MEDLINE=93048835; PubMed=1425352;
RA Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M.,
RA Greenspan R.J., McMahon A.P., Gridley T.;
RT "Expression pattern of Notch, a mouse homolog of Drosophila Notch,
RT suggests an important role in early postimplantation mouse
RT development.";
RN Development 115:737-744(1992).
RN [4]

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RC SEQUENCE OF 1161-1547 FROM N.A.
RP STRAIN-C57BL/6 X CBA; TISSUE=Embryo;
RX MEDLINE=93178563; PubMed=8440332; DOI=10.1006/excr.1993.1044;
RT Lardelli M., Lendahl U.;
RA "Mottch A and Mottch B-two mouse Notch homologues coexpressed in a wide
RT variety of tissues.";
RL Exp. Cell Res. 204:364-372(1993).
RN [5]
RP SEQUENCE OF 1659-1673 FROM N.A.
RX MEDLINE=99364499; PubMed=10437788; DOI=10.1016/S0014-5793(99)00901-1;
RA Lee J.S., Ishimoto A., Yanagawa S.I.;
RT "Murine leukemia provirus-mediated activation of the Notch1 gene leads
RT to induction of HES-1 in a mouse T lymphoma cell line, DL-3.";
RL FEBS Lett. 455:276-280(1999).
RN [6]
RP SEQUENCE OF 1950-2201 FROM N.A.
RX MEDLINE=98029496; PubMed=9384671;
RA Messerle M., Folio M., Nehls M., Eggert H., Boehm T.;
RT "Dynamic changes in gene expression during in vitro differentiation of
RT mouse embryonic stem cells.";
RL Cytokines Cell. Mol. Ther. 1:139-143(1995).
RN [7]
RP SEQUENCE OF 1655-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND
RP MUTAGENESIS OF 1651-ARG--ARG-1654.
RX MEDLINE=98318619; PubMed=9653148; DOI=10.1073/pnas.95.14.8108;
RA Isgrat F., Bessia C., Brou C., LeBail O., Jarriault S., Seidah N.G.,
RA Israel A.;
RT "The Notch1 receptor is cleaved constitutively by a furin-like
RT convertase.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112(1998).
RN [8]
RP SEQUENCE OF 1865-2075 FROM N.A., AND DEVELOPMENTAL STAGE IN HAIR
RP FOLLICLES.
RX PubMed=9486742; DOI=10.1083/jcb.121.3.631;
RA Kopan R., Weintraub H.;
RT "Mouse notch: expression in hair follicles correlates with cell fate
RT determination.";
RL J. Cell Biol. 121:631-641(1993).
RN [9]
RP PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21523956; PubMed=11518718; DOI=10.1074/jbc.M107234200;
RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
RT "Murine notch homologs (N1-4) undergo presenilin-dependent
RT proteolysis.";
RL J. Biol. Chem. 276:40268-40273(2001).
RN [10]
RP POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21374376; PubMed=11459941; DOI=10.1073/pnas.161269998;
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
RT "Conservation of the biochemical mechanisms of signal transduction
RT among mammalian Notch family members.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
RN [11]
RP INTERACTION WITH DTX1 AND DTX2.
RX MEDLINE=21123790; PubMed=11226752; DOI=10.1016/S0736-5748(00)00071-X;
RA Kishi N., Tang Z., Maeda Y., Hirai A., Mo R., Ito M., Suzuki S.,
RA Nakao K., Kinoshita T., Kadesch T., Hui C.-C., Artavanis-Tsakonas S.,
RA Okano H., Matsuno K.;
RT "Murine homologs of Deltex define a novel gene family involved in
RT vertebrate Notch signaling and neurogenesis.";
RL Int. J. Dev. Neurosci. 19:21-35(2001).
RN [12]
RP FUNCTION: Functions as a receptor for membrane-bound ligands
CC Jagged1, Jagged2 and Deltal to regulate cell-fate determination.
CC Upon ligand activation through the released notch intracellular
CC domain (NICD) it forms a transcriptional activator complex with
CC RBP-J kappa and activates genes of the enhancer of split locus.
CC Affects the implementation of differentiation, proliferation and
CC apoptotic programs (By similarity). May play an essential role in
CC postimplantation development, probably in some aspect of cell
CC specification and/or differentiation. May be involved in mesoderm
CC development, somitre formation and neurogenesis. Involved in the
CC maturation of both CD4+ and CD8+ cells in the thymus. Important
CC for follicular differentiation and possibly cell fate selection

CC within the follicle.
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
CC terminal fragment N(EC) which are probably linked by disulfide
CC bonds. Interacts with DTX1 and DTX2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
CC proteolytical processing NICD is translocated to the nucleus.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoID=Q01705-1; Sequences=Displayed;
CC Name=2;
CC IsoID=Q01705-2; Sequence=VSP_001402, VSP_001403, VSP_001404;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in the brain, lung and
CC thymus. Expressed at lower levels in the spleen, bone-marrow,
CC spinal cord, eyes, mammary gland, liver, intestine, skeletal
CC muscle, kidney and heart. In the hair follicle, highly expressed
CC exclusively in the epithelial compartment.
CC -!- DEVELOPMENTAL STAGE: First detected in the mesoderm at 7.5 dpc By
CC 8.5 dpc highly expressed in presomitic mesoderm, mesenchyme and
CC endothelial cells, while much lower levels are seen in the
CC neuroepithelium. Between 9.5-10.5 dpc expressed at high levels in
CC the neuroepithelium. At 13.5 dpc expressed in the surface
CC ectoderm, eye and developing whisker follicles. Hair follicle
CC matrix cells expression starts as different cell types become
CC distinguishable in the developing follicle. Expression persists
CC throughout the growth phase of the follicle and maintains the same
CC expression profile in the second hair cycle. The cells in the
CC follicle that undergo a phase of high level expression are in
CC transition from mitotic precursors to several discreet,
CC differentiating cell types.
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
CC which is proteolytically cleaved by a furin-like convertase in the
CC trans-Golgi network before it reaches the plasma membrane to yield
CC an active, ligand-accessible form. Cleavage results in a C-
CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
CC ligand binding, it is cleaved by TNF-alpha converting enzyme
CC (TACE) to yield a membrane-associated intermediate fragment called
CC notch extracellular truncation (NEXT). This fragment is then
CC cleaved by presenilin dependent gamma-secretase to release a
CC notch-derived peptide containing the intracellular domain (NICD)
CC from the membrane.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Belongs to the NOTCH family.
CC -!- SIMILARITY: Contains 5 ANK repeats.
CC -!- SIMILARITY: Contains 36 EGF-like domains.
CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z11886; CAA77941.1; -
CC EMBL; L02613; AAK14898.1; -
CC EMBL; X68278; CAA48339.1; -
CC EMBL; AJ238029; CAB40733.1; -
CC EMBL; X82562; CAA57909.1; -
CC PIR; A46019; A46019.
CC PIR; B49175; B49175.
CC HSSP; P46531; 1PB5.
CC MGD; MGI-97363; Notch1.
CC GO; GO:0005887; C:integral to plasma membrane; IC.
CC GO; GO:0005515; F:protein binding; IFI.
CC GO; GO:0030154; P:cell differentiation; IMP.
CC GO; GO:0007386; P:compartment specification; IMP.
CC GO; GO:0007369; P:determination of left/right symmetry; IMP.
CC GO; GO:0007215; P:Notch signaling pathway; IC.
CC GO; GO:0045944; P:positive regulation of transcription from P. .; IDA.
CC GO; GO:0048103; P:somatic stem cell renewal; IDA.


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DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR010660; NOD.
DR InterPro; IPR008297; Notch.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00023; Ank; 7.
DR Pfam; PF00008; EGF; 35.
DR Pfam; PF06816; NOD; 1.
DR Pfam; PF00066; Notch; 3.
DR PIRSF; PIRSF002279; Notch; 1.
DR PRINTS; PR01415; ANKYRIN.

Query Match 55.8%; Score 67; DB 1; Length 2531;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXXCNXXNVCV 27
DB 248 GFAGQNCENVDCCPGNNCKNGGACV 273

RESULT 20
NTCL RAT
ID NTCL RAT STANDARD; PRT; 2531 AA.
AC Q07008;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1).
GN Name=Notch1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Schwann cell;
RX MEDLINE=92111383; PubMed=1764995;
RA Weinmaster G., Roberts V.J., Lenke G.;
RT "A homolog of Drosophila Notch expressed during mammalian
RL development.";
RL Development 113:199-205 (1991).
RN [2]
RP REVISIONS TO 1652-1653.
RA Weinmaster G.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=21094508; PubMed=11182080; DOI=10.1016/S0896-6273(01)00179-9;
RA Tanigaki K., Nogaki F., Takahashi J., Tashiro K., Kurooka H.,
RA Honjo T.;
RT "Notch1 and Notch3 instructively restrict bFGF-responsive multipotent
RT neural progenitor cells to an astroglial fate.";
RL Neuron 29:45-55 (2001).
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=93202015; PubMed=1295745;
RA Weinmaster G., Roberts V.J., Lenke G.;
RT "Notch2: a second mammalian Notch gene.";
RL Development 116:931-941 (1992).
RN [5]
RP TISSUE SPECIFICITY.
RX MEDLINE=21331789; PubMed=11438922; DOI=10.1002/cne.1059.abs;
RA Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;
RT "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple
RT functional roles for the Notch-DSL signaling system during brain
RT development.";
RL J. Comp. Neurol. 436:167-181 (2001).
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands

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CC Jagged1, Jagged2 and Deltal to regulate cell-fate determination.
CC Upon ligand activation through the released notch intracellular
CC domain (NICD) it forms a transcriptional activator complex with
CC REP-J kappa and activates genes of the enhancer of split locus.
CC Affects the implementation of differentiation, proliferation and
CC apoptotic programs (By similarity). Acts instructively to control
CC the cell fate determination of CNS multipotent progenitor cells,
CC resulting in astroglial induction and neuron/oligodendrocyte
CC suppression.
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
CC terminal fragment N(EC) which are probably linked by disulfide
CC bonds (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
CC proteolytical processing NICD is translocated to the nucleus (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Expressed in the brain, kidney and spleen.
CC Expressed in postnatal central nervous system (CNS) germinal zones
CC and, in early postnatal life, within numerous cells throughout the
CC CNS. Found in both subventricular and ventricular germinal zones.
CC -!- DEVELOPMENTAL STAGE: In the embryo, highest levels occur between
CC days 12 and 14 and decrease rapidly to much lower levels in the
CC adult.
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
CC which is proteolytically cleaved by a furin-like convertase in the
CC trans-Golgi network before it reaches the plasma membrane to yield
CC an active, ligand-accessible form. Cleavage results in a C-
CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
CC ligand binding, it is cleaved by TNF-alpha converting enzyme
CC (TACE) to yield a membrane-associated intermediate fragment called
CC notch extracellular truncation (NEXT). This fragment is then
CC cleaved by presenilin dependent gamma-secretase to release a
CC notch-derived peptide containing the intracellular domain (NICD)
CC from the membrane (By similarity).
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the NOTCH family.
CC -!- SIMILARITY: Contains 5 ANK repeats.
CC -!- SIMILARITY: Contains 36 EGF-like domains.
CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.

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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/
CC or send an email to license@sib-sib.ch).
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DR EMBL; X57405; CAA40667.1; -.
DR HSSP; P46531; 1PB5.
DR RGD; 3187; Notch1.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR010660; NOD.
DR InterPro; IPR008297; Notch.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 35.
DR Pfam; PF06816; NOD; 1.
DR Pfam; PF00066; Notch; 3.
DR PIRSF; PIRSF002279; Notch; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00010; EGFBELOD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_CA; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.

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PROSITE; PS00022; EGF_1; 35.	FT	DISULFID	106	117	By similarity.
PROSITE; PS01186; EGF_2; 26.	FT	DISULFID	111	127	By similarity.
PROSITE; PS00026; EGF_3; 36.	FT	DISULFID	129	138	By similarity.
PROSITE; PS01187; EGF_CA; 21.	FT	DISULFID	144	155	By similarity.
Activator; ANK repeat. Developmental protein; Differentiation;	FT	DISULFID	149	164	By similarity.
EGF-like domain; Glycoprotein; Notch signaling pathway;	FT	DISULFID	166	175	By similarity.
Phosphorylation; Receptor; Signal; transcription regulation;	FT	DISULFID	182	195	By similarity.
Transmembrane.	FT	DISULFID	189	204	By similarity.
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CHAIN	1711				
CHAIN	1744				
Potential.	2531				
Neurogenic locus notch homolog protein 1.	18				
Notch extracellular truncation (By	19				
similarity).	2531				
Notch intracellular domain (By	1744				
similarity).	2531				
Extracellular (Potential).	19				
Potential.	1723				
Cytoplasmic (Potential).	1747				
EGF-like 1.	20				
EGF-like 2.	59				
EGF-like 3.	102				
EGF-like 4.	140				
EGF-like 5.	176				
EGF-like 6.	218				
EGF-like 7.	255				
EGF-like 8.	293				
EGF-like 9.	333				
EGF-like 10.	371				
EGF-like 11.	412				
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EGF-like 13.	488				
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EGF-like 15.	564				
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EGF-like 281.	10671				
EGF-like 282.					


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DR InterPro; IPR001438; EGF II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR008297; Notch-like.
DR InterPro; IPR008000; Notch_region.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 30.
DR Pfam; PF07645; EGF CA; 5.
DR Pfam; PF00666; Notch; 3.
DR PIRSF; PIRSF002279; Notch; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF CA; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS50088; ANK REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 27.
DR PIRSF; PIRSF002279; Notch; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF CA; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS50088; ANK REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS50026; EGF_3; 36.
DR PROSITE; PS01187; EGF CA; 21.
KW ANK repeat; EGF-like domain.
SQ SEQUENCE 2531 AA; 270819 MW; 7DB7E0DEF799D999 CRC64;

Query Match 55.8%; Score 67; DB 2; Length 2531;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNXCVCV 27
DB 248 GFAGQNCENVDPCGNCKNGGACV 273

RESULT 22
QY7TQ50
ID Q77Q50 PRELIMINARY; PRT; 2531 AA.
AC Q77Q50;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane receptor Notch1.
GN Name=Notch1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C.B-17; TISSUE=Thymus;
RA MEDLINE=22753192; PubMed=12807718; DOI=10.1093/carcin/bgg071;
RX Teuji H., Ishii-Onba H., Ukai H., Katsube T., Ogii T.;
RT "Radiation-induced deletions in the 5' end region of Notch1 lead to
the formation of truncated proteins and are involved in the
development of mouse thymic lymphoma."
RL Carcinogenesis 24:1257-1268 (2003).
DR EMBL; AB106603; BAC77040.1; -.
DR HSSP; P07207; 10T8.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; ASX hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF CA.
DR InterPro; IPR006209; EGF-like.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 31.
DR Pfam; PF07645; EGF CA; 4.
DR Pfam; PF00066; Notch; 3.
DR SMART; SM00248; ANK; 6.

Query Match 55.8%; Score 67; DB 2; Length 2531;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNXCVCV 27
DB 248 GFAGQNCENVDPCGNCKNGGACV 273

RESULT 22
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ID Q77Q50 PRELIMINARY; PRT; 2531 AA.
AC Q77Q50;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane receptor Notch1.
GN Name=Notch1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C.B-17; TISSUE=Thymus;
RA MEDLINE=22753192; PubMed=12807718; DOI=10.1093/carcin/bgg071;
RX Teuji H., Ishii-Onba H., Ukai H., Katsube T., Ogii T.;
RT "Radiation-induced deletions in the 5' end region of Notch1 lead to
the formation of truncated proteins and are involved in the
development of mouse thymic lymphoma."
RL Carcinogenesis 24:1257-1268 (2003).
DR EMBL; AB106603; BAC77040.1; -.
DR HSSP; P07207; 10T8.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; ASX hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF CA.
DR InterPro; IPR006209; EGF-like.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 31.
DR Pfam; PF07645; EGF CA; 4.
DR Pfam; PF00066; Notch; 3.
DR SMART; SM00248; ANK; 6.
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DR SMART; SM00179; EGF CA; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS50026; EGF_3; 36.
DR PROSITE; PS01187; EGF CA; 21.
KW ANK repeat; EGF-like domain; Receptor; Transmembrane.
SQ SEQUENCE 2531 AA; 270832 MW; 97C91F69BABF02BF CRC64;

Query Match 55.8%; Score 67; DB 2; Length 2531;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNXCVCV 27
DB 248 GFAGQNCENVDPCGNCKNGGACV 273

RESULT 23
QYIAT6
ID Q9IAT6 PRELIMINARY; PRT; 664 AA.
AC Q9IAT6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DeltaC.
GN Name=dlc; Synonyms=delC;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RC MEDLINE=20054100; PubMed=10585570; DOI=10.1016/S0925-4773(99)00231-2;
RA Smithers L.E., Haddon C., Jiang Y.-J., Lewis J.;
RT "Sequence and embryonic expression of deltaC in the zebrafish."
RL Mech. Dev. 90:119-123 (2000).
DR EMBL; AF146429; AAF27299.1; -.
DR HSSP; P00740; 1EDM.
DR ZFIN; ZDB-GENE-000125-4; dlc.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; ASX hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF CA.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF-like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 7.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF CA; 2.
KW EGF-like domain.
SQ SEQUENCE 664 AA; 72547 MW; 0AD6C34C8579116B CRC64;

Query Match 55.0%; Score 66; DB 2; Length 664;
Best Local Similarity 30.8%; Pred. No. 1.2e+02;
Matches 8; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNXCVCV 27
DB 411 GFTGRCETNIDDCSSNPQNAGTCV 436
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RESULT 24
Q91902 PRELIMINARY; PRT; 721 AA.
AC Q91902;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE X-Delta-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319507; PubMed=7596411; DOI=10.1038/375787a0;
RA Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
RT "Expression of a Delta homologue in prospective neurons in the
RT chick.";
RL Nature 375:787-790(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319503; PubMed=7596407; DOI=10.1038/375761a0;
RA Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;
RT "Primary neurogenesis in Xenopus embryos regulated by a homologue of
RT the Drosophila neurogenic gene Delta.";
RL Nature 375:761-766(1995).
DR EMBL; L42229; AAC38017.1; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF CA; 4.
DR PROSITE; PS00010; ASX HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;

Query Match 55.0%; Score 66; DB 2; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXGXNXXNC 26
Db 436 GFSGRNCDNLDCTSFPCQNGTC 460

RESULT 25
Q61Q50 PRELIMINARY; PRT; 1317 AA.
AC Q61Q50;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE NOTCH2 protein (Fragment).
GN Name=NOTCH2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 28 EGF-like domains.
DR EMBL; BC071562; AAH71562.1; -.
DR HSSP; P00743; 1APO.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR00152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF; 22.
DR Pfam; PF07645; EGF_CA; 5.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00181; EGF; 31.
DR SMART; SM00179; EGF CA; 30.
DR PROSITE; PS00010; ASX HYDROXYL; 21.
DR PROSITE; PS00022; EGF_1; 28.
DR PROSITE; PS01186; EGF_2; 25.
DR PROSITE; PS00026; EGF_3; 31.
DR PROSITE; PS01187; EGF_CA; 21.
KW EGF-like domain.
FT NON_TER 1
SQ SEQUENCE 1317 AA; 140756 MW; 1A2674F4AF001646 CRC64;

Query Match 55.0%; Score 66; DB 2; Length 1317;
Best Local Similarity 25.8%; Pred. No. 2.2e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 CXIXN-----QXCXQXLDCCSXGXNXXNCV 27
Db 406 CVCVNGSGDDCSENIDDCAFASCTPGSTCI 436

RESULT 26
Q9NGV4 PRELIMINARY; PRT; 1551 AA.
ID Q9NGV4
AC Q9NGV4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE SP1070.
GN Name=SP1070;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

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DR InterPro; IPR008297; Notch.
DR InterPro; IPR008000; Notch_region.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 32.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF00066; Notch; 3.
DR PIRSF; PIRSF002279; Notch; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; Ank; 6.
DR SMART; SM00179; EGF_CA; 22.
DR SMART; SM00004; NL_3.
DR PROSITE; PSS0088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 29.
DR PROSITE; PS00026; EGF_3; 35.
DR PROSITE; PS01187; EGF_CA; 20.
KW ANK repeat; EGF-like domain.
FT NON_TER
SQ SEQUENCE 2447 AA; 262542 MW; 1A8E2A372A085D84 CRC64;

Best Match 55.0%; Score 66; DB 2; Length 2447;
Query Local Similarity 29.0%; Pred.No. 3.9e+02;
Matches 9; Conservative 15; Mismatches 3; Indels 4; Gaps
QY 1 CXTYN----QXCQXLDDCCSXKNXXNKC V 27
| : | : : : : : ||| : : : : :
DB 279 CVCVNGWSGLDCSENIDCDTAACSPGSTCV 309

RESULT 28
NTC2_MOUSE STANDARD; PRT; 2470 AA.
AC Q35516; Q06008; Q60941;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Moch B).
DE Name=Notch2;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NPT SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Thymus;
RA Hamada Y., Higuchi M., Tsujimoto Y.;
RT "Complete amino acid sequence and multiform transcripts encoded by a single copy of mouse Notch2 gene."
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RP [2]
RP NPT SEQUENCE OF 316-1518 FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Embryo;
RX MEDLINE=93178563; PubMed=8440332; DOI=10.1006/excr.1993.1044;
RA Lardelli M., Lendahl U.;
RT "Moch A and Moch B-two mouse Notch homologues coexpressed in a wide variety of tissues."
RL Exp. Cell Res. 204:364-372(1993).
RN [3]
RP NPT SEQUENCE OF 1765-2153 FROM N.A.
RX MEDLINE=97075110; PubMed=8917536; DOI=10.1073/pnas.93.23.13014;
RA Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D., Martin D.I.;
RT "Inhibition of granulocytic differentiation by mNotch1."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
RN [4]
RP FUNCTION.
RX MEDLINE=99396706; PubMed=10393120;
RA Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R.

RA Tsubamoto Y.; "Mutation in ankyrin repeats of the mouse Notch2 gene induces early embryonic lethality.";
RL Development 126:3415-3424 (1999).
RN [5]
RP DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
RX MEDLINE=95333893; PubMed=7609614; DOI=10.1016/0169-328X(94)00257-F;
RA Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsubamoto Y.;
RT "Differential expression of Notch1 and Notch2 in developing and adult mouse brain.";
RL Brain Res. Mol. Brain Res. 29:263-272 (1995).
RN [6]
RP POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
RX MEDLINE=21523956; PubMed=11518718; DOI=10.1074/jbc.M107234200;
RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
RT "Murtine notch homologs (N1-4) undergo presenilin-dependent proteolysis.";
RL J. Biol. Chem. 276:40268-40273 (2001).
RN [7]
RP POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
RX MEDLINE=21374376; PubMed=11459941; DOI=10.1073/pnas.161269998;
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
RT "Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031 (2001).
CC -I- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation.
CC -I- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O35516-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O35516-2; Sequence=VSP_001405;
CC Note=No experimental confirmation available;
CC TISSUE SPECIFICITY: Expressed in the brain, liver, kidney, neuroepithelia, somites, optic vesicles and branchial arches, but not heart.
CC -I- DEVELOPMENTAL STAGE: Expressed in the embryonic ventricular zone, the postnatal ependymal cells, and the choroid plexus throughout embryonic and postnatal development.
CC -I- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane.
CC -I- PTM: Phosphorylated.
CC -I- SIMILARITY: Belongs to the NOTCH family.
CC -I- SIMILARITY: Contains 6 ANK repeats.
CC -I- SIMILARITY: Contains 35 EGF-like domains.
CC -I- SIMILARITY: Contains 2 Lin/Notch repeats.
CC -----
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

CC EMBL: D32210; BAA22094.1; -
CC EMBL: X68279; CAA48340.1; -
CC EMBL: U31881; AAC52924.1; -
CC FIR: A49175; A49175.
CC HSSP: Q9UCV4; INZI.
CC MGD: MGI:97364; Notch2.
CC GO: GO:0009886; C:cell surface; ISS.
CC GO: GO:0005887; C:integral to plasma membrane; IC.
CC GO: GO:0005634; C:nucleus; IDA.
CC GO: GO:0003706; F:ligand-regulated transcription factor activity; ISS.
CC GO: GO:0005915; F:protein binding; IPI.
CC GO: GO:0006916; P:anti-apoptosis; ISS.
CC GO: GO:0007050; P:cell cycle arrest; ISS.
CC GO: GO:0001709; P:cell fate determination; TAS.
CC GO: GO:0016049; P:cell growth; ISS.
CC GO: GO:0007368; P:determination of left/right symmetry; IMP.
CC GO: GO:0007275; P:development; ISS.
CC GO: GO:0030097; P:hemopoiesis; ISS.
CC GO: GO:0006917; P:induction of apoptosis; ISS.
CC GO: GO:0002011; P:morphogenesis of an epithelial sheet; IMP.
CC GO: GO:0008285; P:negative regulation of cell proliferation; ISS.
CC GO: GO:0007399; P:neurogenesis; ISS.
CC GO: GO:0007219; P:Notch signaling pathway; IC.
CC GO: GO:0046579; P:positive regulation of RAS protein signal t. . .; ISS.
CC GO: GO:0042060; P:wound healing; IDA.
CC InterPro: IPR002110; ANK.
CC InterPro: IPR000152; ASX_hydroxyl_S.
CC InterPro: IPR000742; EGF_2.
CC InterPro: IPR001881; EGF_Ca.
CC InterPro: IPR001438; EGF_II.
CC InterPro: IPR006209; EGF_like.
CC InterPro: IPR010660; NOD.
CC InterPro: IPR008297; Notch.
CC InterPro: IPR008000; Notch_region.
CC Pfam: PF00023; Ank; 6.
CC Pfam: PF00008; EGF; 34.
CC Pfam: PF06816; NOD; 1.
CC Pfam: PF00066; Notch; 2.
CC Pfam: PF002279; Notch; 1.
CC PRINTS: PR01415; ANKYRIN.
CC PRINTS: PR00010; EGFLOOD.
CC PRINTS: PR01452; NOTCH.
CC SMART: SM00248; ANK; 6.
CC SMART: SM00179; EGF_CA; 23.
CC SMART: SM00004; NL; 3.
CC PROSITE: PS0297; ANK_REPEAT; 1.
CC PROSITE: PS00088; ANK_REPEAT; 4.
CC PROSITE: PS00010; ASX_HYDROXYL; 22.
CC PROSITE: PS00022; EGF_1; 33.
CC PROSITE: PS01186; EGF_2; 27.
CC PROSITE: PS00026; EGF_3; 35.
CC PROSITE: PS01187; EGF_CA; 22.
CC Activator; Alternative splicing; ANK repeat; Developmental protein;
KW Differentiation; EGF-like domain; Glycoprotein;
KW Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal;
KW Transcription regulation; Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 2470 Neurogenic locus notch homolog protein 2.
FT CHAIN 1666 2470 Notch extracellular truncation.
FT CHAIN 1697 2470 Notch intracellular domain.
FT DOMAIN 26 1677 Extracellular (Potential).
FT TRANSMEM 1678 1698 Potential.
FT DOMAIN 1699 2470 Cytoplasmic (Potential).
FT DOMAIN 26 63 EGF-like 1.
FT DOMAIN 64 102 EGF-like 2.
FT DOMAIN 105 143 EGF-like 3.
FT DOMAIN 144 180 EGF-like 4.
FT DOMAIN 182 219 EGF-like 5, calcium-binding (Potential).
FT DOMAIN 221 256 EGF-like 6 (incomplete).

[6]
 MEDLINE=99180765; PubMed=10079256;
 Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
 Banks A., Lelman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
 "Human ligands of the Notch receptor.";
 Am. J. Pathol. 154:785-794 (1999).
 -!- FUNCTION: Functions as a receptor for membrane-bound ligands
 Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.
 Upon ligand activation through the released notch intracellular
 domain (NICD) it forms a transcriptional activator complex with
 RBP-J kappa and activates genes of the enhancer of split locus.
 Affects the implementation of differentiation, proliferation and
 apoptotic programs (By similarity).
 -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TW) and a N-
 terminal fragment N(EC) which are probably linked by disulfide
 bonds (By similarity).
 -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
 proteolytical processing NICD is translocated to the nucleus.
 -!- TISSUE SPECIFICITY: Expressed in the brain, heart, kidney, lung,
 skeletal muscle and liver.
 -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 which is proteolytically cleaved by a furin-like convertase in the
 trans-Golgi network before it reaches the plasma membrane to yield
 an active, ligand-accessible form. Cleavage results in a C-
 terminal fragment N(TW) and a N-terminal fragment N(EC). Following
 ligand binding, it is cleaved by TNF-alpha converting enzyme
 (TACE) to yield a membrane-associated intermediate fragment called
 notch extracellular truncation (NEXT). This fragment is then
 cleaved by presenilin dependent gamma-secretase to release a
 notch-derived peptide containing the intracellular domain (NICD)
 from the membrane (By similarity).
 -!- PTM: Phosphorylated (By similarity).
 -!- SIMILARITY: Belongs to the NOTCH family.
 -!- SIMILARITY: Contains 6 ANK repeats.
 -!- SIMILARITY: Contains 35 EGF-like domains.
 -!- SIMILARITY: Contains 2 Lin/Notch repeats.

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 cial entities requires a license agreement (See <http://www.isb-sib.ch/annou>
 or send an email to license@isb-sib.ch).

 ENBL; AF308601; AAA36377.2;
 ENBL; AF315356; RAG37073.1;
 ENBL; U77493; AAB19224.1;
 HSP; P00740; IEDM.
 Genew; HGNC:7882; NOTCH2.
 MIM; 600275;
 GO; GO:0009986; C:cell surface; IDA.
 GO; GO:0005887; C:integral to plasma membrane; IDA.
 GO; GO:0005633; C:nucleus; IDA.
 GO; GO:0003706; F:ligand-regulated transcription factor activity; TAS.
 GO; GO:0005515; F:protein binding; NAS.
 GO; GO:0046983; F:protein heterodimerization activity; NAS.
 GO; GO:0004872; F:receptor activity; NAS.
 GO; GO:0006916; P:anti-apoptosis; TAS.
 GO; GO:0007050; P:cell cycle arrest; IDA.
 GO; GO:0001709; P:cell fate determination; TAS.
 GO; GO:0016049; P:cell growth; IDA.
 GO; GO:0007368; P:determination of left/right symmetry; ISS.
 GO; GO:0030097; P:hemoipoiesis; TAS.
 GO; GO:0006917; P:induction of apoptosis; TAS.
 GO; GO:0002011; P:morphogenesis of an epithelial sheet; ISS.
 GO; GO:0008285; P:negative regulation of cell proliferation; IDA.
 GO; GO:0007399; P:neurogenesis; NAS.
 GO; GO:0007219; P:Notch signaling pathway; ISS.
 GO; GO:0046579; P:positive regulation of RAS protein signal t...; IDA
 GO; GO:0019827; P:stem cell maintenance; TAS.
 InterPro; IPR020110; ANK.

Nature 398:525-529 (1999).
[12]
S2 CUEAVAGE BY KUZ.
MEDLINE=21657146; PubMed=11799064; DOI=10.1101/gad.942302;
Lieber T., Kidd S., Young M.W.;
"kuzbanian-mediated cleavage of Drosophila Notch.";
Genes Dev. 16:209-221(2002).
[13]
MUTANT MCD5.
MEDLINE=21575956; PubMed=11719214; DOI=10.1016/S0960-9822(01)00562-0;
Ramin P., Khochumian K., Seugnet L., Arbogast N., Ackermann C.,
Heitler P.;
"Novel Notch alleles reveal a Delta-dependent pathway repressing
neural fate.";
Curr. Biol. 11:1729-1738 (2001).
[14]
REVIEW.
MEDLINE=22256570; PubMed=12369105;
Portin P.;
"General outlines of the molecular genetics of the Notch signalling
pathway in Drosophila melanogaster: a review.";
Hereditas 136:89-96(2002).
-!- FUNCTION: Signaling protein, which regulates, with both positive
and negative signals, the differentiation of at least central and
peripheral nervous system and eye, wing disk, oogenesis, segmental
appendages such as antennae and legs, and muscles, through lateral
inhibition or induction. Functions as a receptor for membrane-
bound ligands Delta and Serrate to regulate cell-fate
determination. Upon ligand activation, and releasing from the cell
membrane, the Notch intracellular domain (NICD) forms a
transcriptional activator complex with Su(H) (Suppressor of
hairless) and activates genes of the E(spl) complex. Essential for
proper differentiation of ectoderm.
-!- SUBUNIT: Interacts with Su(H) when activated. Interacts with Dx
via its ANK repeats.
-!- SUBCELLULAR LOCATION: Type I membrane protein. Upon activation and
S3 cleavage, it is released from the cell membrane and enters into
the nucleus in conjunction with Su(H).
-!- PTM: Upon binding its ligands such as Delta or Serrate, it is
cleaved (S2 cleavage) in its extracellular domain, close to the
transmembrane domain. S2 cleavage is probably mediated by Kuz. It
is then cleaved (S3 cleavage) downstream of its transmembrane
domain, releasing it from the cell membrane. S3 cleavage requires
Psn.
-!- SIMILARITY: Belongs to the NOTCH family.
-!- SIMILARITY: Contains 6 ANK repeats.
-!- SIMILARITY: Contains 36 EGF-like domains.
-!- SIMILARITY: Contains 3 Lin/Notch repeats.

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or send an email to license@isb-sib.ch).

Query Match 55.0%; Score 66; DB 1; Length 2703;
Best Local Similarity 29.2%; Pred. No. 4.3e+02;
Matches 7; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNQCXQXLDDCSXCYNXXNCV 27
:|:::|||||::|::|:
db 822 TGQKCETNDDCVTPNGGTCI 845

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE CG9138-PA.
GN Names=SP1070; ORFNames=CG9138;
OS Drosophila melanogaster [Fruit fly].
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hartis N.L., Harvey D., Heian T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodagat, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
DR EMBL; AB003615; AAF52472.1; -.
DR HSSP; P00740; 1EDM.
DR FlyBase; FBgn0031879; SPI070.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR008985; ConA_like lec_gl.
DR InterPro; IPR000859; CUB_1.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF CA.
DR InterPro; IPR001438; EGF II.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000421; FAS8 C.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR003410; Hyalin.
DR InterPro; IPR002172; LDL receptor A.
DR InterPro; IPR000436; Sushi SCR_CCP.
DR InterPro; IPR001368; TNFR C6.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00431; CUB; 3.
DR Pfam; PF00008; EGF; 12.
DR Pfam; PF07645; EGF CA; 1.
DR Pfam; PF00754; F5_F8 type C; 2.
DR Pfam; PF02494; HVR; 3.
DR Pfam; PF02210; Laminin_G_2; 1.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF00084; Sushi; 7.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00032; CCP; 8.
DR SMART; SM00042; CUB; 3.
DR SMART; SM00179; EGF CA; 9.
DR SMART; SM00231; FAS8C; 2.
DR SMART; SM00192; LDLA; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 11.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS00022; EGF_1; 15.
DR PROSITE; PS01186; EGF_2; 13.
DR PROSITE; PS00026; EGF_3; 16.
DR PROSITE; PS01187; EGF CA; 7.
DR PROSITE; PS01285; FAS8C_1; UNKNOWN_1.
DR PROSITE; PS00022; FAS8C_3; 2.
DR PROSITE; PS00825; HVR; 3.
DR PROSITE; PS01209; LDLA_1; 1.
DR PROSITE; PS00068; LDLA_2; 1.
DR PROSITE; PS00923; SUSHI; 5.
KW EGF-like domain.
SQ SEQUENCE 3396 AA; 369389 MW; E618E9ACEA13E0E5 CRC64;

Query Match 55.0%; Score 66; DB 2; Length 3396;
Best Local Similarity 33.3%; Pred. No. 5.3e+02;


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Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;
QY 4 XNQCXQXLDCCSXCNXXNXC 27
Db 2119 TGNKCQTHIDDCASNPCHGATCV 2142

RESULT 34
Q8AW87
ID Q8AW87 PRELIMINARY; PRT; 726 AA.
AC Q8AW87;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ligand Delta-1.
GN Name=Delta-1;
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
[1]
RN SEQUENCE FROM N.A.
RA Nakamura K., Kikuchi Y., Susaki K., Chiba C., Saito T.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 8 EGF-like domains.
DR EMBL; AB095017; BAC41350.2; -.
DR HSSP; P00740; IEDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR00152; ASX_HYDROXYL_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLLOOD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 17.
DR PROSITE; PS01186; EGF_2; 15.
DR PROSITE; PS01187; EGF_3; 17.
DR PROSITE; PS00026; EGF_3; 17.
DR PROSITE; PS01187; EGF_CA; 7.
DR EGF-like domain; Receptor.
KW EGF-like domain.
FT NON_TER 1
FT NON_TER 752
SQ SEQUENCE 726 AA; 79866 MW; 352A40219AB67F41 CRC64;

Query Match 54.2%; Score 65; DB 2; Length 726;
Best Local Similarity 32.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
QY 2 XIXNQCXQXLDCCSXCNXXNXC 26
Db 437 GFSGRHCDNLDCCASYPANGTGC 461

RESULT 35
O42374
ID O42374 PRELIMINARY; PRT; 752 AA.
AC O42374;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Notch receptor protein (Fragment).
GN Name=notch2; Synonyms=Notch2;
OS Brachydanio rerio (Zebrafish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;
QY 4 XNQCXQXLDCCSXCNXXNXC 27
Db 132 SGDCNQTHIDDCSNPCRNCGTGV 155

RESULT 36
Q9NC90
ID Q9NC90 PRELIMINARY; PRT; 1075 AA.
AC Q9NC90;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Scavenger receptor cysteine-rich protein variant 1.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
[1]
RN SEQUENCE FROM N.A.
RA Pancer Z.;
RL MEDLINE=20542095; PubMed=11069281; DOI=10.1073/pnas.230096397;
RT "Dynamic expresion of multiple scavenger receptor cysteine-rich genes
in coelomocytes of the purple sea urchin.";
Proc. Natl. Acad. Sci. U.S.A. 97:13156-13161(2000).
EMBL; AF228824; AAF76316.1; -.
DR HSSP; P00740; IEDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR InterPro; IPR000152; ASX_hydroxyl_S.
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Query Match          54.2% ; Score 65; DB 2; Length 1290;
Best Local Similarity   26.9%; Pred.No.2.e+02;
Matches      7; Conservative    13; Mismatches     6; Indels       0; Gaps        0;
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OY      2 XIXNOXCXOKLDDCCSXGNXXNKC V 27  
         : . . . . | . . . . ||::|| ::.:|:  
Db      1005 GFTEGCEIDIDDCLSSPCQNGT CI 1030
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RESULT 39  
Q20204 PRELIMINARY; PRT; 1410 AA.  
AC Q20204;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein F4OE10.4.  
GN Names=slt-1; ORFNames=F4OE10.4;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;  
OC Rhabditiidae; Peloderinae; Caenorhabditis.  
OX NCBI_TaxID=6239;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology,";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Smye R.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Smye R.;  
RL Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AL0222270; CAB63434.2; -.  
DR EMBL; Z69792; CAB63434.2; JOINED  
DR EMBL; AL0222270; CAAG93668.3; JOINED.  
DR EMBL; Z69792; CAAG93668.3; -.  
DR PIR; D89711; D89711.  
DR PIR; T22025; T22025.  
DR HSPR; P00740; IEDM.  
DR WormBase; WBGene00004854; slt-1.  
DR WomPep; F4O10.4; CE32412.  
GO; GO:0005509; F:calcium ion binding; IEA.  
GO; GO:0005198; F:structural molecule activity; IEA.  
CO; CO:0007155; P:cell adhesion; IEA.  
InterPro; IPRO00152; Asx hydroxyl S.  
InterPro; IPRO08985; ConA like lec_gl.  
InterPro; IPRO06207; Cys knot_C.  
InterPro; IPRO00742; EGF_2.  
InterPro; IPRO01881; EGF_Ca.  
InterPro; IPRO01438; EGF_I1.  
InterPro; IPRO06209; EGF-like.  
InterPro; IPRO01791; Laminin_G.  
InterPro; IPRO01611; LRR.  
InterPro; IPRO00483; LRR_Cterm.  
InterPro; IPRO00372; LRR_Nterm.  
InterPro; IPRO03591; LRR_TYP.  
InterPro; IPRO03129; TSP_N.  
Pfam; PF00008; EGF_7.  
Pfam; PF02210; Laminin_G_2; 1.  
Pfam; PF01463; LRRC1; 1.  
Pfam; PF01462; LRRT; 4.  
Pfam; PF00560; LRR_1; 17.  
PRINTS; PR00010; EGFBLOOD.  
PRINTS; PR00019; LEURICHPPT.
```


gene in a mouse mammary tumor: generation of truncated Notch4/int3
 mRNAs by retroviral splicing events.";
 J. Virol. 73:5166-5171(1999).
 [6]
 RP MEDLINE=21244657; PubMed=11344305; DOI=10.1073/pnas.091584598;
 RA Uytendaele H., Ho J., Rossant J., Kitajewski J.;
 RT "Vascular patterning defects associated with expression of activated
 Notch4 in embryonic endothelium";
 Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648 (2001).
 [7]
 RP SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS
 OF VAL-1463
 RP MEDLINE=21523956; PubMed=11518718; DOI=10.1074/jbc.M107234200;
 RA Saxena M.T., Schroter E.H., Mumm J.S., Kopan R.;
 RT "Murine notch homologs (N1-4) undergo presenilin-dependent
 proteolysis";
 J. Biol. Chem. 276:40268-40273 (2001).
 [8]
 RP POST-TRANSLATIONAL PROCESSING.
 RP MEDLINE=21374376; PubMed=11459941; DOI=10.1073/pnas.161269998;
 RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
 RT "Conservation of the biochemical mechanisms of signal transduction
 among mammalian Notch family members";
 Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
 Jagged1, Jagged2 and Delta to regulate cell-fate determination.
 Upon ligand activation through the released notch intracellular
 domain (NICD) it forms a transcriptional activator complex with
 RBP-J kappa and activates genes of the enhancer of split locus.
 Affects the implementation of differentiation, proliferation and
 apoptotic programs (By similarity). May regulate branching
 morphogenesis in the developing vascular system.
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 terminal fragment N(EC) which are probably linked by disulfide
 bonds.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
 proteolytical processing NICD is translocated to the nucleus.
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart
 kidney, and at lower levels in the ovary and skeletal muscle. A
 very low expression is seen in the brain, intestine, liver and
 testis.
 CC -1- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during
 embryonic development from 9.0 dpc.
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 which is proteolytically cleaved by a furin-like convertase in the
 trans-Golgi network before it reaches the plasma membrane to yield
 an active, ligand-accessible form. Cleavage results in a C-
 terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 ligand binding, it is cleaved by TNF-alpha converting enzyme
 (TACE) to yield a membrane-associated intermediate fragment called
 notch extracellular truncation (NEXT). This fragment is then
 cleaved by presenilin dependent gamma-secretase to release a
 notch-derived peptide containing the intracellular domain (NICD)
 from the membrane.
 CC -1- PTM: Phosphorylated.
 CC -1- DISEASE: Loss of the extracellular domain causes constitutive
 activation of the Notch protein, which leads to hyperproliferation
 of glandular epithelial tissues and development of mammary
 carcinomas.
 CC -1- SIMILARITY: Belongs to the NOTCH family.
 CC -1- SIMILARITY: Contains 5 ANK repeats.
 CC -1- SIMILARITY: Contains 29 EGF-like domains.
 CC -1- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch.

DR EMBL; M80456; AAB38377.1; -;
 DR EMBL; U43691; AAC52630.1; -;
 DR EMBL; U43691; AAC52631.1; -;
 DR EMBL; AF030001; AAB82004.1; -;
 DR EMBL; AB016771; BAA32281.1; -; ALT SEQ.
 DR EMBL; AB016772; BAA32283.1; -; ALT_INIT.
 DR EMBL; AB016773; BAA32284.1; -; ALT_INIT.
 DR EMBL; AB016774; BAA32285.1; -;
 DR PIR; A38072; TVMVT3.
 DR PIR; T09059; T09059.
 DR HSSP; P08709; 1BP9.
 DR MGD; MGI:107471; Notch4.
 DR GO; GO:0009886; C:cell surface; ISS.
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.
 DR GO; GO:0005634; C:nucleus; ISS.
 DR GO; GO:0003509; F:calcium ion binding; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0049882; F:protein heterodimerization activity; ISS.
 DR GO; GO:0004872; F:receptor activity; ISS.
 DR GO; GO:0001763; P:branching morphogenesis; IMP.
 DR GO; GO:0030154; P:cell fate determination; ISS.
 DR GO; GO:0001709; P:cell fate determination; ISS.
 DR GO; GO:0009790; P:embryonic development; IMP.
 DR GO; GO:0030097; P:hemoiesis; ISS.
 DR GO; GO:0045602; P:negative regulation of endothelial cell dif. .; IMP.
 DR GO; GO:0007219; P:Notch signaling pathway; TAS.
 DR GO; GO:0001569; P:patterning of blood vessels; IMP.
 DR GO; GO:0045893; P:positive regulation of transcription, DNA-d. .; ISS.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; ASX_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR010660; NOD.
 DR InterPro; IPR008297; Notch.
 DR InterPro; IPR000800; Notch_region.
 DR Pfam; PF00023; Ank; 6.
 DR Pfam; PF00008; EGF; 27.
 DR Pfam; PF06816; NOD; 1.
 DR Pfam; PF00666; Notch; 2.
 DR PIRSF; PIRSF02279; Notch; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00010; EGFLOOD.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF_CA; 11.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 5.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 11.
 DR PROSITE; PS00022; EGF_1; 28.
 DR PROSITE; PS01186; EGF_2; 21.
 DR PROSITE; PS50026; EGF_3; 27.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Activator; ANK repeat; Developmental protein; Differentiation;
 KW Direct protein sequencing; EGF-like domain; Glycoprotein;
 KW Notch signaling pathway; Phosphorylation; Proto-oncogene; Receptor;
 KW Repeat; Signal; transcription regulation; Transmembrane.
 FT SIGNAL 1 20
 FT CHAIN 21 1964
 FT CHAIN 1411 1964
 FT CHAIN 1428 1964
 FT CHAIN 1463 1964
 FT CHAIN 1443 1964
 FT DOMAIN 21 1443
 FT TRANSMEM 1444 1464
 FT DOMAIN 1465 1964
 FT DOMAIN 61 112
 FT DOMAIN 115 152
 FT DOMAIN 153 189
 FT DOMAIN 191 229
 EGF-like 5, calcium-binding (Potential).
 EGF-like 4.
 EGF-like 3.
 EGF-like 2.
 EGF-like 1.
 Cytoplasmic (Potential).
 Extracellular (Potential).
 Notch intracellular domain.
 Notch extracellular truncation.
 Transforming protein Int-3.
 Neurogenic locus notch homolog protein 4.
 Potential.


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FT DOMAIN 231 271 EGF-like 6.
FT DOMAIN 273 309 EGF-like 7, calcium-binding (Potential).
FT DOMAIN 311 350 EGF-like 8, calcium-binding (Potential).
FT DOMAIN 352 388 EGF-like 9, calcium-binding (Potential).
FT DOMAIN 389 427 EGF-like 10.
FT DOMAIN 429 470 EGF-like 11, calcium-binding (Potential).
FT DOMAIN 472 508 EGF-like 12, calcium-binding (Potential).
FT DOMAIN 510 546 EGF-like 13, calcium-binding (Potential).

Query Match 54.2%; Score 65; DB 1; Length 1964;
Best Local Similarity 33.3%; Pred. No. 4e+02;
Matches 7; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 7 XCXQXLDCCXXCNXXNCV 27
DB 348 GCENLDDCAATCAPGSTCI 368
      :|::|||::|::|::|::|
      :|::|||::|::|::|::|

RESULT 41
NTC3_MOUSE
ID NTC3_MOUSE STANDARD; PRT; 2318 AA.
AC Q61982;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 25-JAN-2005 (Rel. 46; Last annotation update)
DE Neurogenic locus notch homolog protein 3 precursor (Notch 3).
GN Name=Notch3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR X Swiss Webster;
RX MEDLINE=95001556; PubMed=7918097; DOI=10.1016/0925-4773(94)90081-7;
RA Lardelli M., Dalstrand J., Lendahl U.;
RT "The novel Notch homologue mouse Notch 3 lacks specific epidermal
RT growth factor-repeats and is expressed in proliferating
RT neuroepithelium.";
RL Mech. Dev. 46:123-136(1994).
RN [2]
RN POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21374376; PubMed=11459941; DOI=10.1073/pnas.161269998;
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
RT "Conservation of the biochemical mechanisms of signal transduction
RT among mammalian Notch family members.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands
CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.
CC Upon ligand activation through the released notch intracellular
CC domain (NICD) it forms a transcriptional activator complex with
CC RBP-J kappa and activates genes of the enhancer of split locus.
CC Affects the implementation of differentiation, proliferation and
CC apoptotic programs (By similarity). May play a role during CNS
CC development.
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TW) and a N-
CC terminal fragment N(EC) which are probably linked by disulfide
CC bonds.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
CC proteolytical processing NICD is translocated to the nucleus.
CC -!- TISSUE SPECIFICITY: Proliferating neuroepithelium.
CC -!- DEVELOPMENTAL STAGE: CNS development.
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
CC which is proteolytically cleaved by a furin-like convertase in the
CC trans-Golgi network before it reaches the plasma membrane to yield
CC an active, ligand-accessible form. Cleavage results in a C-

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CC terminal fragment N(TW) and a N-terminal fragment N(EC). Following
CC ligand binding, it is cleaved by TNF-alpha converting enzyme
CC (TACE) to yield a membrane-associated intermediate fragment called
CC notch extracellular truncation (NEXT). This fragment is then
CC cleaved by presenilin dependent gamma-secretase to release a
CC notch-derived peptide containing the intracellular domain (NICD)
CC from the membrane.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Belongs to the NOTCH family.
CC -!- SIMILARITY: Contains 5 ANK repeats.
CC -!- SIMILARITY: Contains 34 EGF-like domains.
CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X74760; CAA52776.1; -.
CC FIRM; S45306; S45306.
CC HSP; P00740; 1EDM.
CC MGD; MGI:99460; Notch3.
CC GO; GO:0005887; C:integral to plasma membrane; IC.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0007219; P:Notch signaling pathway; IC.
CC InterPro; IPR002110; ANK.
CC InterPro; IPR00152; Asx hydroxyl S.
CC InterPro; IPR008985; ConA-like_leg_gl.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR010560; NOD.
CC InterPro; IPR008297; Notch.
CC InterPro; IPR000800; Notch_region.
CC Pfam; PF00023; Ank; 6.
CC Pfam; PF00008; EGF; 33.
CC Pfam; PF08816; NOD; 1.
CC Pfam; PF00066; Notch; 3.
CC PIRSF; PIRSF002279; Notch; 1.
CC PRINTS; PR01415; ANKYRIN.
CC PRINTS; PR00010; EGFBLD.
CC PRINTS; PR01452; NOTCH.
CC SMART; SM00248; ANK; 6.
CC SMART; SM00179; EGF_CA; 19.
CC SMART; SM00004; NL; 3.
CC PROSITE; PS0297; ANK_REPEAT; 1.
CC PROSITE; PS0088; ANK_REPEAT; 4.
CC PROSITE; PS0010; ASX_HYDROXYL; 18.
CC PROSITE; PS00022; EGF_1; 33.
CC PROSITE; PS01186; EGF_2; 27.
CC PROSITE; PS00026; EGF_3; 34.
CC PROSITE; PS01187; EGF_CA; 16.
CC Activator; ANK repeat; Developmental protein; Differentiation;
CC EGF-like domain; Glycoprotein; Notch signaling pathway;
CC Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
CC SIGNAL 1 39 Potential.
CC CHAIN 40 2318 Neurogenic locus notch homolog protein 3.
CC CHAIN 1630 2318 Notch extracellular truncation.
CC CHAIN 1663 2318 Notch intracellular domain.
CC DOMAIN 40 1643 Extracellular.
CC TRANSMEM 1644 1664 Potential.
CC DOMAIN 1665 2318 Cytoplasmic.
CC DOMAIN 2242 2261 PEST.
CC DOMAIN 40 78 EGF-like 1.
CC DOMAIN 79 119 EGF-like 2.
CC DOMAIN 120 157 EGF-like 3.
CC DOMAIN 159 196 EGF-like 4, calcium-binding (Potential).
CC DOMAIN 198 235 EGF-like 5.

```


notch-derived peptide containing the intracellular domain (NICD)
 from the membrane (By similarity).
 -!- PTM: Phosphorylated (By similarity).
 -!- SIMILARITY: Belongs to the NOTCH family.
 -!- SIMILARITY: Contains 5 ANK repeats.
 -!- SIMILARITY: Contains 34 EGF-like domains.
 -!- SIMILARITY: Contains 3 Lin/Notch repeats.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 DR EMBL; AF164486; RAD46653.2; --
 DR HSSP; P00740; 1EDM.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx hydroxyl S.
 DR InterPro; IPR008985; ConA like lec_g1.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001981; EGF Ca.
 DR InterPro; IPR001438; EGF II.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR010660; NOD.
 DR InterPro; IPR008297; Notch.
 DR InterPro; IPR000800; Notch_region.
 DR Pfam; PF00023; Ank; 6.
 DR Pfam; PF00008; EGF; 33.
 DR Pfam; PF06816; NOD; 1.
 DR Pfam; PF00066; Notch; 3.
 DR PIRSF; PIRSF002279; Notch; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00010; EGFLOOD.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF_CA; 20.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS00088; ANK_REPEAT; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 18.
 DR PROSITE; PS00022; EGF 1; 33.
 DR PROSITE; PS01186; EGF 2; 26.
 DR PROSITE; PS00026; EGF 3; 34.
 DR PROSITE; PS01187; EGF_CA; 16.
 KW Activator; ANK repeat; Developmental protein; Differentiation;
 KW EGF-like domain; Glycoprotein; Notch signaling pathway;
 KW Phosphorylation; Receptor; Repeat; Signal; Transcription regulation;
 KW Transmembrane.
 FT SIGNAL 1 40 Potential.
 FT CHAIN 41 2319 Neurogenic locus notch homolog protein 3.
 FT CHAIN 1631 2319 Notch extracellular truncation (By
 similarity).
 FT CHAIN 1664 2319 Notch intracellular domain (By
 similarity).
 FT DOMAIN 41 1645 Extracellular (Potential).
 FT TRANSMEM 1646 1666 Potential.
 FT DOMAIN 1667 2319 Cytoplasmic (Potential).
 FT DOMAIN 41 79 EGF-like 1.
 FT DOMAIN 80 120 EGF-like 2.
 FT DOMAIN 121 158 EGF-like 3.
 FT DOMAIN 160 197 EGF-like 4.
 FT DOMAIN 199 236 EGF-like 5.
 FT DOMAIN 238 274 EGF-like 6.
 FT DOMAIN 276 314 EGF-like 7.
 FT DOMAIN 316 352 EGF-like 8.
 FT DOMAIN 353 391 EGF-like 9.
 FT DOMAIN 393 431 EGF-like 10.
 FT DOMAIN 433 469 EGF-like 11.
 FT DOMAIN 471 507 EGF-like 12.
 FT DOMAIN 509 545 EGF-like 13.
 FT DOMAIN 547 582 EGF-like 14, calcium-binding (Potential).

FT DOMAIN	584	620	EGF-like 15,	calcium-binding (Potential).
FT DOMAIN	622	657	EGF-like 16,	calcium-binding (Potential).
FT DOMAIN	659	695	EGF-like 17,	calcium-binding (Potential).
FT DOMAIN	697	732	EGF-like 18,	
FT DOMAIN	736	772	EGF-like 19,	
FT DOMAIN	773	810	EGF-like 20,	
FT DOMAIN	812	849	EGF-like 21,	calcium-binding (Potential).
FT DOMAIN	851	887	EGF-like 22,	calcium-binding (Potential).
FT DOMAIN	889	924	EGF-like 23,	calcium-binding (Potential).
FT DOMAIN	926	962	EGF-like 24,	calcium-binding (Potential).
FT DOMAIN	964	1000	EGF-like 25,	
FT DOMAIN	1002	1036	EGF-like 26,	
FT DOMAIN	1038	1084	EGF-like 27,	
FT DOMAIN	1086	1122	EGF-like 28,	
FT DOMAIN	1124	1160	EGF-like 29,	calcium-binding (Potential).
FT DOMAIN	1162	1205	EGF-like 30,	calcium-binding (Potential).
FT DOMAIN	1207	1246	EGF-like 31,	
FT DOMAIN	1248	1289	EGF-like 32,	
FT DOMAIN	1291	1327	EGF-like 33,	
FT DOMAIN	1337	1375	EGF-like 34,	
FT REPEAT	1384	1420	Lin/Notch 1.	
FT REPEAT	1425	1461	Lin/Notch 2.	
FT REPEAT	1469	1503	Lin/Notch 3.	
FT REPEAT	1840	1869	ANK 1.	
FT REPEAT	1873	1903	ANK 2.	
FT REPEAT	1907	1936	ANK 3.	
FT REPEAT	1940	1969	ANK 4.	
FT REPEAT	1973	2002	ANK 5.	
FT SITE	1573	1574	Cleavage (by furin-like protease) (By similarity).	
FT DISULFID	44	56	By similarity.	
FT DISULFID	50	67	By similarity.	
FT DISULFID	69	78	By similarity.	
FT DISULFID	84	95	By similarity.	
FT DISULFID	89	108	By similarity.	
FT DISULFID	110	119	By similarity.	
FT DISULFID	125	136	By similarity.	
FT DISULFID	130	146	By similarity.	
FT DISULFID	148	157	By similarity.	
FT DISULFID	164	176	By similarity.	
FT DISULFID	170	185	By similarity.	
FT DISULFID	187	196	By similarity.	
FT DISULFID	203	214	By similarity.	
FT DISULFID	208	224	By similarity.	
FT DISULFID	226	235	By similarity.	
FT DISULFID	242	253	By similarity.	
FT DISULFID	247	262	By similarity.	
FT DISULFID	264	273	By similarity.	
FT DISULFID	280	293	By similarity.	
FT DISULFID	287	302	By similarity.	
FT DISULFID	304	313	By similarity.	
FT DISULFID	320	331	By similarity.	
FT DISULFID	325	340	By similarity.	
FT DISULFID	342	351	By similarity.	
FT DISULFID	357	368	By similarity.	
FT DISULFID	362	379	By similarity.	
FT DISULFID	381	390	By similarity.	
FT DISULFID	397	410	By similarity.	
FT DISULFID	404	419	By similarity.	
FT DISULFID	421	430	By similarity.	
FT DISULFID	437	448	By similarity.	
FT DISULFID	442	457	By similarity.	
FT DISULFID	459	468	By similarity.	
FT DISULFID	475	486	By similarity.	
FT DISULFID	480	495	By similarity.	
FT DISULFID	497	506	By similarity.	
FT DISULFID	513	524	By similarity.	

Query Match 54.2%; Score 65; DB 1; Length 2319;
 Best Local Similarity 30.0%; Pred. NO. 4.7e+02;
 Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;

QY 1 CXIXN---QXCXQXLDCCSXXCNXXNC 26

EMBL; AF058899; AAC14346.1; JOINED.
 DR EMBL; AC004257; AAC04897.1; -.
 DR EMBL; AC004663; AAC15789.1; ALT_INIT.
 DR PIR; S78549; S78549.
 DR HSSP; P00740; IEDM.
 DR Genew; HGNC:7883; NOTCH3.
 DR MIM; 60276; -.
 DR MIM; 125310; -.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx hydroxyl S.
 DR InterPro; IPR008985; ConA-like lec.gl.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR001438; EGF II.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR010660; NOD.
 DR InterPro; IPR008297; Notch.
 DR InterPro; IPR000800; Notch_region.
 DR Pfam; PF00023; ANK; 6.
 DR Pfam; PF00008; EGF; 34.
 DR Pfam; PF06816; NOD; 1.
 DR Pfam; PF00066; Notch; 3.
 DR PIRSF; PIRSF02279; Notch; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00010; EGFLOOD.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF_CA; 19.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS0297; ANK_REPEAT; 1.
 DR PROSITE; PS00088; ANK_REPEAT; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 18.
 DR PROSITE; PS00022; EGF_1; 33.
 DR PROSITE; PS01186; EGF_2; 25.
 DR PROSITE; PS00026; EGF_3; 34.
 DR PROSITE; PS01187; EGF_CA; 16.
 KW Activator; ANK repeat; Developmental protein; Differentiation;
 KW Diseases mutation; EGF-like domain; Glycoprotein;
 KW Notch signaling pathway; Phosphorylation; Polymorphism; Receptor;
 KW Repeat; Signal; Transcription regulation; Transmembrane.
 FT SIGNAL 1 39 Potential.
 FT CHAIN 40 2321 Notch extracellular truncation (By
 FT CHAIN 1629 2321 similarity).
 FT CHAIN 1662 2321 Notch intracellular domain (By
 FT CHAIN 40 1643 similarity).
 FT DOMAIN 1644 1664 Extracellular (Potential).
 FT TRANSMEM 1665 2321 Potential.
 FT DOMAIN 40 77 Cytoplasmic (Potential).
 FT DOMAIN 78 118 EGF-like 1.
 FT DOMAIN 119 156 EGF-like 2.
 FT DOMAIN 158 195 EGF-like 3.
 FT DOMAIN 197 234 EGF-like 5.
 FT DOMAIN 236 272 EGF-like 6.
 FT DOMAIN 312 350 EGF-like 7.
 FT DOMAIN 374 429 EGF-like 8.
 FT DOMAIN 351 389 EGF-like 9.
 FT DOMAIN 391 429 EGF-like 10.
 FT DOMAIN 431 467 EGF-like 11.

Query Match 54.2%; Score 65; DB 1; Length 2321;
 Best Local Similarity 30.0%; Pred. No. 4.7e+02;
 Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;
 QY 1 CXIXN---QXQXLDCCSXCNXNXC 26
 Db 300 CVCVNGWTCESQNIIDCATVCFHGATC 329

RESULT 44
 O16004 PRELIMINARY; PRT; 2531 AA.

AC O16004;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Notch homolog.
 OS Lytechinus variegatus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
 OC Lytechinus.
 OX NCBI_TaxID=7654;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97454256; PubMed=9310331;
 RA Sherwood D.R., McClay D.R.;
 RT "Identification and localization of a sea urchin Notch homologue:
 RT insights into vegetal plate regionalization and Notch receptor
 RT regulation";
 RL Development 124:3363-3374(1997).
 DR EMBL; AF000634; AAB82088.1; -.
 DR PIR; T31070; T31070.
 DR HSSP; P01132; IEGF.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0030154; P:cell differentiation; IEA.
 DR GO; GO:0050793; P:regulation of development; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx hydroxyl S.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR001438; EGF II.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR008297; Notch.
 DR InterPro; IPR000800; Notch_region.
 DR Pfam; PF00023; ANK; 6.
 DR Pfam; PF00008; EGF; 31.
 DR Pfam; PF07645; EGF_CA; 4.
 DR PIRSF; PIRSF02279; Notch; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00010; EGFLOOD.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF_CA; 23.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS00088; ANK_REPEAT; 5.
 DR PROSITE; PS0297; ANK_REPEAT; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 21.
 DR PROSITE; PS00022; EGF_1; 33.
 DR PROSITE; PS01186; EGF_2; 25.
 DR PROSITE; PS00026; EGF_3; 35.
 DR PROSITE; PS01187; EGF_CA; 20.
 KW ANK repeat; EGF-like domain.
 SQ SEQUENCE 2531 AA; 273982 MW; 5BF42BEC627CA303 CRC64;
 Query Match 54.2%; Score 65; DB 2; Length 2531;
 Best Local Similarity 38.1%; Pred. No. 5.1e+02;
 Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;
 QY 7 XCQXLDCCSXCNXNXC 27
 Db 661 NCEEDIDDCSRPCHNGGTCV 681

RESULT 45
 Q25253 PRELIMINARY; PRT; 2653 AA.
 ID O25253
 AC O25253
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Notch homolog Scalloped wings.
 GN Name=Sci;
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).

DE	Phytoxin-like SCR74.
OS	Phytophthora infestans (Potato late blight fungus).
OC	Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OX	Phytophthora.
NCBI_TaxID=4787;	
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA	Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA	Kamoun S.;
RT	"Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene"
RT	Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
RL	EMBL: AY723713; AAU21454.1; -
DR	EMBL: AY723713; AAU21454.1; -
SQ	SEQUENCE 74 AA; 7942 MW; CE020986B607E796 CRC64;
Query Match	53.8%; Score 64.5; DB 2; Length 74;
Best Local Similarity	33.3%; Pred. No.23;
Matches	9; Conservative 11; Mismatches 0; Indels 7; Gaps
Qy	7 XCXQLD-----DCSXXCNXXNC 26 : ::: : :::
Dd	45 KCQAINPDVAFYDCCKSKCNTGSPC 71
RESULT 47	
Q646V5	PRELIMINARY; PRT; 74 AA.
ID	Q646V5
AC	Q646V5;
DT	23-OCT-2004 (TREMBlrel. 28, Created)
DT	25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT	25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE	Phytoxin-like SCR74.
OS	Phytophthora infestans (Potato late blight fungus).
OC	Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OX	Phytophthora.
NCBI_TaxID=4787;	
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA	Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA	Kamoun S.;
RT	"Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene"
RT	Family of Phytophthora infestans;"
RL	Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR	EMBL: AY723711; AAU21452.1; -
SQ	SEQUENCE 74 AA; 7825 MW; 537318AAFF612545 CRC64;
Query Match	53.8%; Score 64.5; DB 2; Length 74;
Best Local Similarity	33.3%; Pred. No.23;
Matches	9; Conservative 11; Mismatches 0; Indels 7; Gaps
Qy	7 XCXQLD-----DCSXXCNXXNC 26 : ::: : :::
Dd	45 KCQAINADPIAFHDCCKSKCNTGSPC 71
RESULT 48	
Q646W1	PRELIMINARY; PRT; 74 AA.
ID	Q646W1
AC	Q646W1;
DT	25-OCT-2004 (TREMBlrel. 28, Created)
DT	25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT	25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE	Phytoxin-like SCR74.
OS	Phytophthora infestans (Potato late blight fungus).
OC	Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OX	Phytophthora.
NCBI_TaxID=4787;	
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA	Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,

SEQUENCE FROM N.A.


```

RX MEDLINE=98148073; PubMed=9478979; DOI=10.1074/jbc.273.9.5235;
RA Moestrup S.K., Kozyraki R., Kristiansen M., Kayen J.H.,
RA Rasmussen H.H., Braut D., Pontillon F., Goda F.O., Christensen E.I.,
RA Hammond T.G., Verroust P.J.;
RT "The intrinsic factor-vitamin B12 receptor and target of teratogenic
RT antibodies is a metal-binding peripheral membrane protein with
RT homology to developmental proteins.";
RL J. Biol. Chem. 273:5235-5242(1998).
DR EMBL; AF022247; AAC71661.1;
DR PIR; T08618; T08618.
DR HSP; P00740; 11XA.
DR GO; GO:000509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_Ca.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00431; CUB; 4.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF_Ca; 3.
DR SMART; SM00042; CUB; 27.
DR SMART; SM00179; EGF_Ca; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS01180; CUB; 27.
DR PROSITE; PS00022; EGF_1; 4.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_Ca; 4.
KW EGF-like domain; Receptor; Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 3623 intrinsic factor-B12 receptor.
SQ SEQUENCE 3623 AA; 398984 MW; 39FB792AC6545240 CRC64;

Query Match 53.3%; Score 64; DB 2; Length 3623;
Best Local Similarity 29.2%; Pred. No. 8.9e+02;
Matches 7; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

OY 4 XNOXCXQXLDCCSXCNXNKCXV 27
DB 425 SGQNTENINDSSNPLNGGTGCI 448

RESULT 55
MTB COLVI
ID MTB COLVI STANDARD; PRT; 43 AA.
AC P27087;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metallothionein B (MTB) (Fragment)
OS Colinus virginianus (Bobwhite quail) (Common bobwhite).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Odontophoridae; Colinus.
OX NCBI_TaxID=9014;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93247066; PubMed=8493164;
RA Shartzer K.L., Kage K., Sobleski R.J., Andrews G.K.;
RA "Evolution of avian metallothionein: DNA sequence analyses of the
RT turkey metallothionein gene and metallothionein cDNAs from pheasant
RT and quail.";
RL J. Mol. Evol. 36:255-262(1993).
CC -!- FUNCTION: Metallothioneins have a high content of cysteine
CC residues that bind various heavy metals.
CC -!- DOMAIN: Class I metallothioneins contain 2 metal-binding domains:
CC four divalent ions are chelated within cluster A of the alpha
CC domain and are coordinated via cysteinyl thiolate bridges to 11
CC cysteine ligands. Cluster B, the corresponding region within the
CC beta domain, can ligate three divalent ions to 9 cysteines.
CC -!- SIMILARITY: Belongs to the metallothionein superfamily. Family 1.
CC -----

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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X62512; CAA44371.1;
DR PIR; S33379; S18174.
DR HSP; P04355; IMRT.
DR InterPro; IPR003019; Metallthion.
DR InterPro; IPR000066; Metallthion_1.
DR InterPro; IPR001212; Somatomedin_B.
DR Pfam; PF00131; Metallothio; 1.
DR PRINTS; PR00860; MTVERTEBRATE.
DR PROSITE; PR00022; SOMATOMEDINE.
DR PROSITE; PS00203; METALLOTHIONEIN_VRT; PARTIAL.
KW Metal-binding; Metal-thiolate cluster.
FT NON_TER 1 1
FT DOMAIN <1 16 Beta.
FT DOMAIN 17 >43 Alpha.
FT METAL 2 2 Cluster B.
FT METAL 6 6 Cluster B.
FT METAL 8 8 Cluster B.
FT METAL 11 11 Cluster B.
FT METAL 13 13 Cluster B.
FT METAL 16 16 Cluster B.
FT METAL 20 20 Cluster A.
FT METAL 21 21 Cluster A.
FT METAL 23 23 Cluster A.
FT METAL 24 24 Cluster A.
FT METAL 28 28 Cluster A.
FT METAL 31 31 Cluster A.
FT METAL 35 35 Cluster A.
FT METAL 37 37 Cluster A.
FT NON_TER 43 43
SQ SEQUENCE 43 AA; 4429 MW; 1612EB40E6EB875 CRC64;

Query Match 52.5%; Score 63; DB 1; Length 43;
Best Local Similarity 33.3%; Pred. No. 20;
Matches 9; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

OY 1 CXIXNQXCQXLDCCSXCNXNKCXV 27
DB 6 CKCKNCRCSRCKSCSCCPCAGNVCV 32

RESULT 56
FBP3 STRPU
ID FBP3 STRPU STANDARD; PRT; 570 AA.
AC P49013;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibropellin-C precursor (Epidermal growth factor-related protein 3)
DE (EGF III) (Fibropellin III).
GN Name=EGF3;
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinozoa;
OC Echinoida; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gastrula;
RX MEDLINE=93273088; PubMed=8500658; DOI=10.1006/dbio.1993.1155;
RA Bisgrove B.W., Raff R.A.;
RA "The SpSGF III gene encodes a member of the fibropellins: EGF repeat-
RT containing proteins that form the apical lamina of the sea urchin
RT embryo.";
RL Dev. Biol. 157:526-538(1993).
CC -!- FUNCTION: Forms the apical lamina, a component of the

```


extracellular matrix.

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- DEVELOPMENTAL STAGE: Low levels in unfertilized eggs and during

CC early cleavage, then rapidly increases in abundance between late

CC morula and mesenchyme blastula stages to maximal levels maintained

CC through subsequent stages.

CC -1- MISCELLANEOUS: Expressed both maternally and zygotically.

CC -1- SIMILARITY: Contains 1 avidin domain.

CC -1- SIMILARITY: Contains 1 CUB domain.

CC -1- SIMILARITY: Contains 8 EGF-like domains.

CC -----

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CC -----

CC EMBL: L07045; AAA30045.1; -.

CC PIR: A48836; A48836.

CC HSP: P00740; IEDM.

CC InterPro: IPR000152; Asx_hydroxyl_S.

CC InterPro: IPR005469; Avidin.

CC InterPro: IPR005468; Avidin/str.

CC InterPro: IPR000859; CUB.

CC InterPro: IPR000742; EGF_2.

CC InterPro: IPR001881; EGF_Ca.

CC InterPro: IPR001438; EGF_II.

CC InterPro: IPR006209; EGF_like.

CC Pfam: PF01382; Avidin; 1.

CC Pfam: PF00431; CUB; 1.

CC Pfam: PF00008; EGF; 8.

CC PRINTS: PR00709; AVIDIN.

CC PROSITE: PR00010; EGF_BLOOD.

CC PROSITE: PS00010; ASX_HYDROXYL; 8.

CC PROSITE: PS00577; AVIDIN; 1.

CC PROSITE: PS01180; CUB; 1.

CC PROSITE: PS00022; EGF_1; 8.

CC PROSITE: PS01186; EGF_2; 7.

CC PROSITE: PS00026; EGF_3; 8.

CC PROSITE: PS01187; EGF_CA; 6.

CC Biotin; Calcium-binding; EGF-like domain; Glycoprotein; Repeat;

KW Signal.

FT CHAIN 1 17 Potential.

FT CHAIN 18 570 Fibropellin C.

FT DOMAIN 18 55 EGF-like 1.

FT DOMAIN 62 175 CUB.

FT DOMAIN 176 212 EGF-like 2, calcium-binding (Potential).

FT DOMAIN 214 250 EGF-like 3, calcium-binding (Potential).

FT DOMAIN 252 288 EGF-like 4, calcium-binding (Potential).

FT DOMAIN 290 326 EGF-like 5, calcium-binding (Potential).

FT DOMAIN 328 364 EGF-like 6, calcium-binding (Potential).

FT DOMAIN 366 402 EGF-like 7.

FT DOMAIN 404 440 EGF-like 8, calcium-binding (Potential).

FT DOMAIN 442 570 Avidin.

FT DISULFID 23 34 By similarity.

FT DISULFID 28 43 By similarity.

FT DISULFID 45 54 By similarity.

FT DISULFID 180 191 By similarity.

FT DISULFID 185 200 By similarity.

FT DISULFID 202 211 By similarity.

FT DISULFID 218 229 By similarity.

FT DISULFID 223 238 By similarity.

FT DISULFID 240 249 By similarity.

FT DISULFID 256 267 By similarity.

FT DISULFID 261 276 By similarity.

FT DISULFID 278 287 By similarity.

FT DISULFID 294 305 By similarity.

FT DISULFID 299 314 By similarity.

FT DISULFID 316 325 By similarity.

FT DISULFID 332 343 By similarity.

FT DISULFID 337 352 By similarity.

FT DISULFID 354 363 By similarity.

FT DISULFID 370 381 By similarity.

FT DISULFID 375 390 By similarity.

FT DISULFID 392 401 By similarity.

FT DISULFID 408 419 By similarity.

FT DISULFID 413 428 By similarity.

FT DISULFID 430 439 By similarity.

FT CARBOHYD 30 30 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 357 357 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 570 AA; 61116 MW; BE665E3E1C05B6EE CRC64;

Query Match 52.5%; Score 63; DB 1; Length 570;

Best Local Similarity 26.9%; Pred. No. 2.1e+02;

Matches 7; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXQXQXLDCCSXXCNXXKCV 27

DB 205 GFTGNCDETDICASAPCRNGACV 230

RESULT 57

Q80W06 PRELIMINARY; PRT; 585 AA.

ID Q80W06

AC Q80W06; 01-JUN-2003 (Tremblrel. 24, Created)

DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)

DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Delta-like 3, isoform 1.

GN Name=Dll3;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altshuler S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Ustin T.B., Toshuyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RL and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RA Strausberg R.

RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Contains 6 EGF-like domains.

DR EMBL: BC052002; AAHS2002.1; -.

DR HSP: P00740; IEDM.

DR MGD: MGI:1096877; Dll3.

DR GO: GO:0005615; C:extracellular space; TAS.

DR GO: GO:0016021; C:integral to membrane; TAS.

DR GO: GO:0007386; P:compartment specification; IMP.

DR InterPro: IPR000742; EGF_2.

DR InterPro: IPR001438; EGF_II.

DR InterPro: IPR006209; EGF_like.


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DR InterPro; IPR006210; IEFG.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00008; EGF; 5.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00181; EGF; 6.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00026; EGF_3; 5.
DR PROSITE; PS00334; MYB_2; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 585 AA; 61125 MW; EB276F508998D4E9 CRC64;

Query Match          52.5%; Score 63; DB 2; Length 585;
Best Local Similarity 30.8%; Pred. No. 2.1e+02;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 2 XIXNQXQXQXLDCCSXXCNXXNXC 27
Db 380 GFAGPRCEHLDLDCAGRACANGTCV 405

RESULT 58
Q8NBS4
AC Q8NBS4; PRELIMINARY; PRT; 587 AA.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein FLJ90821.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano A., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
DR EMBL; AK075302; BAC11535.1; -.
DR HSSP; P00740; 1EDM.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEFG.
DR Pfam; PF00008; EGF; 5.
DR PRINTS; PR00010; EGFBL00D.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS00334; MYB_2; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 587 AA; -61144 MW; 2FF5E3E66789B1B CRC64;

Query Match          52.5%; Score 63; DB 2; Length 587;
Best Local Similarity 30.8%; Pred. No. 2.1e+02;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 2 XIXNQXQXQXLDCCSXXCNXXNXC 27
Db 382 GFAGPRCEHLDLDCAGRACANGTCV 407

RESULT 59:
DL3 RAT
ID DL3 RAT STANDARD; PRT; 589 AA.
AC O88671;
DT 16-OCT-2001 (Rel. 40, Created)

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Delta-like protein 3 precursor (Drosophila Delta homolog 3).
GN Name=Dll3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulter J., Greenfield A., Weinmaster G.;
RT "Rattus norvegicus mRNA for Delta 3: a putative ligand for Notch.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Inhibits primary neurogenesis. May be required to divert
CC neurons along a specific differentiation pathway. Play a role in
CC the formation of somite boundaries during segmentation of the
CC paraxial mesoderm (By similarity).
CC -1- SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The DSL domain is required for binding to the Notch
CC receptor.
CC -1- SIMILARITY: Contains 1 DSL domain.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
CC
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CC
CC EMBL; AF084576; AAC33303.1; -.
DR HSSP; P00740; 1EDM.
DR RGD; 70953; Dll3.
DR GO; GO:0005112; P:Notch binding; ISS.
DR GO; GO:0001709; P:cell fate determination; ISS.
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
DR GO; GO:0007399; P:neurogenesis; ISS.
DR GO; GO:0007219; P:Notch signaling pathway; ISS.
DR GO; GO:0001501; P:skeletal development; ISS.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 5.
DR PRINTS; PR00010; EGFBL00D.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 6.
DR Developmental protein; Differentiation; EGF-like domain;
DR Notch signaling pathway; Repeat; Signal; Transmembrane.
FT SIGNAL 1 32
FT CHAIN 33 589
FT DOMAIN 33 494
FT TRANSMEM 495 515
FT DOMAIN 516 589
FT DOMAIN 174 213
FT DOMAIN 218 251
FT DOMAIN 276 312
FT DOMAIN 314 353
FT DOMAIN 355 391
FT DOMAIN 393 429
FT DOMAIN 431 467
FT DOMAIN 503 511
FT DISULFID 222 233
FT DISULFID 226 239
FT DISULFID 241 250
FT DISULFID 280 291
FT DISULFID 285 300
FT DISULFID 302 311
FT DISULFID 318 329
FT DISULFID 323 341

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L -> P (in dbSNP:1110627).


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FT VARIANT 385 385 /FTID=VAR_016776.
FT FT G->D (in_SCD01).
FT FT /FTID=VAR_009952.
SQ SEQUENCE 618 AA; 64617 MW; 58A9BC0A7DEAD1A0 CRC64;

Query Match 52.5%; Score 63; DB 1; Length 618;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 2 XIXNQXCQXLDCCSXXCNXKCV 27
Db 382 GFAGPRCEHLDCCAGCACAGGTCTV 407

RESULT 62
P79941 PRELIMINARY; PRT; 642 AA.
AC P79941;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Notch ligand X-Delta-2.
GN Name=X-Delta-2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Jen W.C., Wettstein D.A., Chitnis A.B., Kintner C.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U70843; AAB37131.1; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0005509; F.calcium ion binding; IEA.
DR GO; GO:0007154; P.cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF07645; EGF_Ca; 1.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00179; EGF_CA; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
DR EGF-like domain.
SQ SEQUENCE 642 AA; 70667 MW; D7DC31EB9D92820C CRC64;

Query Match 52.5%; Score 63; DB 2; Length 642;
Best Local Similarity 30.8%; Pred. No. 2.3e+02;
Matches 8; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXCQXLDCCSXXCNXKCV 27
Db 415 GFSGPRCELNIDCCASSPCAGGTCTV 440

RESULT 63
Q72XT4 PRELIMINARY; PRT; 642 AA.
AC Q72XT4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE MCS2561 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/gvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044262; AAH44262.1; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0005509; F.calcium ion binding; IEA.
DR GO; GO:0007154; P.cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF07645; EGF_Ca; 1.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
DR EGF-like domain.
SQ SEQUENCE 642 AA; 70655 MW; 56APB4013E1C2AE2 CRC64;

Query Match 52.5%; Score 63; DB 2; Length 642;
Best Local Similarity 30.8%; Pred. No. 2.3e+02;
Matches 8; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

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QY      2 XIXNOXCXOXLDCCSXCNXXNCV 27
Db      415 GFSGPCELNIDDCASSPCANGTCV 440

RESULT 64
JAG2_RAT
ID      JAG2_RAT      STANDARD;      PRT;      1202 AA.
AC      P97607;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DE      Jagged2 (Jagged2) (Fragment).
GN      Name=Jag2;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      NCBI_Taxid=10116;
RP      [1]
RC      SEQUENCE FROM N.A.
RX      MEDLINE=97105852; PubMed=8948600; DOI=10.1006/dbio.1996.0310;
RA      Shawber C., Boulter J., Lindsell C.E., Weinmaster G.;
RT      "Jagged2: a serrate-like gene expressed during rat embryogenesis.";
RL      Dev. Biol. 180:370-376(1996).
CC      -!- FUNCTION: Putative Notch ligand involved in the mediation of Notch
CC      signaling. May have a role in neurogenesis in the peripheral
CC      nervous system, limb development and in the adult brain.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- DEVELOPMENTAL STAGE: At stage E12.5 it is detected in dorsal root
CC      ganglia, AER, and surface ectoderm. At E14.5, found as well in
CC      cranial ganglia, thymus and olfactory epithelia. At E16.5, found as
CC      well in salivary gland, tooth buds and hair follicles.
CC      -!- SIMILARITY: Contains 1 DSL domain.
CC      -!- SIMILARITY: Contains 16 EGF-like domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U70050; AC52946.1; -
DR      HSP; P00743; ICCF.
DR      RGD; 2938; Jag2.
DR      GO; GO:0005887; C: integral to plasma membrane; ISS.
DR      GO; GO:0008083; F: growth factor activity; ISS.
DR      GO; GO:0005112; F: Notch binding; NAS.
DR      GO; GO:0007049; P: cell cycle; ISS.
DR      GO; GO:0030154; P: cell differentiation; NAS.
DR      GO; GO:0001709; P: cell fate determination; NAS.
DR      GO; GO:0009912; P: hair cell fate commitment; ISS.
DR      GO; GO:0030326; P: limb morphogenesis; NAS.
DR      GO; GO:0007219; P: Notch signaling pathway; NAS.
DR      GO; GO:0007605; P: perception of sound; ISS.
DR      GO; GO:0030334; P: regulation of cell migration; ISS.
DR      GO; GO:0042127; P: regulation of cell proliferation; ISS.
DR      GO; GO:0007283; P: spermatogenesis; IEP.
DR      GO; GO:0030217; P: T-cell differentiation; ISS.
DR      GO; GO:0045061; P: thymic T-cell selection; ISS.
DR      InterPro; IPR000152; Asx_hydroxyl_s.
DR      InterPro; IPR001774; DSL.
DR      InterPro; IPR000742; EGF_2.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR001438; EGF_II.
DR      InterPro; IPR006209; EGF_like.
DR      InterPro; IPR009041; PMP_SGCI.
DR      Pfam; PF01414; DSL_1.
DR      Pfam; PF00008; EGF_14.
DR      PRINTS; PR00010; EGFBLD.
DR      PROSITE; PS00010; ASX_HYDROXYL; 10.

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DR      PROSITE; PS00022; EGF_1; 15.
DR      PROSITE; PS01186; EGF_2; 11.
DR      PROSITE; PS00026; EGF_3; 15.
DR      PROSITE; PS01187; EGF_CA; 7.
KW      Calcium-binding; Developmental protein; EGF-like domain; Glycoprotein;
KW      Notch signaling pathway; Repeat; Transmembrane.
FT      NON_TER 1
FT      DOMAIN <1 1085 Extracellular (Potential).
FT      TRANSMEM 1086 1102 Potential.
FT      DOMAIN 1103 1202 Cytoplasmic (Potential).
FT      DOMAIN 132 194 DSL-like 1.
FT      DOMAIN 195 228 EGF-like 2.
FT      DOMAIN 229 259 EGF-like 3.
FT      DOMAIN 261 299 EGF-like 4.
FT      DOMAIN 301 337 EGF-like 5, calcium-binding (Potential).
FT      DOMAIN 339 375 EGF-like 6, calcium-binding (Potential).
FT      DOMAIN 377 413 EGF-like 7, calcium-binding (Potential).
FT      DOMAIN 415 450 EGF-like 8.
FT      DOMAIN 452 488 EGF-like 9.
FT      DOMAIN 490 527 EGF-like 10 (atypical).
FT      DOMAIN 529 589 EGF-like 11, calcium-binding (Potential).
FT      DOMAIN 591 627 EGF-like 12, calcium-binding (Potential).
FT      DOMAIN 629 665 EGF-like 13.
FT      DOMAIN 667 703 EGF-like 14.
FT      DOMAIN 706 742 EGF-like 15, calcium-binding (Potential).
FT      DOMAIN 744 780 EGF-like 16, calcium-binding (Potential).
FT      DISULFID 782 818 By similarity.
FT      DISULFID 199 210 By similarity.
FT      DISULFID 203 216 By similarity.
FT      DISULFID 218 227 By similarity.
FT      DISULFID 230 241 By similarity.
FT      DISULFID 246 258 By similarity.
FT      DISULFID 249 258 By similarity.
FT      DISULFID 265 277 By similarity.
FT      DISULFID 271 287 By similarity.
FT      DISULFID 289 298 By similarity.
FT      DISULFID 305 316 By similarity.
FT      DISULFID 310 325 By similarity.
FT      DISULFID 327 336 By similarity.
FT      DISULFID 343 354 By similarity.
FT      DISULFID 368 374 By similarity.
FT      DISULFID 381 392 By similarity.
FT      DISULFID 386 401 By similarity.
FT      DISULFID 403 412 By similarity.
FT      DISULFID 419 429 By similarity.
FT      DISULFID 423 438 By similarity.
FT      DISULFID 440 449 By similarity.
FT      DISULFID 456 467 By similarity.
FT      DISULFID 461 476 By similarity.
FT      DISULFID 478 487 By similarity.
FT      DISULFID 495 506 By similarity.
FT      DISULFID 500 515 By similarity.
FT      DISULFID 517 526 By similarity.
FT      DISULFID 544 567 Potential.
FT      DISULFID 561 577 By similarity.
FT      DISULFID 579 588 By similarity.
FT      DISULFID 595 606 By similarity.
FT      DISULFID 600 615 By similarity.
FT      DISULFID 617 626 By similarity.
FT      DISULFID 633 644 By similarity.
FT      DISULFID 638 653 By similarity.
FT      DISULFID 655 664 By similarity.
FT      DISULFID 671 682 By similarity.
FT      DISULFID 676 691 By similarity.
FT      DISULFID 693 702 By similarity.
FT      DISULFID 710 721 By similarity.
FT      DISULFID 715 730 By similarity.
FT      DISULFID 732 741 By similarity.
FT      DISULFID 748 759 By similarity.
FT      DISULFID 753 768 By similarity.
FT      DISULFID 770 779 By similarity.
FT      DISULFID 786 797 By similarity.

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FT DISULFID 791 806 By similarity.
FT DISULFID 808 817 By similarity.
SQ SEQUENCE 1202 AA; 129703 MW; 08CB44E571FF8BE CRC64;

Query Match 52.5%; Score 63; DB 1; Length 1202;
Best Local Similarity 23.1%; Pred.No. 4.1e+02;
Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNOXCXQXLDCCSXCNXNXCXV 27
Db 582 GFTGTYCHENIDDCMQPCRNGGTCTI 607

RESULT 65
JAG2_HUMAN
ID JAG2_HUMAN STANDARD; PRT; 1238 AA.
AC Q9Y2I9; Q9UE99; Q9UNK8; Q9V6P9; Q9V6Q0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Jagged 2 precursor (Jagged2) (H2).
GN Names=JAG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=97459705; PubMed=9315665;
RA Luo B., Aster J.C., Hassarjian R.P., Kuo F., Sklar J.;
RT "Isolation and functional analysis of a cDNA for human Jagged2, a gene
RL encoding a ligand for the Notch1 receptor."
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Retal brain;
RX MEDLINE=99180765; PubMed=10079256;
RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
RT "Human ligands of the Notch receptor."
RL Am. J. Pathol. 154:785-794(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Bone marrow;
RX MEDLINE=20130121; PubMed=10626252; DOI=10.1006/geno.1999.6045;
RA Deng Y., Madan A., Banta A.B., Friedman C., Trask B.J., Hood L.,
RA Li L.;
RT "Characterization, chromosomal localization, and the complete 30-kb
RL DNA sequence of the human Jagged2 (JAG2) gene."
RN [4]
RP SEQUENCE OF 17-1238 FROM N.A. (ISOFORM LONG).
RC TISSUE=Heart;
RX MEDLINE=98145947; PubMed=9486542; DOI=10.1016/S0925-4773(97)00146-9;
RA Valsecchi C., Ghezzi C., Ballabio A., Ruggeri E.I.;
RT "JAGGED2: a putative Notch ligand expressed in the apical ectodermal
RL ridge and in sites of epithelial-mesenchymal interactions."
RL Mech. Dev. 69:203-207(1997).

CC -1- FUNCTION: Putative Notch ligand involved in the mediation of Notch
CC signaling. Involved in limb development (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q9Y2I9-1; Sequence=Displayed;
CC Name=Short; Synonyms=HJAG2.del-E6;
CC IsoId=Q9Y2I9-2; Sequence=VSP_001395;
CC -1- TISSUE SPECIFICITY: Expressed in heart, placenta and skeletal
CC muscle and to a lesser extent in pancreas. Very low expression in
CC brain, lung, liver and kidney.
CC -1- DISEASE: May be associated to Usher syndrome type 1A (USH1A)
CC which describes a congenital sensory deafness associated with
CC retinitis pigmentosa and feeble-mindedness.

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CC -1- SIMILARITY: Contains 1 DSL domain.
CC -1- SIMILARITY: Contains 16 EGF-like domains.
CC -1- SIMILARITY: Contains 1 VWFC domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF020201; AAB71189.1; -
CC EMBL; AF003521; AAB61285.1; -
CC EMBL; AF029778; AAB84215.1; -
CC EMBL; AF029779; AAB84216.1; -
CC EMBL; AF111170; AAD15562.1; -
CC EMBL; Y14330; CAA74706.1; -
CC HSSP; P01132; LGK5.
CC DR Genew; HGNC:6189; JAG2.
CC DR MIM; 602570; -
CC DR GO; GO:0005887; C:integral to plasma membrane; ISS.
CC DR GO; GO:0008083; P:growth factor activity; IDA.
CC DR GO; GO:0005112; P:Notch binding; IPI.
CC DR GO; GO:0007049; P:cell cycle; NAS.
CC DR GO; GO:0030154; P:cell differentiation; IDA.
CC DR GO; GO:0001709; P:cell fate determination; NAS.
CC DR GO; GO:0007267; P:cell-cell signaling; ISS.
CC DR GO; GO:0009912; P:hair cell fate commitment; ISS.
CC DR GO; GO:0030326; P:limb morphogenesis; ISS.
CC DR GO; GO:0007213; P:Notch signaling pathway; NAS.
CC DR GO; GO:0007605; P:perception of sound; ISS.
CC DR GO; GO:0030334; P:regulation of cell migration; NAS.
CC DR GO; GO:0042127; P:regulation of cell proliferation; IDA.
CC DR GO; GO:0007283; P:spermatogenesis; ISP.
CC DR GO; GO:0030217; P:T-cell differentiation; IDA.
CC DR GO; GO:0045061; P:thymic T-cell selection; IDA.
CC DR InterPro; IPR000152; Asx_hydroxyl_S.
CC DR InterPro; IPR001774; DSL.
CC DR InterPro; IPR000742; EGF_2.
CC DR InterPro; IPR001881; EGF_Ca.
CC DR InterPro; IPR001438; EGF_II.
CC DR InterPro; IPR006209; EGF_Like.
CC DR InterPro; IPR009041; PMP_SGCI.
CC DR Pfam; PF01414; DSL; 1.
CC DR Pfam; PF00008; EGF; 14.
CC DR PRINTS; PRO0010; EGFBLD.
CC DR PROSITE; PS00010; ASX_HYDROXYL; 10.
CC DR PROSITE; PS00022; EGF_1; 16.
CC DR PROSITE; PS01186; EGF_2; 12.
CC DR PROSITE; PS00026; EGF_3; 15.
CC DR PROSITE; PS01187; EGF_Ca; 7.
CC DR PROSITE; PS0184; VWFC_2; 1.
KW Alternative splicing; Calcium-binding; Developmental protein;
KW EGF-like domain; Glycoprotein; Notch signaling pathway; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 1238 Jagged 2.
FT DOMAIN 27 1080 Extracellular (Potential).
FT TRANSMEM 1081 1105 Potential.
FT DOMAIN 1106 1238 Cytoplasmic (Potential).
FT DOMAIN 178 240 DSL.
FT DOMAIN 241 274 EGF-like 1.
FT DOMAIN 275 305 EGF-like 2.
FT DOMAIN 307 345 EGF-like 3.
FT DOMAIN 347 383 EGF-like 4.
FT DOMAIN 385 421 EGF-like 5.
FT DOMAIN 423 459 EGF-like 6.
FT DOMAIN 461 496 EGF-like 7.
FT DOMAIN 498 534 EGF-like 8.
FT DOMAIN 536 572 EGF-like 9.
FT DOMAIN 574 634 EGF-like 10 (atypical).

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RC STRAIN=C57BL/6J; TISSUE=Whole embryo;
RX MEDLINE=98142023; PubMed=9473344; DOI=10.1006/excr.1997.3865;
RA Hoff H.B. III, Tresini M., Li S., Sell C.;
RT "DBI-1, a novel gene related to the notch family, modulates mitogenic
RL response to insulin-like growth factor 1.";
DR EMBL; U57368; AAB01338.1; -.
DR PIR; T30176; T30176.
DR HSP; P08709; 1F7E.
DR MGD; MGI:1202397; Ddx26.
DR GO; GO:0015021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000629; DEAD box.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF07645; EGF_Ca; 1.
DR SMART; SM00179; EGF_CA; 2.
DR PROSITE; PS00010; ASX HYDROXYL; 2.
DR PROSITE; PS00039; DEAD ATP HELICASE; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR EGF-like domain; Transmembrane.
SQ SEQUENCE 1687 AA; 188528 MW; DA3B5302B67545D3 CRC64;

Query Match 52.5%; Score 63; DB 2; Length 1687;
Best Local Similarity 26.9%; Pred. No. 5.6e+02;
Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSXXCNXNKCXV 27
Db 480 GFEGSTCERNIDCPNFKONGVCV 505

RESULT 68
Q7QCP4
ID Q7QCP4 PRELIMINARY; PRT; 3523 AA.
AC Q7QCP4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP1653 (Fragment).
GN Name=agCGS0053; ORFNames=ENSANGG00000007782;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAB0100859; EAA08121.1; -.
DR HSP; P00740; 1EDM.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000859; CUB_like_1.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
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DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR003410; Hyalin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 3.
DR Pfam; PF00008; EGF; 11.
DR Pfam; PF07645; EGF_Ca; 2.
DR Pfam; PF02494; F5_F8 type_C; 2.
DR Pfam; PF02494; HYR; 3.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; Sushi; 8.
DR PRINTS; PR00010; EGFBL00D.
DR PROSITE; PS00010; ASX HYDROXYL; 11.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS00041; C TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 15.
DR PROSITE; PS01186; EGF_2; 13.
DR PROSITE; PS00026; EGF_3; 17.
DR PROSITE; PS01187; EGF_CA; 7.
DR PROSITE; PS00022; FAS8C_3; 2.
DR PROSITE; PS00825; HYR; 3.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00688; LDLRA_2; 1.
DR PROSITE; PS00923; SUSHI; 6.
DR EGF-like domain.
KW EGF-like domain.
FT NON_TER 1
FT NON_TER 3523
SQ SEQUENCE 3523 AA; 385001 MW; B58BB588E2A484E6 CRC64;

Query Match 52.5%; Score 63; DB 2; Length 3523;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 4 XNOXCXQXLDCCSXXCNXNKCXV 27
Db 2247 TGKNCQHTVDDCESAPQNGGTCV 2270

RESULT 69
CX07_CONGE
ID CX07 CONGE STANDARD; PRT; 29 AA.
AC P05483;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Omega-conotoxins GVIIA/GVIIB (Shaker peptides GVIIA/GVIIB) (SNX-178).
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=86070213; PubMed=4071055;
RA Olivera B.M., Gray W.R., Zeikus R.D., McIntosh J.M., Varga J.,
RA Rivier J.E., de Santos V., Cruz L.J.;
RT "Peptide neurotoxins from fish-hunting cone snails.";
RL Sequence 230:1338-1343(1985).
CC -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
CC and block voltage-sensitive calcium channels (VSCC).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MISCELLANEOUS: The sequence shown is that of conotoxin GVIIA.
CC -1- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
CC family.
DR PIR; A43620; A43620.
DR PIR; B43620; B43620.
DR KW Calcium channel inhibitor; Direct protein sequencing; Hydroxylation;
DR KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
FT MOD_RES 4 4 4 4-hydroxyproline.
```



```

CC similarity). This toxin blocks N-type calcium channels.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
CC family.
CC
CC HSSP; P05484; 1DM4.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
DR Amidation; Calcium channel inhibitor; Direct protein sequencing;
KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Signal;
KW
KW Toin.
KW SIGNAL 1 22 Potential.
KW PROPEP 23 45
KW PEPTIDE 46 72 .Omega-conotoxin CVID.
KW DISULFID 46 61 By similarity.
KW DISULFID 53 65 By similarity.
KW DISULFID 60 72 By similarity.
KW MOD_RES 72 72 Cysteine amide (G-73 provides amide
FT group).
FT SEQUENCE 73 AA; 7748 MW; C4CEBD30C77DAEC3 CRC64;
SQ
Query Match 51.7%; Score 62; DB 1; Length 73;
Best Local Similarity 30.4%; Pred. No. 41;
Matches 7; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQLDDCCSXXCNXX 23
DB 46 CRSKGAKCSKLMYDCGSGCSGT 68
| : : : : : | | | | : : :
| : : : : : | | | | : : :
RESULT 72
Q646U3 PRELIMINARY; PRT; 74 AA.
ID AC Q646U3;
AC Q646U3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Phytoxin-like SCR74.
DE Phytrophthora infestans (Potato late blight fungus).
OS Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytrophthora.
OC NCBI_TaxID=4787;
OX [1]
RN SEQUENCE FROM N.A.
RP Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Tarto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RA "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
RT Family of Phytrophthora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723724; GAU21465.1; -
SQ SEQUENCE 74 AA; 7910 MW; C925922881E5EA3C CRC64;
Query Match 51.7%; Score 62; DB 2; Length 74;
Best Local Similarity 25.8%; Pred. No. 41;
Matches 8; Conservative 14; Mismatches 3; Indels 6; Gaps 1;
QY 2 XIXNQXCQ-----XLDCCSXXCNXXNC 26
DB 41 KVTSKCKKAINADPIAFHDCCKSCNTGSPC 71
| : : : : : | : : : : : |
| : : : : : | : : : : : |
RESULT 73
Q646U4 PRELIMINARY; PRT; 74 AA.
ID AC Q646U4;
AC Q646U4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Phytoxin-like SCR74.
DE Phytrophthora infestans (Potato late blight fungus).
OS Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytrophthora.

```



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OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
RL Family of Phytoththora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723723; AAU21444.1; -
SQ SEQUENCE 74 AA; 7879 MW; F19FBA1F67B8A3E CRC64;

Query Match
Best Local Similarity 51.7%; Score 62; DB 2; Length 74;
Matches 8; Conservative 14; Mismatches 3; Indels 6; Gaps 1;

OY 2 XIXNQXCQ-----XLDCCSXXCNXXNC 26
Db 41 DVVSKCKKAINADPIAFHDCCKSCNTGSPC 71

RESULT 74
O646W2
ID Q646W2 PRELIMINARY; PRT; 74 AA.
AC Q646W2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Phytoxin-like SCR74.
OS Phytoththora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytoththora.
OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
RL Family of Phytoththora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723704; AAU21445.1; -
SQ SEQUENCE 74 AA; 7807 MW; D9D10BA1F26FC5B0 CRC64;

Query Match
Best Local Similarity 51.7%; Score 62; DB 2; Length 74;
Matches 8; Conservative 14; Mismatches 3; Indels 6; Gaps 1;

OY 2 XIXNQXCQ-----XLDCCSXXCNXXNC 26
Db 41 DVVSKCKKAINADPIAFHDCCKSCNTGSPC 71

RESULT 75
O646W3
ID Q646W3 PRELIMINARY; PRT; 74 AA.
AC Q646W3;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Phytoxin-like SCR74.
OS Phytoththora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytoththora.
OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
RL Family of Phytoththora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY723703; AAU21444.1; -
SQ SEQUENCE 74 AA; 7817 MW; 5373030B547B94FF CRC64;

Query Match
Best Local Similarity 51.7%; Score 62; DB 2; Length 74;
Matches 8; Conservative 14; Mismatches 3; Indels 6; Gaps 1;

OY 2 XIXNQXCQ-----XLDCCSXXCNXXNC 26
Db 41 DVVSKCKKAINADPIAFHDCCKSCNTGSPC 71

RESULT 76
O646W6
ID Q646W6 PRELIMINARY; PRT; 74 AA.
AC Q646W6;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Phytoxin-like SCR74.
OS Phytoththora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytoththora.
OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
RL Family of Phytoththora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723700; AAU21441.1; -
DR EMBL; AY723701; AAU21442.1; -
DR EMBL; AY723702; AAU21443.1; -
DR EMBL; AY723699; AAU21440.1; -
SQ SEQUENCE 74 AA; 7851 MW; D9D10BA1F67B94F1 CRC64;

Query Match
Best Local Similarity 51.7%; Score 62; DB 2; Length 74;
Matches 8; Conservative 14; Mismatches 3; Indels 6; Gaps 1;

OY 2 XIXNQXCQ-----XLDCCSXXCNXXNC 26
Db 41 DVVSKCKKAINADPIAFHDCCKSCNTGSPC 71

RESULT 77
O9AUD1
ID Q9AUD1 PRELIMINARY; PRT; 153 AA.
AC Q9AUD1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Pedaliaceae; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RP SEQUENCE FROM N.A.
RA Tai S.S.K., Lee T.T., Tsai C.C.Y., Yiu T.-J., Tzen J.T.C.;
RT "Expression pattern and deposition of three storage proteins, 11S
globulin, 2S albumin and 7S globulin in maturing sesame seeds.";
RL Plant Physiol. Biochem. 39:981-992(2001).
DR EMBL; AF240005; AAK15088.1; -
DR HSP; P01085; IHSS.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR000480; Glutelin.
DR InterPro; IPR000617; Napin.
DR Pfam; PF00234; Tryp_alpha_amyl; 1.

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CC ENBL; BC019431; AAH19431.1;
CC EMBL; AB011019; BAA8686.1; ALT_INIT.
CC HSSP; P00750; ITPG.
CC MGD; MGI:2146838; Egfl9.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
CC InterPro; IPR006209; EGF_Like.
CC Pfam; PF00008; EGF; 5.
CC PRINTS; PR00010; EGFBL00D.
CC SMART; SM00179; EGF_CA; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 2.
CC PROSITE; PS00022; EGF_1; 6.
CC PROSITE; PS00186; EGF_2; 6.
CC PROSITE; PS00026; EGF_3; 6.
CC PROSITE; PS01187; EGF_CA; 2.
CC Alternative splicing; Calcium; Calcium-binding; EGF-like domain;
CC Repeat; Signal; Transmembrane.
CC SIGNAL 1 26 Potential.
CC CHAIN 27 382 Multiple EGF-like-domain protein 9.
CC DOMAIN 306 326 Extracellular (Potential).
CC TRANSMEM 327 382 Potential.
CC DOMAIN 27 58 Cytoplasmic (Potential).
CC DOMAIN 62 89 EGF-like 1.
CC DOMAIN 91 129 EGF-like 2.
CC DOMAIN 131 172 EGF-like 3.
CC DOMAIN 174 210 EGF-like 4.
CC DOMAIN 212 248 EGF-like 5, calcium-binding (Potential).
CC DISULFID 29 40 EGF-like 6, calcium-binding (Potential).
CC DISULFID 33 46 By similarity.
CC DISULFID 48 57 By similarity.
CC DISULFID 66 71 By similarity.
CC DISULFID 79 88 By similarity.
CC DISULFID 95 107 By similarity.
CC DISULFID 101 117 By similarity.
CC DISULFID 119 128 By similarity.
CC DISULFID 135 148 By similarity.
CC DISULFID 142 160 By similarity.
CC DISULFID 162 171 By similarity.
CC DISULFID 178 189 By similarity.
CC DISULFID 183 198 By similarity.
CC DISULFID 200 209 By similarity.
CC DISULFID 216 227 By similarity.
CC DISULFID 221 236 By similarity.
CC DISULFID 238 247 By similarity.
CC CARBOHYD 157 157 N-linked (GlcNAc..) (Potential).
CC VARSPPLIC 295 311 Missing (in isoform 2).
CC SEQUENCE 382 AA; 40404 MW; F2C82AD649CA0B3C CRC64;
Query Match 51.7%; Score 62; DB 1; Length 382;
Best Local Similarity 32.0%; Pred. NO. 1.8e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
QY 2 XIXNQYCXOXLDCCSXCNXXNC 26
: : : : : : : : : : : : : :
DB 203 GFAGRECTINLDDCASRPCQRGARC 227
RESULT 79
EFL9_HUMAN
ID EFL9_HUMAN STANDARD; PRT; 383 AA.
AC Q6UY11; Q9BQ54;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Multiple EGF-like-domain protein 9 precursor (UNQ2903/PRO28633).
GN Name=Egfl9;
OS Homo sapiens (Human).

```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu J., Hase P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RN Genome Res. 13:2265-2270(2003).
 RL [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Eye;
 RX MEDLINE=20388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=2;
 CC IsoId=Q6UY11-1; Sequence=Displayed;
 CC IsoId=Q6UY11-2; Sequence=VSP_011767;
 CC Note=Splicing acceptor site not canonical. No experimental
 CC confirmation available;
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; AV358126; AAQ88493.1; -;
 CC EMBL; BC000230; AAH00230.1; -;
 CC EMBL; BC006425; AAH06425.1; -;
 CC GenBank; U01113; EGF.L9.
 DR InterPro; IPR000152; Asx hydroxyl S.
 DR InterPro; IPR008985; ConA like_1ec_g1.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR001438; EGF-II.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.

DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00008; EGF_5.
 DR PRINTS; PR00010; EGFBL00D.
 DR SMART; SM00181; EGF_6.
 DR SMART; SM00179; EGF_CA_4.
 DR PROSITE; PS00010; ASX HYDROXYL; 2.
 DR PROSITE; PS00022; EGF_1; 6.
 DR PROSITE; PS01186; EGF_2; 6.
 DR PROSITE; PS00026; EGF_3; 6.
 DR PROSITE; PS01187; EGF_CA; 2.
 KW Alternative splicing; Calcium; Calcium-binding; EGF-like domain;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 383 Multiple EGF-like-domain protein 9.
 FT DOMAIN 27 306 Extracellular (Potential).
 FT TRANSMEM 307 327 Potential.
 FT DOMAIN 328 383 Cytoplasmic (Potential).
 FT DOMAIN 27 58 EGF-like 1.
 FT DOMAIN 62 89 EGF-like 2.
 FT DOMAIN 91 129 EGF-like 3.
 FT DOMAIN 131 172 EGF-like 4.
 FT DOMAIN 174 210 EGF-like 5, calcium-binding (Potential).
 FT DOMAIN 212 248 EGF-like 6, calcium-binding (Potential).
 FT DISULFID 29 40 By similarity.
 FT DISULFID 33 46 By similarity.
 FT DISULFID 48 57 By similarity.
 FT DISULFID 66 71 By similarity.
 FT DISULFID 79 88 By similarity.
 FT DISULFID 95 107 By similarity.
 FT DISULFID 101 117 By similarity.
 FT DISULFID 119 128 By similarity.
 FT DISULFID 135 148 By similarity.
 FT DISULFID 142 160 By similarity.
 FT DISULFID 162 171 By similarity.
 FT DISULFID 178 189 By similarity.
 FT DISULFID 193 198 By similarity.
 FT DISULFID 200 209 By similarity.
 FT DISULFID 216 227 By similarity.
 FT DISULFID 221 236 By similarity.
 FT DISULFID 238 247 By similarity.
 FT CARBOHYD 157 157 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 1 179 Missing (in isoform 2).
 FT /FTId=VSP_011767;
 SQ SEQUENCE 383 AA; 40547 MW; 701AC6B043863EA7 CRC64;
 Query Match 51.7%; Score 62; DB 1; Length 383;
 Best Local Similarity 32.0%; Pred. No. 1.8e+02;
 Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
 OY 2 XIXNQXCNQXLDCCSXCNXNXC 26
 Db 203 GFAGRFCTINLDDCASRPCQRC 227
 ID Q7PM27 PRELIMINARY; PRT; 638 AA.
 AC Q7PM27;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE ENSANGP0000014402 (Fragement).
 GN Name=ENSANGG0000011913;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an


```
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008980; ERA14483.2; -.
DR HSP; P19438; 1EXT.
DR InterPro; IPR003341; DUF139.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF02363; CtripleX; 15.
DR Pfam; PF00008; EGF; 1.
DR PROSITE; PS01186; EGF_2; 4.
FT NON TER 1
FT NON TER 638
SQ SEQUENCE 638 AA; 69390 MW; 026DB4846AB483F CRC64;

Query Match 51.78; Score 62; DB 2; Length 638;
Best Local Similarity 26.98; Pred. No. 2.9e+02;
Matches 7; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Oy 2 XIXNQXCXQLDDCCSXXCNXNKC 26
Db 30 RLSNHRICPHCDCCDNGICTKPGYC 54

RESULT 81
Oy62W9 PRELIMINARY; PRT; 713 AA.
AC Q962W9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE EGF-like protein (Fragment).
OS Podocoryne carnea.
OC Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydroidea; Anthomedusae;
OC Hydrozoa; Podocorynidae; Podocoryninae.
OX NCBI_TaxID=6096;
RN [1]
RP SEQUENCE FROM N.A.
RA Bauer P., Plickert G.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397902; AAK92130.1; -.
DR HSP; P00740; 1EDM.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR00152; Aax_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 18.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00179; EGF_CA; 16.
DR PROSITE; PS00010; ASX_HYDROXYL; 17.
DR PROSITE; PS00022; EGF_1; 18.
DR PROSITE; PS01186; EGF_2; 18.
DR PROSITE; PS50026; EGF_3; 18.
DR PROSITE; PS01187; EGF_CA; 16.
KW EGF-like domain.
FT NON TER 1
FT NON TER 713
SQ SEQUENCE 713 AA; 76908 MW; 980E392B533E42D0 CRC64;

Query Match 51.78; Score 62; DB 2; Length 713;
Best Local Similarity 26.98; Pred. No. 3.2e+02;
Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Oy 2 XIXNQXCXQLDDCCSXXCNXNKC 27
Db 489 GFTGETCEIIDECSPPCQNGCTCV 514

RESULT 82
ID_DLL1_RAT
AC P97677;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
```

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DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1).
GN Names=Dll1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Disibio G., Hebehi L., Boulter J., Weinmaster G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May be involved in cell-to-cell communication in
CC mammalian embryos. May have a role in cellular interactions
CC underlying somitogenesis and development of the nervous system (By
CC similarity).
CC -1- SUBUNIT: Interacts with Notch receptors.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 1 DSL domain.
CC -1- SIMILARITY: Contains 8 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U78889; AAB37343.1; -.
CC HSP; P08709; 1BF9.
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0005112; F:Notch binding; IPI.
CC GO; GO:0030154; P:cell differentiation; ISS.
CC GO; GO:0001709; P:cell fate determination; ISS.
CC GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
CC GO; GO:0009912; P:hair cell fate commitment; NAS.
CC GO; GO:0030097; P:hemopoiesis; ISS.
CC GO; GO:0042472; P:inner ear morphogenesis; ISS.
CC GO; GO:0007399; P:neurogenesis; NAS.
CC GO; GO:0007219; P:Notch signaling pathway; NAS.
CC GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.
CC GO; GO:0030155; P:regulation of cell adhesion; ISS.
CC InterPro; IPR00152; Aax_hydroxyl_S.
CC InterPro; IPR001774; DSL.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
CC Pfam; PF01414; DSL; 1.
CC Pfam; PF00008; EGF; 6.
CC PRINTS; PR00010; EGFBL00D.
CC SMART; SM00051; DSL; 1.
CC SMART; SM00179; EGF_CA; 4.
CC PROSITE; PS00010; ASX_HYDROXYL; 3.
CC PROSITE; PS00022; EGF_1; 8.
CC PROSITE; PS01186; EGF_2; 8.
CC PROSITE; PS50026; EGF_3; 7.
CC PROSITE; PS01187; EGF_CA; 2.
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW Notch signaling pathway; Repeat; Signal; Transmembrane.
FT SIGNAL 1 17
FT CHAIN 18 714
FT DOMAIN 18 537
FT TRANSMEM 538 560
FT DOMAIN 561 714
FT DOMAIN 158 220
FT DOMAIN 225 253
FT DOMAIN 256 284
FT DOMAIN 291 324
FT DOMAIN 331 362
FT DOMAIN 369 401
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STRAIN=C57BL/6J;
RA Brattwatt M., Waeltz P., Dudek D., Nagaraja R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 8 EGF-like domains.
DR ENBL; BC057400; AAH57400.1; -;
DR ENBL; BC065063; AAH65063.1; -;
DR ENBL; AY497019; AAR30869.1; -;
DR HSSP; P00743; IAP0.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007386; P:compartment specification; IMP.
DR GO; GO:0007368; P:determination of left/right symmetry; IMP.
DR GO; GO:0001757; P:somite specification; IMP.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; P000010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
DR EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match 51.7%; Score 62; DB 2; Length 722;
Best Local Similarity 28.0%; Pred.No. 3.2e+02;
Matches 7; Conservative 12; Mismatches 6; Indels 0; Gaps 0

QY 2 XIXNXQXCXQXLDCCSXXCNXKNC 26
DB 433 GFSGRYCDNVDDCASSPCANGGTC 457

RESULT 85
DPLL_HUMAN
ID DPLL_HUMAN STANDARD; PRT; 723 AA.
AC 000548; Q9NU41; Q9UUV2;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1)
DE (H-Delta-1) (UNQ146/PRO172).
GN Name=DLL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99180765; PubMed=10079256;
RA Gray G.B., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.
RT "Human ligands of the Notch receptor."
RL Am. J. Pathol. 154:785-794 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX Han W., Ye Q., Moore M.A.S.;
RT "A soluble form of human delta-like-1 inhibits differentiation of
RT hematopoietic progenitor cells."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

DR	InterPro; IPR001774; DSL.
DR	InterPro; IPR000742; EGF_2.
DR	InterPro; IPR001881; EGF_Ca.
DR	InterPro; IPR001438; EGF_II.
DR	InterPro; IPR006209; EGF_like.
DR	Pfam; PF01414; DSL; 1.
DR	Pfam; PF00008; EGF; 6.
DR	PRINTS; PRO0010; EGFBLD.
DR	SMART; SM00051; DSL; 1.
DR	SMART; SM00179; EGF_CA; 4.
DR	PROSITE; PS00010; ASX HYDROXYL; 3.
DR	PROSITE; PS00022; EGF_1; 8.
DR	PROSITE; PS01186; EGF_2; 8.
DR	PROSITE; PS50026; EGF_3; 7.
DR	PROSITE; FS01187; EGF_CA; 1.
KW	Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW	Notch signaling pathway; Repeat; Signal; Transmembrane.
FT	SIGNAL 1 17 Potential.
FT	CHAIN 18 723 Delta-like protein 1.
FT	DOMAIN 18 545 Extracellular (Potential).
FT	TRANSMEM 546 568 Potential.
FT	DOMAIN 569 723 Cytoplasmic (Potential).
FT	DOMAIN 159 221 DSL.
FT	DOMAIN 226 254 EGF-like 1.
FT	DOMAIN 257 285 EGF-like 2.
FT	DOMAIN 292 325 EGF-like 3.
FT	DOMAIN 332 363 EGF-like 4, calcium-binding (Potential).
FT	DOMAIN 370 402 EGF-like 5.
FT	DOMAIN 409 440 EGF-like 6.
FT	DOMAIN 447 478 EGF-like 7, calcium-binding (Potential).
FT	DOMAIN 485 516 EGF-like 8.
FT	DISULFID 226 237 By similarity.
FT	DISULFID 230 243 By similarity.
FT	DISULFID 245 254 By similarity.
FT	DISULFID 257 268 By similarity.
FT	DISULFID 263 274 By similarity.
FT	DISULFID 276 285 By similarity.
FT	DISULFID 292 304 By similarity.
FT	DISULFID 298 314 By similarity.
FT	DISULFID 316 325 By similarity.
FT	DISULFID 332 343 By similarity.
FT	DISULFID 337 352 By similarity.
FT	DISULFID 354 363 By similarity.
FT	DISULFID 370 381 By similarity.
FT	DISULFID 375 391 By similarity.
FT	DISULFID 393 402 By similarity.
FT	DISULFID 409 420 By similarity.
FT	DISULFID 414 429 By similarity.
FT	DISULFID 431 440 By similarity.
FT	DISULFID 447 467 By similarity.
FT	DISULFID 469 478 By similarity.
FT	DISULFID 485 496 By similarity.
FT	DISULFID 490 505 By similarity.
FT	DISULFID 507 516 By similarity.
FT	CARBOHYD 477 477 N-linked (GlcNAc...) (Potential).
FT	CONFLICT 498 498 E -> Q (in Ref. 2).
FT	CONFLICT 502 502 G -> R (in Ref. 4 and 5).
FT	CONFLICT 510 510 G -> S (in Ref. 2).
SQL	SEQUENCE 723 AA; 77956 MW; B4EC455FFA32A12B CRC64;
Query Match	51.7%; Score 62; DB 1; Length 723;
Best Local Similarity	28.0%; Pred.No. 3.3e+02;
Matches	7; Conservative 12; Mismatches 6; Indels 0; Gaps
Qy	2 XIXNQXCXQLDDCCSXKNKNC 26 : : :::: :: ::: :
Dd	434 GPSGRHCDNDVDCASSPCANGTC 458
RESULT 86	
Q66S04	PRELIMITINARY; PRT; 824 AA.
ID	Q66S04
AC	Q66S04

DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Notch receptor-like protein.
 GN ORFNames=008-50;
 OS Oikopleura dioica.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
 OC Oikopleuridae; Oikopleura.
 OX NCBI_TaxID=34765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=1534333; DOI=10.1038/nature02709;
 RA Sso H.C., Edvardsen R.B., Maeland A.D., Bjordal M., Jensen M.F.,
 RA Hansen A., Flaot M., Weissenbach J., Leirach H., Wincker P.,
 RA Reinhardt R., Chourout D.;
 RT "Hox cluster integration with persistent anteroposterior order of
 RT expression in Oikopleura dioica";
 RL Nature 431:67-71(2004)
 RL EMBL; AY613856; AAY4887.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000152; ASX_HYDROXYL_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF00008; EGF_11.
 DR PRINTS; PR00010; EGFBL00D.
 DR SMART; SM00181; EGF; 17.
 DR SMART; SM00179; EGF_CA; 15.
 DR PROSITE; PS00010; ASX_HYDROXYL; 10.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 17.
 DR PROSITE; PS01186; EGF_2; 14.
 DR PROSITE; PS00028; EGF_3; 2.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Receptor.
 SQ SEQUENCE 824 AA; 89253 MW; 955ABAE53CFC86A CRC64;
 Query Match 51.78; Score 62; DB 2; Length 824;
 Best Local Similarity 30.88; Pred. No. 3.7e+02;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXQXLDQCCSXCNXNXC 26
 DB 154 CELEKSFCEQFPNYCENGDCNDGFC 179
 RESULT 87
 FBPI STRPU STANDARD; PRT; 1064 AA.
 AC P10079;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Fibropellin I precursor (Epidermal growth factor-related protein 1)
 DE (UEGF-1)
 GN Name=EGF1;
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90112459; PubMed=25114273;
 RA Delgadillo-Reynoso M.G., Rolio D.R., Hursh D.A., Raff R.A.;
 RT "Structural analysis of the UEGF gene in the sea urchin
 RT strongylocentrotus purpuratus reveals more similarity to vertebrate
 RT than to invertebrate genes with EGF-like repeats.";
 RL J. Mol. Evol. 29:314-327(1989).
 RN [2]

RP SEQUENCE OF 279-476 AND 781-1064 FROM N.A.
 RX MEDLINE=87319677; PubMed=3498216;
 RA Hursh D.A., Andrews M.E., Raff R.A.;
 RT "A sea urchin gene encodes a polypeptide homologous to epidermal
 RT growth factor";
 RL Science 237:1487-1490(1987).
 RN [3]
 RP AVIDIN-LIKE DOMAIN.
 RX MEDLINE=89196806; PubMed=2784773;
 RA Hunt L.T., Barker W.C.;
 RT "Avidin-like domain in an epidermal growth factor homolog from a sea
 RT urchin";
 RL FASEB J. 3:1760-1764(1989).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=91285254; PubMed=2060714;
 RA Bisgrove B.W., Andrews M.E., Raff R.A.;
 RT "Fibropellins, products of an EGF repeat-containing gene, form a
 RT unique extracellular matrix structure that surrounds the sea urchin
 RT embryo";
 RL Dev. Biol. 146:89-99(1991).
 CC -I- FUNCTION: Forms the apical lamina, a component of the
 CC extracellular matrix.
 CC -I- SUBCELLULAR LOCATION: Extracellular. In vesicles in the cytoplasm
 CC of unfertilized eggs, then to the base of the hyalin layer
 CC throughout development and finally in the apical lamina in late
 CC embryos and early larvae.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=IA;
 CC IsoId=P10079-1; Sequence=Displayed;
 CC Name=IB;
 CC IsoId=P10079-2; Sequence=VSP_000451;
 CC -I- DEVELOPMENTAL STAGE: Moderate levels in unfertilized eggs and
 CC during early cleavage, then rapidly increases in abundance between
 CC late morula and mesenchyme blastula stages to maximal levels
 CC maintained through subsequent stages. Expressed both maternally
 CC and zygotically.
 CC -I- SIMILARITY: Contains 1 avidin domain.
 CC -I- SIMILARITY: Contains 1 CUB domain.
 CC -I- SIMILARITY: Contains 21 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L08692; AAA62164.1; -;
 CC EMBL; L08692; AAA62163.1; -;
 CC EMBL; X17530; CAA35571.1; -;
 CC EMBL; M17421; CAA30050.1; -;
 CC EMBL; X17533; CAA35573.1; -;
 CC PIR; A40136; A40136.
 CC HSSP; P01132; 1EGF.
 CC InterPro; IPR000152; ASX_hydroxyl_s.
 CC InterPro; IPR005469; Avidin.
 CC InterPro; IPR005468; Avidin/str.
 CC InterPro; IPR000859; CUB.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR001438; EGF_II.
 CC InterPro; IPR006209; EGF_like.
 CC Pfam; PF01382; Avidin; 1.
 CC Pfam; PF00431; CUB; 1.
 CC Pfam; PF00008; EGF; 21.
 CC PRINTS; PR00709; AVIDIN.
 CC PRINTS; PR00010; EGFBL00D.
 CC PROSITE; PS00010; ASX_HYDROXYL; 19.
 CC PROSITE; PS00577; AVIDIN; 1.
 CC PROSITE; PS01180; CUB; 1.

[illegible]

RESULT 91

Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

EMBL; AF537369; AAN06819.1; -, HSSP; P07207; IOT8.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0030154; P:cell differentiation; IEA.

GO; GO:0050793; P:regulation of development; IEA.

InterPro; IPR002110; ANK.

InterPro; IPR000154; Asx_hydroxyl_S.

InterPro; IPR000742; EGF_2.

InterPro; IPR001881; EGF_Ca.

InterPro; IPR001438; EGF_II.

InterPro; IPR006209; EGF-like.

InterPro; IPR008297; Notch.

InterPro; IPR000800; Notch_region.

Pfam; PF00023; Ank; 6.

Pfam; PF00008; EGF; 29.

Pfam; PF07645; EGF_Ca; 4.

Pfam; PF00056; Notch; 3.

PIRSF; PIRSF02279; Notch; 1.

PRINTS; PR01415; ANKYRIN.

PRINTS; PR00010; EGFBLD.

PRINTS; PR01452; NOTCH.

SMART; SM00248; ANK; 7.

SMART; SM00179; EGF_Ca; 25.

SMART; SM00004; NL; 3.

PROSITE; PS00088; ANK_REPEAT; 4.

PROSITE; PS0297; ANK_REPEAT_REGION; 1.

PROSITE; PS00010; ASX_HYDROXYL; 22.

PROSITE; PS00022; EGF_1; 34.

PROSITE; PS01186; EGF_2; 27.

PROSITE; PS00026; EGF_3; 35.

PROSITE; PS01187; EGF_Ca; 22.

ANK repeat; EGF-like domain.

SEQUENCE 2428 AA; 260842 MW; 766A9362CE37CB9F CRC64;

Query Match 51.7%; Score 62; DB 2; Length 2428;

Best Local Similarity 29.2%; Pred. No. 9.8e+02;

Matches 7; Conservative 11; Mismatches 6; Indels 0;

OY 4 XNQCXQXLDCCSXCNXNXCVCV 27

DB 794 SGRNCETNLDCCSPNCRNGGSCI 817

RESULT 93

Q8GPA5 PRELIMINARY; PRT; 2524 AA.

ID Q8GPA5

AC Q8GPA5

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Putative notch receptor protein.

GN Name=notch;

OS Branchiostoma floridae (Florida lancelet) (Amphioxus).

OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

OC Branchiostoma.

OX NCBI_TaxID=7739;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Whole larvae;

RA Holland L.Z., Burgdorf C., Holland N.D., Lehrach H., Tamme R.,

RA Abi-Rached L., Pontarotti P., Lardelli M.,

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

[2]

RP SEQUENCE FROM N.A.

RC TISSUE=Whole larvae;

RA Lardelli M.T.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

EMBL; Y12539; CAC19873.1; -.

HSSP; P07207; IOT8.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

CC -l- FUNCTION: Causes irreversible paralysis in lepidopterous insects
CC by massive transmitter release (which is mediated by glutamate
CC receptors) from presynaptic stores at neuromuscular junctions.
CC

Q8LAG1	
ID	Q8LAG1
AC	Q8LAG1;
DT	01-OCT-2002 (Tremblrel. 22, Created)
	PRELIMINARY; PRT; 471 AA.

```
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -I- SIMILARITY: Belongs to the mu-agatoxin family.
DR PIR; A32038; A32038.
DR PDB; LEIT; NMR; @=1-36.
DR InterPro; IPR009243; Toxin_7.
DR Pfam; PF05980; Toxin_7; 1..7.
KW 3D-structure; Amidation; Direct protein sequencing; Neurotoxin; Toxin.
FT DISULFID 2 17
FT FT 9 22
FT FT DISULFID 16 32
FT FT DISULFID 24 30
FT MOD_RES 36 36 Asparagine amide.
FT STRAND 3 3
FT TURN 5 6
FT STRAND 16 16
FT TURN 18 19
FT STRAND 20 26
FT TURN 27 28
FT STRAND 29 34
SQ SEQUENCE 36 AA; 4273 MW; 3B973A605B90DE85 CRC64;

Query Match          51.2%; Score 61.5; DB 1; Length 36;
Best Local Similarity 26.7%; Pred.No.24;
Matches      8; Conservative 12; Mismatches       7; Indels   3; Gaps    1;

QY      1 CXIXNXCXOXLDLDCGS---XXCNXXNXCXV 27
         |:|::||::||::||::||::||::||::||:
Db       2 CVPENGHCRDWYDECCEGFCVCSCRQPPKCI 31

RESULT 95
Q9BP77 PRELIMINARY; PRT; 81 AA.
AC Q9BP77;
DT 01-JUN-2001 (TRMBLrel. 17, Created)
DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DE Conotoxin scaffold VI/VII.
OS Conus arenatus (Sand-dusted cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsobagastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=89451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.;
RL "Mechanisms for evolving hypervariability: the case of conopeptides.";
RT Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF215061; AAC60489.1; -.
DR GO; GO:0005576; Cytoplasmic; IEA.
DR GO; GO:0008200; F-ion channel inhibitor activity; IEA.
DR GO; GO:0009405; Pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
SQ SEQUENCE 81 AA; 8697 MW; 99EB0139D26851D5 CRC64;

Query Match          51.2%; Score 61.5; DB 2; Length 81;
Best Local Similarity 27.6%; Pred.No.50;
Matches      8; Conservative 12; Mismatches       6; Indels   3; Gaps    1;

QY      1 CXIXNXCXOXLDLDCGSXXC---NXXNXC 26
         |:::::||::||||::||::||::||:
Db     46 CTVDSDCFDPDNHDCCSGRCIDEGGGVC 74

RESULT 96
Q8LAG1 PRELIMINARY; PRT; 471 AA.
ID Q8LAG1;
AC Q8LAG1;
DT 01-OCT-2002 (TRMBLrel. 22, Created)
```


DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22088475; PubMed=12093376;
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY087835; AAM65388.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 53428 MW; 3573C789C54FB28A CRC64;

Query Match 51.2%; Score 61.5; DB 2; Length 471;
 Best Local Similarity 22.2%; Pred. No. 2.5e+02;
 Matches 8; Conservative 12; Mismatches 7; Indels 9; Gaps 1;

QY 1 CXIXNQCXQXLDLC-----CSXXCNXXKVCV 27
 DB 150 CAGNEKCRSLMPOCEATLPAMPDCICGGERKFCV 185

RESULT 97
 Q9VZ55
 ID Q8VZ55 PRELIMINARY; PRT; 471 AA.
 AC Q8VZ55;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Atlg05410/T25N20_5 (Hypothetical protein Atlg05410).
 GN Name=Atlg05410;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesena E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.

RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY065014; AAL57658.1; -;
 DR EMBL; AY074502; AAL69486.1; -;
 DR EMBL; AY096601; AAM20251.1; -;
 DR EMBL; AY142043; AAM98307.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 53368 MW; 582512E495010DDA CRC64;

Query Match 51.2%; Score 61.5; DB 2; Length 471;
 Best Local Similarity 22.2%; Pred. No. 2.5e+02;
 Matches 8; Conservative 12; Mismatches 7; Indels 9; Gaps 1;

QY 1 CXIXNQCXQXLDLC-----CSXXCNXXKVCV 27
 DB 150 CAGNEKCRSLMPOCEATLPAMPDCICGGERKFCV 185

RESULT 98
 Q9VZV7
 ID Q9VZV7 PRELIMINARY; PRT; 481 AA.
 AC Q9VZV7;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE T25N20.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,
 RA Shinn P., Altafi H., Bei B., Chin C., Chio J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 RA Kim C., Altafi H., Bei B., Chin C., Chio J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chio J., Choi E.,
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

Search completed: April 18, 2005, 20:37:46
Job time : 121 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 19:58:50 ; Search time 125 Seconds
(without alignments)
83.540 Million cell updates/sec

Title: US-10-627-685a-26

Perfect score: 161

Sequence: 1 CRXNQKCFQHLDDCCSKCNKFNKCV 27

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161	100.0	27	2	AAW35723 Kappa-con
2	161	100.0	27	4	AAU10218 Snail Kap
3	161	100.0	27	6	AAE38358 Conus pur
4	158	98.1	27	4	AAU10212 Snail Kap
5	158	98.1	27	4	AAU10206 Snail Kap
6	158	98.1	27	4	AAU10203 Snail Kap
7	158	98.1	27	6	AAE38352 Conus pur
8	158	98.1	27	6	AAE38346 Conus pur
9	158	98.1	27	6	AAE38343 Conus pur
10	157	97.5	27	4	AAU10207 Snail Kap
11	157	97.5	27	4	AAU10217 Snail Kap
12	157	97.5	27	6	AAE38357 Conus pur
13	157	97.5	27	6	AAE38347 Conus pur
14	156	96.9	27	4	AAU10214 Snail Kap
15	156	96.9	27	4	AAU10198 Snail Kap
16	156	96.9	27	6	AAE38338 Conus pur
17	156	96.9	27	6	AAE38354 Conus pur
18	155	96.3	27	4	AAU10200 Snail Kap
19	155	96.3	27	4	AAU10216 Snail Kap
20	155	96.3	27	4	AAU10205 Snail Kap
21	155	96.3	27	4	AAU10199 Snail Kap
22	155	96.3	27	4	AAU10196 Snail Kap
23	155	96.3	27	4	AAU10202 Snail Kap
24	155	96.3	27	4	AAU10210 Snail Kap
25	155	96.3	27	4	AAU10197 Snail Kap

26	155	96.3	27	4	AAU10204
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28	155	96.3	27	6	AAE38344
29	155	96.3	27	6	AAE38336
30	155	96.3	27	6	AAE38339
31	155	96.3	27	6	AAE38345
32	155	96.3	27	6	AAE38337
33	155	96.3	27	6	AAE38340
34	155	96.3	27	6	AAE38356
35	155	96.3	27	6	AAE38350
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43	153	95.0	27	6	AAE38351
44	153	95.0	27	6	AAE38341
45	153	95.0	27	6	AAE38355
46	153	95.0	27	6	AAE38349
47	153	95.0	27	6	AAE38359
48	151	93.8	27	4	AAU10208
49	151	93.8	27	6	AAE38348
50	78.5	48.8	27	5	ABE96846
51	78.5	48.8	72	5	ABE96638
52	75	46.6	26	2	AAE39628
53	75	46.6	26	2	AAE37774
54	75	46.6	26	2	AAU19570
55	75	46.6	26	2	AAU12985
56	75	46.6	26	2	AAW72625
57	75	46.6	26	2	AAW95584
58	75	46.6	26	3	AAV56496
59	75	46.6	26	3	AAU14370
60	75	46.6	26	4	AAU19462
61	74	46.0	26	5	ABE96887
62	74	46.0	30	5	ABE96679
63	73	45.3	72	5	ABE96666
64	71	44.1	26	2	AAE39615
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66	71	44.1	26	2	AAU19551
67	71	44.1	26	2	AAU12974
68	71	44.1	26	2	AAW72612
69	71	44.1	26	2	AAW95571
70	71	44.1	26	3	AAV56480
71	71	44.1	26	3	AAU14359
72	71	44.1	26	4	AAE92221
73	71	44.1	26	4	AAU19449
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75	71	44.1	27	5	ABE96876
76	71	44.1	72	5	ABE96668
77	67	41.6	26	5	ABE96786
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79	64	39.8	27	5	ABE96772
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81	63.5	39.4	27	5	ABE96842
82	63.5	39.4	73	5	ABE96626
83	63	39.1	38	2	AAW06589
84	62.5	38.8	36	5	ABE88797
85	62.5	38.8	37	5	ABE88659
86	62	38.5	27	5	ABE96774
87	62	38.5	76	4	AAU05927
88	61.5	38.2	27	5	ABE96741
89	61	37.9	26	2	AAE39616
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91	61	37.9	26	2	AAE37762
92	61	37.9	26	2	AAE37761
93	61	37.9	26	2	AAU19552
94	61	37.9	26	2	AAW72614
95	61	37.9	26	2	AAW72613
96	61	37.9	26	2	AAW95572
97	61	37.9	26	2	AAW95573
98	61	37.9	26	3	AAV56481

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AAE38342	Conus pur
AAE38344	Conus pur
AAE38336	Conus pur
AAE38339	Conus pur
AAE38345	Conus pur
AAE38337	Conus pur
AAE38340	Conus pur
AAE38356	Conus pur
AAE38350	Conus pur
AAU10213	Snail Kap
AAU10209	Snail Kap
AAU10219	Snail Kap
AAU10201	Snail Kap
AAU10215	Snail Kap
AAU10211	Snail Kap
AAE38353	Conus pur
AAE38351	Conus pur
AAE38341	Conus pur
AAE38355	Conus pur
AAE38349	Conus pur
AAE38359	Conus pur
AAU10208	Snail Kap
AAE38348	Conus pur
ABE96846	Omega-con
ABE96638	Omega-con
AAE39628	SNX-202
AAE37774	SNX-202
AAU19570	SNX-202
AAU12985	Omega-con
AAW72625	Conus gen
AAW95584	Analog om
AAV56496	Analogue
AAU14370	Omega-con
AAU19462	Sequence
ABE96887	Omega-con
ABE96679	Omega-con
ABE96666	Omega-con
AAE39615	SVIB/SNX1
AAE37760	SVIB/SNX1
AAU19551	Natural o
AAU12974	Omega-con
AAW72612	Conus gen
AAW95571	Omega-con
AAV56480	Natural o
AAU14359	Omega-con
AAE92221	Toxin pep
AAU19449	Primary s
AAU15126	Cone snail
ABE96876	Omega-con
ABE96668	Omega-con
ABE96786	Omega-con
ABE96790	Omega-con
ABE96772	Omega-con
ABE96874	Omega-con
ABE96842	Omega-con
ABE96626	Omega-con
AAW06589	Tyrosinas
ABE88797	Conus bet
ABE88659	Conus bet
ABE96774	Omega-con
AAU05927	Cone snail
ABE96741	Omega-con
AAE39616	MVIC/SNX
AAE39617	MVIC/SNX
AAE37762	SNX-231
AAE37761	MVIC/SNX
AAU19552	Natural o
AAW72614	Conus gen
AAW72613	Conus gen
AAW95572	Omega-con
AAW95573	Omega-con
AAV56481	Natural o

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100 61 37.9 26 3 AAB14377 Aab14377 Omega-con

ALIGNMENTS

```

RESULT 1
AAW35723
ID ID AAW35723 standard; peptide; 27 AA.
XX AC AAW35723;
XX DT 03-APR-1998 (first entry)
XX DE Kappa-conotoxin PVIIA.
XX KW Kappa-conotoxin PVIIA; potassium channel; neurotransmitter release;
XX KW cone snail; venom; goldfish; delta-conotoxin PVIIA; disulphide.
XX OS Conus purpurascens.
XX FH Key Location/Qualifiers
FT Disulfide-bond 1..16
FT /note= "disulphide bond"
FT Modified-site 4
FT /note= "Optionally 4-trans-hydroxyproline, hydroxyproline
FT or proline"
FT Disulfide-bond 8..20
FT /note= "disulphide bond"
FT Disulfide-bond 15..26
FT /note= "disulphide bond"
XX W09734925-A1.
XX PD 25-SEP-1997.
XX PF 14-MAR-1997; 9TWO-US003483.
XX PR 18-MAR-1996; 96US-00619936.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Terlau H, Shon K, Grilley MM, Olivera BM;
XX WPI; 1997-480162/44.
XX PT New kappa-conotoxin peptides - which target potassium channels and can be
XX used to augment neurotransmitter release in e.g. autoimmune diseases.
XX PS Claim 1; Page 23; 29pp; English.
XX CC The present sequence represents a new kappa-conotoxin PVIIA which targets
XX potassium channels and can be used to augment neurotransmitter release in
XX pathological situations such as autoimmune diseases, e.g. Alzheimer's
XX disease, Lambert-Raton syndrome or myasthenia gravis. This peptide
XX together with delta-conotoxin PVIIA act synergistically to rapidly
XX immobilize fish which are injected with the two peptides. Injection of
XX kappa-conotoxin PVIIA alone results in different symptoms with an
XX injected fish becoming hyperactive and then contracting and suddenly
XX in a series of jerky movements. This "fin-popping" occurs repeatedly resulting
XX in PVIIA does not immobilize or kill the fish
SQ Sequence 27 AA;
Query Match 100.0%; Score 161; DB 2; Length 27;
Best Local Similarity 96.3%; Pred. No. 1e-10;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRXNKKCFQHLDDCCSRKCNFNKCV 27
DB 1 CRIPNKKCFQHLDDCCSRKCNFNKCV 27

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RESULT 2
AAU10218
ID AAU10218 standard; peptide; 27 AA.
XX AC AAU10218;
XX DT 16-JAN-2002 (first entry)
XX DE Snail Kappa-conotoxin PVIIA analogue O4A.
XX KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
XX KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
XX KW cerebral ischaemia; ocular ischaemia; asthma; O4A.
XX OS Conus purpurascens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "Hydroxyproline"
FT Modified-site 27
FT /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX W0200121648-A1.
XX PD 29-MAR-2001.
XX PF 21-SEP-2000; 2000WO-US025827.
XX PR 22-SEP-1999; 99US-0155135P.
XX PR 20-JUL-2000; 2000US-0219438P.
XX PA (COGN-) COGNETIX INC.
XX PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX Jones RR;
XX WPI; 2001-648090/74.
XX PT Treating disorders associated with radical depolarization of excitable
XX membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
XX activating a KATP channel by administering to an individual a kappa-
XX conotoxin PVIIA peptide.
XX PS Claim 1; Page 28; 46pp; English.
XX CC The invention relates to treating disorders associated with radical
XX depolarisation of excitable membrane by activating a KATP channel
XX comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
XX PVIIA) peptide or its analogue, derivative or physiologically active
XX salt. The conotoxins are used for treating disorders associated with
XX radical depolarisation of excitable membrane by activating a KATP
XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular
XX ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX analogue of the invention
SQ Sequence 27 AA;
Query Match 100.0%; Score 161; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 1e-10;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRXNKKCFQHLDDCCSRKCNFNKCV 27
DB 1 CRXNKKCFQHLDDCCSRKCNFNKCV 27

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RESULT 3
AAE38358
ID AAE38358 standard; peptide; 27 AA.

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XX AC AAE38358;
 XX DT 20-NOV-2003 (first entry)
 XX DE Conus purpurascens kappa-PVIIA analogue peptide, Q4A.
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX PN WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PF 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 8; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX SQ Sequence 27 AA;
 Query Match 100.0%; Score 161; DB 6; Length 27;
 Best Local Similarity 96.3%; Pred. No. 1e-10; Indels 0; Gaps 0;
 Matches 26; Conservative 1; Mismatches 0;
 QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 4
 AAU10212
 ID AAU10212 standard; peptide; 27 AA.
 XX AC AAU10212;
 XX DT 16-JAN-2002 (first entry)
 XX DE Snail Kappa-conotoxin PVIIA analogue S17A.
 XX KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;

KW cerebral ischaemia; ocular ischaemia; asthma; S17A.
 XX OS Conus purpurascens.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Modified-site 4 /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX PN WO200121648-A1.
 XX PD 29-MAR-2001.
 XX PF 21-SEP-2000; 2000WO-US025827.
 XX PR 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX PA (COGN-) COGNETIX INC.
 XX PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX DR WPI; 2001-648090/74.
 XX PT Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.
 XX PS Claim 1; Page 28; 46pp; English.
 XX CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX SQ Sequence 27 AA;
 Query Match 98.1%; Score 158; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 2.2e-10; Indels 0; Gaps 0;
 Matches 26; Conservative 1; Mismatches 0;
 QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 5
 AAU10206
 ID AAU10206 standard; peptide; 27 AA.
 XX AC AAU10206;
 XX DT 16-JAN-2002 (first entry)
 XX DE Snail Kappa-conotoxin PVIIA analogue F9Y.
 XX KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; F9Y.
 XX OS Conus purpurascens.
 XX OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 FT
 XX WO200121648-A1.
 XX
 XX 29-MAR-2001.
 XX
 XX 21-SEP-2000; 2000WO-US025827.
 XX
 XX 22-SEP-1999; 99US-0155135P.
 XX
 XX 20-JUL-2000; 2000US-0219438P.
 XX
 XX (COGN-) COGNETIX INC.
 XX
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX Jones RR;
 XX WPI; 2001-648090/74.
 XX
 XX Treating disorders associated with radical depolarization of excitable
 XX membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 XX activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.
 XX
 XX Claim 1; Page 28; 46pp; English.
 XX
 XX The invention relates to treating disorders associated with radical
 XX depolarisation of excitable membrane by activating a KATP channel
 XX comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 XX PVIIA) peptide or its analogue, derivative or physiologically active
 XX salt. The conotoxins are used for treating disorders associated with
 XX radical depolarisation of excitable membrane by activating a KATP
 XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 XX ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 XX analogue of the invention
 XX
 XX Sequence 27 AA;
 SQ
 Query Match 98.1%; Score 158; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 2.2e-10;
 Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CRXNOKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRXNOKCYQHLDDCCSRKCNRFNKCVCV 27
 RESULT 6
 AAU10203
 ID AAU10203 standard; peptide; 27 AA.
 XX
 XX AAU10203;
 XX
 XX 16-JAN-2002 (first entry)
 XX
 XX Snail Kappa-conotoxin PVIIA analogue R2K.
 XX
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 XX cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 XX cerebral ischaemia; ocular ischaemia; asthma; R2K.
 XX
 XX Conus purpurascens.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an

FT amide group"
 XX WO200121648-A1.
 XX
 XX 29-MAR-2001.
 XX
 XX 21-SEP-2000; 2000WO-US025827.
 XX
 XX 22-SEP-1999; 99US-0155135P.
 XX
 XX 20-JUL-2000; 2000US-0219438P.
 XX
 XX (COGN-) COGNETIX INC.
 XX
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX Jones RR;
 XX WPI; 2001-648090/74.
 XX
 XX Treating disorders associated with radical depolarization of excitable
 XX membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 XX activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.
 XX
 XX Claim 1; Page 27; 46pp; English.
 XX
 XX The invention relates to treating disorders associated with radical
 XX depolarisation of excitable membrane by activating a KATP channel
 XX comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 XX PVIIA) peptide or its analogue, derivative or physiologically active
 XX salt. The conotoxins are used for treating disorders associated with
 XX radical depolarisation of excitable membrane by activating a KATP
 XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 XX ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 XX analogue of the invention
 XX
 XX Sequence 27 AA;
 SQ
 Query Match 98.1%; Score 158; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 2.2e-10;
 Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CRXNOKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRXNOKCFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 7
 AAEE38352
 ID AAEE38352 standard; peptide; 27 AA.
 XX
 XX AAEE38352;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Conus purpurascens kappa-PVIIA analogue peptide, S17A.
 XX
 XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 XX ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 XX organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 XX retinopathy; coronary artery bypass graft surgery; acute heart failure;
 XX congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 XX Conus purpurascens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /label= Hyp
 XX
 XX WO2003063782-A2.
 XX
 XX 07-AUG-2003.
 XX
 XX 28-JAN-2003; 2003WO-US002384..

XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 XX PI Olivera BM;
 XX WPI; 2003-679464/64.
 XX DR Protection and preservation of an organ e.g. heart of a mammal comprises
 XX PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 7; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 XX CC organ protectants. The invention also relates to a method of arresting,
 XX CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 XX CC related conotoxins. The conotoxins can also be used for arresting,
 XX CC protecting or preserving somatic cells. The invention is for the
 XX CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 XX CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 XX CC peripheral circulation disturbances, hypertension, angina, cerebral
 XX CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 XX CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 XX CC ischaemic heart disease, asthma and congestive heart failure. The present
 XX CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX CC peptide
 XX SQ Sequence 27 AA;
 Query Match 98.1%; Score 158; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 2.2e-10;
 Matches 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIPNQKCFQHLDDCCARKCNRFNKCVCV 27
 RESULT 8
 AAE38346
 ID AAE38346 standard; peptide; 27 AA.
 AC AAE38346;
 DT 20-NOV-2003 (first entry)
 DE Conus purpurascens kappa-PVIIA analogue peptide, F9Y.
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 OS Conus purpurascens.
 XX Key Location/Qualifiers
 FH Modified-site 4 /label= Hyp
 FT WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PN 28-JAN-2003; 2003WO-US002384.
 XX PP 07-AUG-2003.
 XX PR 28-JAN-2003; 2003WO-US002384.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 XX PI Olivera BM;
 XX WPI; 2003-679464/64.

XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 XX PI Olivera BM;
 XX WPI; 2003-679464/64.
 XX DR Protection and preservation of an organ e.g. heart of a mammal comprises
 XX PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 7; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 XX CC organ protectants. The invention also relates to a method of arresting,
 XX CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 XX CC related conotoxins. The conotoxins can also be used for arresting,
 XX CC protecting or preserving somatic cells. The invention is for the
 XX CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 XX CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 XX CC peripheral circulation disturbances, hypertension, angina, cerebral
 XX CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 XX CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 XX CC ischaemic heart disease, asthma and congestive heart failure. The present
 XX CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX CC peptide
 XX SQ Sequence 27 AA;
 Query Match 98.1%; Score 158; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 2.2e-10;
 Matches 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIPNQKCFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 9
 AAE38343
 ID AAE38343 standard; peptide; 27 AA.
 AC AAE38343;
 DT 20-NOV-2003 (first entry)
 DE Conus purpurascens kappa-PVIIA analogue peptide, R2K.
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 OS Conus purpurascens.
 XX Key Location/Qualifiers
 FH Modified-site 4 /label= Hyp
 FT WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PN 28-JAN-2003; 2003WO-US002384.
 XX PP 07-AUG-2003.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 XX PI Olivera BM;
 XX WPI; 2003-679464/64.

XX
PT Protection and preservation of an organ e.g. heart of a mammal comprises
PT use of a compound binding to kappa-PVIIA-binding site.
XX
PS Disclosure; Page 7; 32pp; English.
XX
CC The invention relates to kappa-PVIIA-related conotoxins and their use as
CC organ protectants. The invention also relates to a method of arresting,
CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC related conotoxins. The conotoxins can also be used for arresting,
CC protecting or preserving somatic cells. The invention is for the
CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
CC peripheral circulation disturbances, hypertension, angina, cerebral
CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
CC peptide
XX
SQ Sequence 27 AA;

Query Match 98.1%; Score 158; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 2.2e-10;
Matches 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CKIPNKKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 10

AAU10207

ID AAU10207 standard; peptide; 27 AA.

XX AC AAU10207;

XX DT 16-JAN-2002 (first entry)

XX DE Snail Kappa-conotoxin PVIIA analogue E2Q.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; R2Q.
XX
OS Conus purpurascens.
XX Synthetic.

XX Key Location/Qualifiers
FH Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27
FT /note= "The C-terminus is either a carboxyl group or an
FT amide group"

XX WO200121648-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US025827.

XX 22-SEP-1999; 99US-0155135P.

XX 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.

XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

XX Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises

PT activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.

XX Claim 1; Page 28; 46pp; English.

XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
CC analogue of the invention

XX Sequence 27 AA;

Query Match 97.5%; Score 157; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 2.8e-10;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27

Db 1 CQIXNKKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 11

AAU10217

ID AAU10217 standard; peptide; 27 AA.

XX AC AAU10217;

XX DT 16-JAN-2002 (first entry)

XX DE Snail Kappa-conotoxin PVIIA analogue V27A.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; V27A.
XX
OS Conus purpurascens.
XX Synthetic.

XX Key Location/Qualifiers
FH Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27
FT /note= "The C-terminus is either a carboxyl group or an
FT amide group"

XX WO200121648-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US025827.

XX 22-SEP-1999; 99US-0155135P.

XX 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.

XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

XX Jones RR;

XX WPI; 2001-648090/74.

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PT conotoxin PVIIA peptide.
XX Claim 1; Page 28; 46pp; English.

CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 SQ Sequence 27 AA;

Query Match 97.5%; Score 157; DB 4; Length 27;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 |||||
 DB 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 |||||

RESULT 12
 AAE38357
 ID AAE38357 standard; peptide; 27 AA.
 XX
 AC AAE38357;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Conus purpurascens kappa-PVIIA analogue peptide, V27A.
 XX
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 OS Conus purpurascens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT
 PN WO2003063782-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 28-JAN-2003; 2003WO-US002384.
 XX
 PR 29-JAN-2002; 2002US-0352219P.
 XX
 PA (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX
 DR WPI; 2003-679464/64.
 XX
 PS Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX
 PS Disclosure; Page 8; 32pp; English.
 XX
 CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,

CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide
 SQ Sequence 27 AA;

Query Match 97.5%; Score 157; DB 6; Length 27;
 Best Local Similarity 96.2%; Pred. No. 2.8e-10;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 |||||
 DB 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 |||||

RESULT 13
 AAE38347
 ID AAE38347 standard; peptide; 27 AA.
 XX
 AC AAE38347;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Conus purpurascens kappa-PVIIA analogue peptide, R2Q.
 XX
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 OS Conus purpurascens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT
 PN WO2003063782-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 28-JAN-2003; 2003WO-US002384.
 XX
 PR 29-JAN-2002; 2002US-0352219P.
 XX
 PA (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX
 DR WPI; 2003-679464/64.
 XX
 PS Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX
 PS Disclosure; Page 7; 32pp; English.
 XX
 CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide

Matches	26;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
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RESULT 16
AAE38338
ID AAE38338 standard; peptide; 27 AA.
XX AC AAE38338;
XX AC AAE38338;
XX DT 20-NOV-2003 (first entry)
XX DE Conus purpurascens kappa-PVIIA analogue peptide, I3A.
XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX KW congestive heart failure; neuropathy; nephropathy; CABG.
XX OS Conus purpurascens.
XX FH Key Location/Qualifiers
XX FT Modified-site 4 /label= Hyp
XX FT
XX PN WO2003063782-A2.
XX PD 07-AUG-2003.
XX PN 28-JAN-2003; 2003WO-US002384.
XX PD 29-JAN-2002; 2002US-0352219P.
XX PR (COGN-) COGNETIX INC.
XX PA (UTAH) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
XX PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
XX PT use of a compound binding to kappa-PVIIA-binding site.
XX PS Disclosure; Page 6; 32pp; English.
XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
XX CC organ protectants. The invention also relates to a method of arresting,
XX CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
XX CC related conotoxins. The conotoxins can also be used for arresting,
XX CC protecting or preserving somatic cells. The invention is for the
XX CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
XX CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
XX CC peripheral circulation disturbances, hypertension, angina, cerebral
XX CC vasoospasm accompanying subarachnoid haemorrhage, anxiety disorder,
XX CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
XX CC ischaemic heart disease, asthma and congestive heart failure. The present
XX CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX CC peptide
XX SQ Sequence 27 AA;
Query Match 96.9%; Score 156; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 3.6e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRINXOKCFQHLDDCCSRKCNRFKCV 27
DB 1 CRAPNOKCFQHLDDCCSRKCNRFKCV 27
RESULT 17
AAE38354
ID AAE38354 standard; peptide; 27 AA.
XX AC AAE38354;
XX DT 20-NOV-2003 (first entry)
XX DE Conus purpurascens kappa-PVIIA analogue peptide, L12A.
XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX KW congestive heart failure; neuropathy; nephropathy; CABG.
XX OS Conus purpurascens.
XX FH Key Location/Qualifiers
XX FT Modified-site 4 /label= Hyp
XX FT
XX PN WO2003063782-A2.
XX PD 07-AUG-2003.
XX PN 28-JAN-2003; 2003WO-US002384.
XX PD 29-JAN-2002; 2002US-0352219P.
XX PR (COGN-) COGNETIX INC.
XX PA (UTAH) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
XX PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
XX PT use of a compound binding to kappa-PVIIA-binding site.
XX PS Disclosure; Page 8; 32pp; English.
XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
XX CC organ protectants. The invention also relates to a method of arresting,
XX CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
XX CC related conotoxins. The conotoxins can also be used for arresting,
XX CC protecting or preserving somatic cells. The invention is for the
XX CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
XX CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
XX CC peripheral circulation disturbances, hypertension, angina, cerebral
XX CC vasoospasm accompanying subarachnoid haemorrhage, anxiety disorder,
XX CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
XX CC ischaemic heart disease, asthma and congestive heart failure. The present
XX CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX CC peptide
XX SQ Sequence 27 AA;
Query Match 96.9%; Score 156; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 3.6e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRINXOKCFQHLDDCCSRKCNRFKCV 27
DB 1 CRAPNOKCFQHLDDCCSRKCNRFKCV 27
RESULT 18
AAU10200
ID AAU10200 standard; peptide; 27 AA.
XX AC AAU10200;
XX AC AAU10200;
XX DT 16-JAN-2002 (first entry)
XX DE Snail Kappa-conotoxin PVIIA analogue R2A.

AC AAE38354;
XX 20-NOV-2003 (first entry)
XX Conus purpurascens kappa-PVIIA analogue peptide, L12A.
XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX KW congestive heart failure; neuropathy; nephropathy; CABG.
XX OS Conus purpurascens.
XX FH Key Location/Qualifiers
XX FT Modified-site 4 /label= Hyp
XX FT
XX PN WO2003063782-A2.
XX PD 07-AUG-2003.
XX PN 28-JAN-2003; 2003WO-US002384.
XX PD 29-JAN-2002; 2002US-0352219P.
XX PR (COGN-) COGNETIX INC.
XX PA (UTAH) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
XX PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
XX PT use of a compound binding to kappa-PVIIA-binding site.
XX PS Disclosure; Page 8; 32pp; English.
XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
XX CC organ protectants. The invention also relates to a method of arresting,
XX CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
XX CC related conotoxins. The conotoxins can also be used for arresting,
XX CC protecting or preserving somatic cells. The invention is for the
XX CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
XX CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
XX CC peripheral circulation disturbances, hypertension, angina, cerebral
XX CC vasoospasm accompanying subarachnoid haemorrhage, anxiety disorder,
XX CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
XX CC ischaemic heart disease, asthma and congestive heart failure. The present
XX CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX CC peptide
XX SQ Sequence 27 AA;
Query Match 96.9%; Score 156; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 3.6e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRINXOKCFQHLDDCCSRKCNRFKCV 27
DB 1 CRIPNOKCFQHADCCSRKCNRFKCV 27
RESULT 18
AAU10200
ID AAU10200 standard; peptide; 27 AA.
XX AC AAU10200;
XX AC AAU10200;
XX DT 16-JAN-2002 (first entry)
XX DE Snail Kappa-conotoxin PVIIA analogue R2A.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; RZA.
 XX Conus purpurascens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX WO200121648-A1.
 PN 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025827.
 XX 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX (COGN-) COGNETIX INC.
 PA Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 PI WPI; 2001-648090/74.
 DR Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.
 PS Claim 1; Page 27; 46pp; English.
 XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX Sequence 27 AA;
 SQ Query Match 96.3%; Score 155; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 4.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CRXNKKCFQHLDDCCSRKCNRFKCV 27
 Db 1 CAIXNKKCFQHLDDCCSRKCNRFKCV 27
 RESULT 19
 AAU10216
 ID AAU10216 standard; peptide; 27 AA.
 XX AAU10216;
 AC AAU10216;
 XX 16-JAN-2002 (first entry)
 DT Snail Kappa-conotoxin PVIIA analogue Q10A.
 DE Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; Q10A.
 XX

OS Conus purpurascens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX WO200121648-A1.
 PN 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025827.
 XX 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX (COGN-) COGNETIX INC.
 PA Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 PI WPI; 2001-648090/74.
 DR Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.
 PS Claim 1; Page 28; 46pp; English.
 XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX Sequence 27 AA;
 SQ Query Match 96.3%; Score 155; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 4.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CRXNKKCFQHLDDCCSRKCNRFKCV 27
 Db 1 CRXNKKCFQHLDDCCSRKCNRFKCV 27
 RESULT 20
 AAU10205
 ID AAU10205 standard; peptide; 27 AA.
 XX AAU10205;
 AC AAU10205;
 XX 16-JAN-2002 (first entry)
 DT Snail Kappa-conotoxin PVIIA analogue F9M.
 DE Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; F9M.
 XX Conus purpurascens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 4

FT Modified-site 27 /note= "Hydroxyproline"
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX
 PN WO200121648-A1.
 XX
 PD 29-MAR-2001.
 FT
 XX
 PF 21-SEP-2000; 2000WO-US025827.
 XX
 XX
 PR 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX
 XX (COGN-) COGNETIX INC.
 XX
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX
 DR WPI; 2001-648090/74.
 XX
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.
 XX
 PS Claim 1; Page 28; 46pp; English.
 XX
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 SQ Sequence 27 AA;
 XX
 Query Match 96.3%; Score 155; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 4.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 XX
 RESULT 21
 AAU10199
 ID AAU10199 standard; peptide; 27 AA.
 XX
 AC AAU10199;
 XX
 XX 16-JAN-2002 (first entry)
 DT
 DE Snail Kappa-conotoxin PVIIA analogue K19A.
 XX
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; K19A.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX
 PN WO200121648-A1.
 XX
 PD 29-MAR-2001.
 FT
 XX 21-SEP-2000; 2000WO-US025827.

PN WO200121648-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-US025827.
 XX
 XX
 PR 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX
 XX (COGN-) COGNETIX INC.
 XX
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX
 DR WPI; 2001-648090/74.
 XX
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.
 XX
 PS Claim 1; Page 27; 46pp; English.
 XX
 CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 SQ Sequence 27 AA;
 XX
 Query Match 96.3%; Score 155; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 4.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 XX
 RESULT 22
 AAU10196
 ID AAU10196 standard; peptide; 27 AA.
 XX
 AC AAU10196;
 XX
 XX 16-JAN-2002 (first entry)
 DT
 DE Snail Kappa-conotoxin PVIIA analogue R18A.
 XX
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; R18A.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX
 PN WO200121648-A1.
 XX
 PD 29-MAR-2001.
 FT
 XX 21-SEP-2000; 2000WO-US025827.

XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
PT activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.
XX Claim 1; Page 28; 46pp; English.
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX analogue of the invention
SQ Sequence 27 AA;
Query Match 96.3%; Score 155; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 4.7e-10;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
RESULT 25
AAU10197
ID AAU10197 standard; peptide; 27 AA.
XX AC AAU10197;
XX DT 16-JAN-2002 (first entry)
XX DE Snail Kappa-conotoxin PVIIA analogue R22A.
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; R22A.
XX Conus purpurascens.
OS Synthetic.
XX Key Location/Qualifiers
FT Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX WO200121648-A1.
XX PD 29-MAR-2001.
XX PF 21-SEP-2000; 2000WO-US025827.
XX PR 22-SEP-1999; 99US-0155135P.
XX PR 20-JUL-2000; 2000US-0219438P.
XX PA (COGN-) COGNETIX INC.
XX PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX WPI; 2001-648090/74.
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
PT activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.

XX Claim 1; Page 27; 46pp; English.
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX analogue of the invention
SQ Sequence 27 AA;
Query Match 96.3%; Score 155; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 4.7e-10;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
RESULT 26
AAU10204
ID AAU10204 standard; peptide; 27 AA.
XX AC AAU10204;
XX DT 16-JAN-2002 (first entry)
XX DE Snail Kappa-conotoxin PVIIA analogue K7A.
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; K7A.
XX Conus purpurascens.
OS Synthetic.
XX Key Location/Qualifiers
FT Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX WO200121648-A1.
XX PD 29-MAR-2001.
XX PF 21-SEP-2000; 2000WO-US025827.
XX PR 22-SEP-1999; 99US-0155135P.
XX PR 20-JUL-2000; 2000US-0219438P.
XX PA (COGN-) COGNETIX INC.
XX PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX WPI; 2001-648090/74.
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
PT activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.
XX Claim 1; Page 28; 46pp; English.
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel

Query Match 96.3%; Score 155; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 4.7e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRINQKCFQHLDDCCSRKCNRFKCV 27
DB 1 CRIPNACFQHLDDCCSRKCNRFKCV 27

RESULT 29
AAE38336
ID AAE38336 standard; peptide; 27 AA.
XX AAE38336;
AC AAE38336;
DT 20-NOV-2003 (first entry)
XX Conus purpurascens kappa-PVIIA analogue peptide, R18A.
DE
XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
KW congestive heart failure; neuropathy; nephropathy; CABG.
XX Conus purpurascens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 4 /label= Hyp
FT
FT
PN WO2003063782-A2.
XX
XX 07-AUG-2003.
XX
XX 28-JAN-2003; 2003WO-US002384.
XX
XX 29-JAN-2002; 2002US-0352219P.
XX
XX (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX
XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
PI Olivera BM;
XX
XX WPI; 2003-679464/64.
XX
XX Protection and preservation of an organ e.g. heart of a mammal comprises
PT use of a compound binding to kappa-PVIIA-binding site.
XX
XX Disclosure; Page 6; 32pp; English.
XX
XX The invention relates to kappa-PVIIA-related conotoxins and their use as
CC organ protectants. The invention also relates to a method of arresting,
CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC related conotoxins. The conotoxins can also be used for arresting,
CC protecting or preserving somatic cells. The invention is for the
CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
CC peripheral circulation disturbances, hypertension, angina, cerebral
CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX peptide
SQ Sequence 27 AA;

Query Match 96.3%; Score 155; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 4.7e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRINQKCFQHLDDCCSRKCNRFKCV 27

Db 1 CRIPNKCFOHLDDCCSAKCNRFKCV 27

RESULT 30
AAE38339
ID AAE38339 standard; peptide; 27 AA.
XX AAE38339;
AC AAE38339;
DT 20-NOV-2003 (first entry)
XX Conus purpurascens kappa-PVIIA analogue peptide, K19A.
DE
XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
KW congestive heart failure; neuropathy; nephropathy; CABG.
XX Conus purpurascens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 4 /label= Hyp
FT
FT
PN WO2003063782-A2.
XX
XX 07-AUG-2003.
XX
XX 28-JAN-2003; 2003WO-US002384.
XX
XX 29-JAN-2002; 2002US-0352219P.
XX
XX (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX
XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
PI Olivera BM;
XX
XX WPI; 2003-679464/64.
XX
XX Protection and preservation of an organ e.g. heart of a mammal comprises
PT use of a compound binding to kappa-PVIIA-binding site.
XX
XX Disclosure; Page 7; 32pp; English.
XX
XX The invention relates to kappa-PVIIA-related conotoxins and their use as
CC organ protectants. The invention also relates to a method of arresting,
CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC related conotoxins. The conotoxins can also be used for arresting,
CC protecting or preserving somatic cells. The invention is for the
CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
CC peripheral circulation disturbances, hypertension, angina, cerebral
CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX peptide
SQ Sequence 27 AA;

Query Match 96.3%; Score 155; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 4.7e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRINQKCFQHLDDCCSRKCNRFKCV 27
DB 1 CRIPNKCFOHLDDCCSRKCNRFKCV 27

RESULT 31

AAE38345
ID AAE38345 standard; peptide; 27 AA.
XX AC AAE38345;
XX AC AAE38345;
DT DT 20-NOV-2003 (first entry)
XX DE Conus purpurascens kappa-PVIIA analogue peptide, F9M.
XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; KW ischemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina; KW retinopathy; coronary artery bypass graft surgery; acute heart failure; KW congestive heart failure; neuropathy; nephropathy; CABG. OS OS XX OS Conus purpurascens.
XX FH Key Location/Qualifiers
FT Modified-site 4
FT /label= HYP
XX WO2003063782-A2.
PX PD
XX PD 07-AUG-2003.
PX PF 28-JAN-2003; 2003WO-US002384.
XX PX 29-JAN-2002; 2002US-0352219P.
PR COGN-) COGNETIX INC.
XX PA (UTAH) UNIV UTAH RES FOUND.
PX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM; PI Olivera BM;
XX WIPI; 2003-679464/64.
DR PT Protection and preservation of an organ e.g. heart of a mammal comprises PT use of a compound binding to kappa-PVIIA-binding site.
PS Disclosure; Page 7; 32pp; English.
CC The invention relates to kappa-PVIIA-related conotoxins and their use as CC organ protectants. The invention also relates to a method of arresting, CC protecting and/or preserving an organ of a mammal using kappa-PVIIA- CC related conotoxins. The conotoxins can also be used for arresting, CC protecting or preserving somatic cells. The invention is for the CC treatment of arrhythmia, urinary incontinence, reperfusion injury, CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, CC peripheral circulation disturbances, hypertension, angina, cerebral CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery, CC ischaemic heart disease, asthma and congestive heart failure. The present CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analoque XX QY Sequence 27 AA;
SQ Query Match 96.3%; Score 155; DB 6; Length 27; Best Local Similarity 92.6%; Pred.No. 4.7e-10; Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0
OY 1 CRINQKCFQHLDCCSRKCNRFNKCV 27
DB 1 CRIPNQCMQHLLDCCSRKCNRFNKCV 27
RESULT 32
AAP38337
ID AAP38337 standard; peptide; 27 AA.
XX AP AAP38337;
XX X

KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

XX Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp

XX WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

XX (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;

XX Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 7; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide

XX Sequence 27 AA;

Query Match 96.3%; Score 155; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 4.7e-10;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27

DB 1 CAIPNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 34

AAE38356

ID AAE38356 standard; peptide; 27 AA.

XX AAE38356;

XX 20-NOV-2003 (first entry)

DE Conus purpurascens kappa-PVIIA analogue peptide, Q10A.

XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

XX Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp

XX WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

XX (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;

XX Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 8; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide

XX Sequence 27 AA;

Query Match 96.3%; Score 155; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 4.7e-10;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27

DB 1 CRIPNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 35

AAE38350

ID AAE38350 standard; peptide; 27 AA.

XX AAE38350;

XX 20-NOV-2003 (first entry)

DE Conus purpurascens kappa-PVIIA analogue peptide, Q6A.

XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

XX Key Location/Qualifiers

FT Modified-site 4 /label= Hyp

FT

XX WO2003063782-A2.
 XX 07-AUG-2003.
 XX 28-JAN-2003; 2003WO-US002384.
 XX 29-JAN-2002; 2002US-0352219P.
 XX (COGN-) COGNETIX INC.
 XX (UTAH) UNIV UTAH RES FOUND.
 XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 XX Olivera BM;
 XX WPI; 2003-679464/64.
 XX Protection and preservation of an organ e.g. heart of a mammal comprises
 XX use of a compound binding to kappa-PVIIA-binding site.
 XX Disclosure; Page 7; 32pp; English.
 XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 XX organ protectants. The invention also relates to a method of arresting,
 XX protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 XX related conotoxins. The conotoxins can also be used for arresting,
 XX protecting or preserving somatic cells. The invention is for the
 XX treatment of arrhythmia, urinary incontinence, reperfusion injury,
 XX diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 XX peripheral circulation disturbances, hypertension, angina, cerebral
 XX vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 XX cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 XX ischaemic heart disease, asthma and congestive heart failure. The present
 XX sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide
 XX Sequence 27 AA;
 XX Query Match 96.3%; Score 155; DB 6; Length 27;
 XX Best Local Similarity 92.6%; Pred. No. 4.7e-10;
 XX Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 27
 DB 1 CRIPNAKCFQHLDDCCSRKCNRFNKC 27
 RESULT 36
 AAU10213
 ID AAU10213 standard; peptide; 27 AA.
 AC AAU10213;
 XX 16-JAN-2002 (first entry)
 DE Snail Kappa-conotoxin PVIIA analogue N24A.
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; N24A.
 OS Conus purpurascens.
 OS Synthetic.
 XX Key Location/Qualifiers
 XX Modified-site 4 /note= "Hydroxyproline"
 XX Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
 XX amide group"
 XX WO200121648-A1.

PD 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025827.
 XX 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX (COGN-) COGNETIX INC.
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX WPI; 2001-648090/74.
 XX Treating disorders associated with radical depolarization of excitable
 XX membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises
 XX activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.
 XX Claim 1; Page 28; 46pp; English.
 XX The invention relates to treating disorders associated with radical
 XX depolarisation of excitable membrane by activating a KATP channel
 XX comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 XX PVIIA) peptide or its analogue, derivative or physiologically active
 XX salt. The conotoxins are used for treating disorders associated with
 XX radical depolarisation of excitable membrane by activating a KATP
 XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 XX ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 XX analogue of the invention
 XX Sequence 27 AA;
 XX Query Match 95.0%; Score 153; DB 4; Length 27;
 XX Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 XX Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 27
 DB 1 CRXNKKCFQHLDDCCSRKCNRFNKC 27
 RESULT 37
 AAU10209
 ID AAU10209 standard; peptide; 27 AA.
 XX AAU10209;
 AC AAU10209;
 XX 16-JAN-2002 (first entry)
 DT Snail Kappa-conotoxin PVIIA analogue D14A.
 DE Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; D14A.
 OS Conus purpurascens.
 OS Synthetic.
 XX Key Location/Qualifiers
 XX Modified-site 4 /note= "Hydroxyproline"
 XX Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
 XX amide group"
 XX WO200121648-A1.
 XX 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025827.
 XX 22-SEP-1999; 99US-0155135P.

PR 20-JUL-2000; 2000US-0219438P.
XX (COGN-) COGNETIX INC.
XX
PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises
PT activating a KATP channel by administering to an individual a kappa-
XX conotoxin PVIIA peptide.
XX
XX Claim 1; Page 28; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
CC analogue of the invention
XX
XX Sequence 27 AA;
SQ

Query Match 95.0%; Score 153; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 7.7e-10;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 38
AAU10219
ID AAU10219 standard; peptide; 27 AA.
XX
XX AAU10219;
AC
XX
XX 16-JAN-2002 (first entry)
DT
DE
DE Snail Kappa-conotoxin PVIIA analogue NSA.
XX
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; NSA.
XX
XX Conus purpurascens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27
FT Modified-site /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX
XX WO200121648-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 21-SEP-2000; 2000WO-US025827.
PF
XX
XX 22-SEP-1999; 99US-0155135P.
PR
XX 20-JUL-2000; 2000US-0219438P.
XX
XX (COGN-) COGNETIX INC.
PA
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable

PI Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises
PT activating a KATP channel by administering to an individual a kappa-
XX conotoxin PVIIA peptide.
XX
XX Claim 1; Page 28; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
CC analogue of the invention
XX
XX Sequence 27 AA;
SQ

Query Match 95.0%; Score 153; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 7.7e-10;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 39
AAU10201
ID AAU10201 standard; peptide; 27 AA.
XX
XX AAU10201;
AC
XX
XX 16-JAN-2002 (first entry)
DT
DE
DE Snail Kappa-conotoxin PVIIA analogue F9A.
XX
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; F9A.
XX
XX Conus purpurascens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27
FT Modified-site /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX
XX WO200121648-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 21-SEP-2000; 2000WO-US025827.
PF
XX
XX 22-SEP-1999; 99US-0155135P.
PR
XX 20-JUL-2000; 2000US-0219438P.
XX
XX (COGN-) COGNETIX INC.
PA
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable

PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.

PS Claim 1; Page 27; 46pp; English.

XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention

XX Sequence 27 AA;

Query Match 95.0%; Score 153; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFKCV 27
 |||||
 DB 1 CRXNQKCAQHLDDCCSRKCNRFKCV 27

RESULT 40

AAU10215
 ID AAU10215 standard; peptide; 27 AA.

XX AC AAU10215;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue D13A.

KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; D13A.

OS Conus purpurascens.
 OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 4

FT /note= "Hydroxyproline"

FT Modified-site 27

FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"

XX WO200121648-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US025827.

XX 22-SEP-1999; 99US-0155135P.

XX 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.

XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.

PS Claim 1; Page 28; 46pp; English.

XX

CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention

XX Sequence 27 AA;

Query Match 95.0%; Score 153; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFKCV 27
 |||||
 DB 1 CRXNQKCFQHLDDCCSRKCNRFKCV 27

RESULT 41

AAU10211

ID AAU10211 standard; peptide; 27 AA.

XX AC AAU10211;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue N21A.

KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; N21A.

OS Conus purpurascens.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 4

FT /note= "Hydroxyproline"

FT Modified-site 27

FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"

XX WO200121648-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US025827.

XX 22-SEP-1999; 99US-0155135P.

XX 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.

XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.

PS Claim 1; Page 28; 46pp; English.

CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active

CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention

XX Sequence 27 AA;

Query Match 95.0%; Score 153; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27
 |||||
 DB 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 42

AAE38353
 ID AAE38353 standard; peptide; 27 AA.

AC AAE38353;

DT 20-NOV-2003 (first entry)

DE Conus purpurascens kappa-PVIIA analogue peptide, N24A.

XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

XX Conus purpurascens.

XX Key Location/Qualifiers
 FH Modified-site 4 /label= Hyp
 FT

PN WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 7; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide

XX Sequence 27 AA;

Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 7.7e-10;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27
 |||||
 DB 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 43

AAE38351
 ID AAE38351 standard; peptide; 27 AA.

AC AAE38351;

DT 20-NOV-2003 (first entry)

DE Conus purpurascens kappa-PVIIA analogue peptide, N21A.

XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

XX Conus purpurascens.

XX Key Location/Qualifiers
 FH Modified-site 4 /label= Hyp
 FT

PN WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 7; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide

XX Sequence 27 AA;

Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 7.7e-10;

XX AC AAE38349;
 XX DT 20-NOV-2003 (first entry)
 XX DE Conus purpurascens kappa-PVIIA analogue peptide, D14A.
 XX DE
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX FT Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 XX WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PF 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 XX PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 7; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide
 XX SQ Sequence 27 AA;
 Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 7.7e-10;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRIPNKCQFQHLDDCCSRKCNRFNKCVCV 27
 Db |||||
 1 CRIPNKCQFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 47
 ID AAE38359
 XX AAE38359 standard; peptide; 27 AA.
 XX AC AAE38359;
 XX DT 20-NOV-2003 (first entry)
 XX DE Conus purpurascens kappa-PVIIA analogue peptide, D14A.
 XX DE
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX FT Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 XX WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PF 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 XX PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 7; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide
 XX SQ Sequence 27 AA;
 Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 7.7e-10;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRIPNKCQFQHLDDCCSRKCNRFNKCVCV 27
 Db |||||
 1 CRIPNKCQFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 47
 ID AAE38359
 XX AAE38359 standard; peptide; 27 AA.
 XX AC AAE38359;
 XX DT 20-NOV-2003 (first entry)
 XX DE Conus purpurascens kappa-PVIIA analogue peptide, D14A.
 XX DE
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX FT Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 XX WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PF 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 XX PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 8; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide
 XX SQ Sequence 27 AA;
 Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRIXNKCQFQHLDDCCSRKCNRFNKCVCV 27
 Db |||||
 1 CRIXNKCQFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 48
 ID AAU10208
 XX AAU10208 standard; peptide; 27 AA.
 XX AC AAU10208;
 XX DT 16-JAN-2002 (first entry)
 XX DE Snail kappa-conotoxin PVIIA analogue H11A.
 XX DE
 XX KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KARP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; H11A.

DE Conus purpurascens kappa-PVIIA analogue peptide, NSA.
 XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 XX ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX FT Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 XX WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PF 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 XX PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 8; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide
 XX SQ Sequence 27 AA;
 Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRIXNKCQFQHLDDCCSRKCNRFNKCVCV 27
 Db |||||
 1 CRIXNKCQFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 48
 ID AAU10208
 XX AAU10208 standard; peptide; 27 AA.
 XX AC AAU10208;
 XX DT 16-JAN-2002 (first entry)
 XX DE Snail kappa-conotoxin PVIIA analogue H11A.
 XX DE
 XX KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KARP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; H11A.

XX OS Conus purpurascens.
 XX OS Synthetic.
 XX FH Key
 XX FT Modified-site 4
 XX FT Location/Qualifiers
 XX FT /note= "Hydroxyproline"
 XX FT Modified-site 27
 XX FT /note= "The C-terminus is either a carboxyl group or an
 XX FT amide group"
 XX PN WO200121648-A1.
 XX XX
 XX PD 29-MAR-2001.
 XX XX
 XX PF 21-SEP-2000; 2000WO-US025827.
 XX XX
 XX PR 22-SEP-1999; 99US-0155135P.
 XX PR 20-JUL-2000; 2000US-0219438P.
 XX XX
 XX PA (COGN-) COGNETIX INC.
 XX XX
 XX PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX PI Jones RR;
 XX DR WPI; 2001-648090/74.
 XX XX
 XX FT Treating disorders associated with radical depolarization of excitable
 XX FT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 XX FT activating a KATP channel by administering to an individual a kappa-
 XX FT conotoxin PVIIA peptide.
 XX XX
 XX PS Claim 1; Page 28; 46pp; English.
 XX XX
 XX CC The invention relates to treating disorders associated with radical
 XX CC depolarisation of excitable membrane by activating a KATP channel
 XX CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 XX CC PVIIA) peptide or its analogue, derivative or physiologically active
 XX CC salt. The conotoxins are used for treating disorders associated with
 XX CC radical depolarisation of excitable membrane by activating a KATP
 XX CC channel, especially cardiac ischemia, cerebral ischemia, ocular
 XX CC ischemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 XX CC analogue of the invention
 XX SQ Sequence 27 AA;
 XX XX
 XX Query Match 93.8%; Score 151; DB 4; Length 27;
 XX Best Local Similarity 96.3%; Pred. No. 1.3e-09;
 XX Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRXNKKCFQALDDCCSRKCNRFNKCVCV 27
 RESULT 49
 AAEE38348
 ID RAE38348 standard; peptide; 27 AA.
 XX AC RAE38348;
 XX XX
 XX DT 20-NOV-2003 (first entry)
 XX XX
 XX DE Conus purpurascens kappa-PVIIA analogue peptide, H11A.
 XX XX
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 XX KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 XX KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 XX KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 XX KW congestive heart failure; neuropathy; nephropathy; CAGB.
 XX OS Conus purpurascens.
 XX XX

FH Key Location/Qualifiers
 FT Modified-site 4
 FT /label= Hyp
 XX WO2003063782-A2.
 XX PN 07-AUG-2003.
 XX PD 28-JAN-2003; 2003WO-US002384.
 XX PF 29-JAN-2002; 2002US-0352219P.
 XX PR (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX XX
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 XX PI Olivera BM;
 XX XX
 XX DR WPI; 2003-679464/64.
 XX XX
 XX FT Protection and preservation of an organ e.g. heart of a mammal comprises
 XX FT use of a compound binding to kappa-PVIIA-binding site.
 XX XX
 XX PS Disclosure; Page 7; 32pp; English.
 XX XX
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 XX CC organ protectants. The invention also relates to a method of arresting,
 XX CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 XX CC related conotoxins. The conotoxins can also be used for arresting,
 XX CC protecting or preserving somatic cells. The invention is for the
 XX CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 XX CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 XX CC peripheral circulation disturbances, hypertension, angina, cerebral
 XX CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 XX CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 XX CC ischaemic heart disease, asthma and congestive heart failure. The present
 XX CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX CC peptide
 XX SQ Sequence 27 AA;
 XX XX
 XX Query Match 93.8%; Score 151; DB 6; Length 27;
 XX Best Local Similarity 92.6%; Pred. No. 1.3e-09;
 XX Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIPNKKCFQALDDCCSRKCNRFNKCVCV 27
 RESULT 50
 ABB96846
 ID ABB96846 standard; peptide; 27 AA.
 XX AC ABB96846;
 XX XX
 XX DT 12-JUL-2002. (first entry)
 XX XX
 XX DE Omega-conopeptide E6.2 toxin sequence.
 XX XX
 XX KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 XX KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 XX KW antimigraine; antidiabetic; tranquiliser; vulnery; antipsychotic;
 XX KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 XX KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 XX KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 XX KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 XX KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 XX KW psychosis; anxiety; schizophrenia.
 XX OS Conus ermineus.
 XX XX
 XX PN WO200207675-A2.

XX 31-JAN-2002.
 XX 23-JUL-2001; 2001WO-US023041.
 XX 21-JUL-2000; 2000US-0219616P.
 PR 05-FEB-2001; 2001US-0265888P.
 XX (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;
 XX WPI; 2002-257318/30.
 XX New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.
 XX Claim 1(a); Page 71; 195pp; English.
 XX The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96807-ABB96905 represent omega-conopeptide
 CC toxin sequences
 XX Sequence 27 AA;
 SQ
 Query Match 48.8%; Score 78.5; DB 5; Length 27;
 Best Local Similarity 46.2%; Pred. No. 0.098;
 Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
 QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
 | : : ||| | ||| : : |||
 Db 2 CKPKGRKCFPHQKDCNKTCTR-SKC 26
 | : : ||| | ||| : : |||
 RESULT 51
 ABB96638
 ID ABB96638 standard; peptide; 72 AA.
 XX
 AC ABB96638;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Omega-conopeptide E6.2 propeptide.
 XX
 KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.
 XX Conus ermineus.
 OS

XX WO200207675-A2.
 XX 31-JAN-2002.
 XX 23-JUL-2001; 2001WO-US023041.
 XX 21-JUL-2000; 2000US-0219616P.
 PR 05-FEB-2001; 2001US-0265888P.
 XX (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;
 XX WPI; 2002-257318/30.
 DR N-PSDB; ABL98897.
 XX New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.
 XX Claim 1(c); Page 42; 195pp; English.
 XX The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96595-ABB96697 represent omega-conopeptide
 CC propeptide sequences
 XX Sequence 72 AA;
 SQ
 Query Match 48.8%; Score 78.5; DB 5; Length 72;
 Best Local Similarity 46.2%; Pred. No. 0.22;
 Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
 QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
 | : : ||| | ||| : : |||
 Db 47 CKPKGRKCFPHQKDCNKTCTR-SKC 71
 | : : ||| | ||| : : |||
 RESULT 52
 AAR39628
 ID AAR39628 standard; peptide; 26 AA.
 XX
 AC AAR39628;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-DEC-1993 (first entry)
 XX
 DE SNX-202.
 XX Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
 KW calcium channel; neuron; contraction; guinea pig; ileum; MVIIA;
 KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
 KW narcotics.
 XX Synthetic.
 OS

FH Key Location/Qualifiers
 FT Disulfide-bond 1. .16
 FT Disulfide-bond 8. .20
 FT Disulfide-bond 15. .26
 FT Modified-site 26
 FT /note= "Amidated C-terminal"
 XX
 PN WO9313128-A1.
 XX
 PD 08-JUL-1993.
 XX
 PF 30-DEC-1992; 92WO-US011349.
 XX
 PR 30-DEC-1991; 91US-00814759.
 XX
 PA (NEUR-) NEUREX CORP.
 XX
 PI Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;
 XX WPI; 1993-227270/28.
 DR
 PT Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
 PT calcium channels - to induce analgesia, enhance opiate analgesics, treat
 PT pain etc.
 XX
 PS Claim 1; Fig 2; 90pp; English.
 XX
 CC The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
 CC derivatives of these, which may be used to produce analgesia in a mammal.
 CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
 CC tissue. This is shown by the peptides ability to stimulate contraction in
 CC guinea pig ileum and to bind to OCT MVIIR binding sites present in
 CC neuronal tissue. OCTs are components of peptide toxins derived from
 CC marine snails of the genus Conus, and act as calcium channel blockers.
 CC These OCTs may be used to replace opioids in the treatment of chronic pain
 CC or to reduce the opiod dosage required. This helps to reduce dependence
 CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 CC
 SQ Sequence 26 AA;
 Query Match 46.6%; Score 75; DB 2; Length 26;
 Best Local Similarity 42.3%; Pred. No. 0.23;
 Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
 DB 1 CKLKGQSCSLMYDCCSGCGSGKC 26
 RESULT 53
 AAR37774
 ID AAR37774 standard; peptide; 26 AA.
 AC AAR37774;
 XX
 DT 25-MAR-2003 (revised)
 DT 08-SEP-1993 (first entry)
 XX
 DE SNX-202.
 XX
 KW Ischaemia; neuronal; omega-conotoxin; OCT; MVIIR; MVIIC; MVIID; MVIIB;
 KW GVIA; GVIIA; GVIA; GVIA; GVIA; GVIA; GVIA; GVIA; GVIA; GVIA;
 KW antihistamine; blood pressure; stroke; SNX-207; delayed treatment;
 KW N-channel mediated neurotransmitter release.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1. .16
 FT Disulfide-bond 8. .20
 FT Disulfide-bond 15. .26
 XX

PN WO9310145-A1.
 XX
 PD 27-MAY-1993.
 XX
 PF 12-NOV-1992; 92WO-US009766.
 XX
 PR 12-NOV-1991; 91US-00789913.
 PR 17-JUL-1992; 92US-00916478.
 XX
 PA (NEUR-) NEUREX CORP.
 XX
 PI Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;
 FI Yamashiro DH;
 XX WPI; 1993-182487/22.
 DR
 XX
 PT Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
 PT bind specifically to omega-conotoxin MVIIR binding sites.
 XX
 PS Disclosure; Fig 2; 103pp; English.
 XX
 CC The C-terminal is amidated. Ischaemia-related neuronal damage in mammals
 CC is reduced by admin. 4-24 hr after onset of ischaemia, of a cpd. (I)
 CC which binds selectively to an omega-conotoxin (OCT) MVIIR site in
 CC neuronal tissue. (I) has selectivity at least 100 expressed as ratio of
 CC binding affinity for the MVIIR site to that for the MVIIC site. (I) is
 CC one of the OCTs MVIIR, MVIIB, GVIA, GVIIA or RVIA or it is the cpd. SNX-
 CC 207. (I) is esp. used to reduce neuronal damage caused by stroke. By
 CC delaying admin. for some time (compare US5051403 where cpds. are given
 CC within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage
 CC is achieved. (I) is admin. e.g. by intracerebroventricular (ICV)
 CC injection at 0.1-20 microg/kg, but can also be given i.v. (opt. after
 CC treatment with antihistamines to minimise redn. in blood pressure caused
 CC by (I)). (I) is also at least as effective as the specified conotoxins
 CC for (1) selective inhibition of N-type voltage-gated Ca currents in
 CC neuronal tissue and (2) selective inhibition of N-channel mediated
 CC neurotransmitter release in neuronal tissue. Primary sequences of omega-
 CC conopeptides are given in AAR37752-62. Several analog omega-conopeptides
 CC are given in AAR37763-76. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 26 AA;
 Query Match 46.6%; Score 75; DB 2; Length 26;
 Best Local Similarity 42.3%; Pred. No. 0.23;
 Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
 DB 1 CKLKGQSCSLMYDCCSGCGSGKC 26
 RESULT 54
 AAR19570
 ID AAR19570 standard; peptide; 26 AA.
 AC AAR19570;
 XX
 DT 14-OCT-1997 (first entry)
 XX
 DE SNX-202, omega conopeptide derivative used for pain relief.
 XX
 KW Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;
 KW N-type voltage-sensitive calcium channel; block; Conus.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 26
 FT /note= "amidated"
 XX
 PN WO9701351-A1.
 XX
 PD 16-JAN-1997.


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XX PF 26-JUN-1996; 96WO-US011041.
XX PF
XX PR 27-JUN-1995; 95US-00496947.
XX PR 08-MAR-1996; 96US-00613400.
XX XX
XX PA (NEUR-) NEUREX CORP.
XX
XX PI Amstutz GA, Bowersox SS, Gohil K, Adriaenssens PI, Kristipati R;
XX PI Gadbois T, Pettus MR, Luther RR;
XX XX
XX DR WPI; 1997-100012/09.
XX
XX PT Stable omega-conopeptide compositions - for producing analgesia and for
XX PT inhibiting progression of neuropathic pain disorders.
XX XX
XX PS Disclosure; Fig 4; 47pp; English.
XX
XX CC AAW19555-W19572 are omega conopeptides (OCs) derived from natural
XX CC peptides from Conus sp. (cone snails). The peptides and their analogues
XX CC are used as analgesics acting by blocking N-type voltage-sensitive
XX CC calcium channels. The OCs can be used to treat neuropathic pain as a
XX CC result of e.g. insult to the spinal cord or peripheral nerves, cancer,
XX CC bone degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes
XX CC zoster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or
XX CC hyperalgesia. The OCs are preferably administered in a medicament via an
XX CC epidural route in a continuous infusion or sustained release formulation.
XX CC The OCs can provide pain relief when administered epidurally in the
XX CC absence of a permeation enhancer, at doses that are comparable to
XX CC effective analgesic doses using intrathecal administration. OC
XX CC formulations comprising an OC and a carboxylic acid buffer anti-oxidant.
XX CC They also confer stability to solutions containing them for prolonged
XX CC treatment methods and long-term storage
XX XX
XX SQ Sequence 26 AA;

Query Match 46.6%; Score 75; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.23;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CRIXNQKCFQHLDDCCSRKCNRENKC 26
|:::|:::|:::|:::|:::|
Db 1 CLKUGQSCSRLMYDCCSGCGRSGKC 26

RESULT 55
AAW12985
ID AAW12985 standard; peptide; 26 AA.
XX
XX AC AAW12985;
XX
XX DT 25-MAR-2003 (revised)
XX DT 22-APR-1997 (first entry)
XX
XX DE Omega conopeptide SNX-202.
XX
XX KW Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition;
XX KW neuronal damage; schizophrenia; tardive dyskinesia; analgesia;
XX KW acute dystonic reactions; inflammation; epilepsy.
XX
XX OS Synthetic.
XX
XX PN US5587454-A.
XX
XX XX 24-DEC-1996.
XX
XX PF 15-APR-1993; 93US-00049794.
XX
XX PR 30-DEC-1991; 91US-00814759.
XX PR 30-DEC-1992; 92WO-US011349.
XX
XX PA (NEUR-) NEUREX CORP.
XX

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PI Gohil KC, Miljanich GP, Valentino KL, Justice A, Singh T;
XX
XX DR WPI; 1997-064830/06.
XX
XX PT Omega conopeptide(s) - useful as analgesics, esp. for treating
XX PT neuropathic pain.
XX
XX PS Disclosure; Col 51-52; 58pp; English.
XX
XX CC The present peptide is an omega conopeptide, useful as an analgesic,
XX CC especially for treating neuropathic pain. The peptide, which can be
XX CC prepared by solid phase synthesis, can also be used to inhibit neuronal
XX CC damage and treat schizophrenia, tardive dyskinesia, acute dystonic
XX CC reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
XX CC PF field.)
XX
XX SQ Sequence 26 AA;

Query Match 46.6%; Score 75; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.23;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CRIXNQKCFQHLDDCCSRKCNRENKC 26
|:::|:::|:::|:::|:::|
Db 1 CLKUGQSCSRLMYDCCSGCGRSGKC 26

RESULT 56
AAW72625
ID AAW72625 standard; peptide; 26 AA.
XX
XX AC AAW72625;
XX
XX DT 27-AUG-2003 (revised)
XX DT 06-JAN-1999 (first entry)
XX
XX DE Conus genus analogue omega-conopeptide SNX-202.
XX
XX KW Conus genus; marine snail; cone snail; omega-conopeptide; analgesia;
XX KW nociceptive pain; neuropathic pain; neuronal tissue; conotoxin;
XX KW inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction;
XX KW rheumatoid arthritis; epilepsy.
XX
XX OS Conus.
XX
XX PN US5824645-A.
XX
XX PD 20-OCT-1998.
XX
XX PF 01-NOV-1996; 96US-00742774.
XX
XX PR 30-DEC-1991; 91US-00814759.
XX PR 15-APR-1993; 93US-00049794.
XX PR 03-JUL-1996; 96US-00675354.
XX
XX PA (NEUR-) NEUREX CORP.
XX
XX PI Miljanich GP, Valentino KL, Gohil KC, Justice A, Singh T;
XX
XX DR WPI; 1998-582596/49.
XX
XX PT Treatment of inflammation, comprises administration of omega-conopeptide
XX PT - effective to block voltage-gated calcium channels, bind with high
XX PT affinity to omega-conopeptide binding site, and inhibit neurotransmitter
XX PT release.
XX
XX PS Disclosure; Fig 2; 58pp; English.
XX
XX CC A method has been developed for the treatment of inflammation in a
XX CC subject. The method comprises administration of an omega-conopeptide
XX CC effective to: (i) block voltage-gated calcium channels, (ii) bind with
XX CC high affinity to an omega-conopeptide binding site; and (iii) inhibit
XX CC neurotransmitter release from nervous tissue. The method is used to treat

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QY 1 CRXNKCFOHLDCCSRKCNRFNC 26
 Db 1 CKLKGSCSLMWYDCCSGSGRGKC 26

RESULT 61
 ID ABB96887
 AC ABB96887;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Omega-conopeptide S6.2 toxin sequence.

XX Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.

OS Conus striatus.

XX WO200207675-A2.

PN 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023041.

XX 21-JUL-2000; 2000US-0219616P.

PR 05-FEB-2001; 2001US-0265888P.

XX (UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;

XX WPI; 2002-257318/30.

XX New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.

XX Claim 1(a); Page 72; 195pp; English.

XX The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96807-ABB96905 represent omega-conopeptide
 CC toxin sequences

XX Sequence 26 AA;

Query Match 46.0%; Score 74; DB 5; Length 26;

Best Local Similarity 42.3%; Pred. No. 0.29;
 Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 CRXNKCFOHLDCCSRKCNRFNC 26
 Db 1 CKLKGSCSLMWYDCCSGSGRGKC 26

RESULT 62
 ID ABB96679
 AC ABB96679 standard; peptide; 30 AA.

XX ABB96679;

XX 12-JUL-2002 (first entry)

XX Omega-conopeptide S6.2 propeptide.

XX Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.

OS Conus striatus.

XX WO200207675-A2.

PN 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023041.

XX 21-JUL-2000; 2000US-0219616P.

PR 05-FEB-2001; 2001US-0265888P.

XX (UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;

XX WPI; 2002-257318/30.

DR N-PSDB; ABL98938.

XX New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.

XX Claim 1(c); Page 62; 195pp; English.

XX The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96595-ABB96697 represent omega-conopeptide
 CC propeptide sequences

Query Match	44.1%;	Score 71;	DB 2;	Length 26;
Best Local Similarity	42.3%;	Pred. No. 0.62;		

Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNFNKC 26
 Db 1 CKLKGOSCRKTSYDCCSGSGRSGKC 26

RESULT 65

AAW19551
 ID AAR37760 standard; peptide; 26 AA.

AC AAR37760;

DT 25-MAR-2003 (revised)

DT 08-SEP-1993 (first entry)

XX SVIB/SNX-183.

XX Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB;
 KW GVIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment;
 KW antihistamine; blood pressure; N-type voltage-gated Ca currents;
 KW N-channel mediated neurotransmitter release.

XX Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..16
 FT Disulfide-bond 8..20
 FT Disulfide-bond 15..26

XX WO9310145-A1.

XX 27-MAY-1993.

XX 12-NOV-1992; 92WO-US009766.

XX 12-NOV-1991; 91US-00789913.

XX 17-JUL-1992; 92US-00916478.

XX (NEUR-) NEUREX CORP.

XX Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;
 FI Yamashiro DH;

XX WPI; 1993-182487/22.

XX Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
 bind specifically to omega-conotoxin MVIIA binding sites.

XX Disclosure; Fig 1; 103pp; English.

XX Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24
 CC hr after onset of ischaemia, of a cpd. (I) which binds selectively to an
 CC omega-conotoxin (OCT) MVIIA site in neuronal tissue. (I) has selectivity
 CC at least 100 expressed as ratio of binding affinity for the MVIIA site to
 CC that for the MVIIC site. (I) is one of the OCTs MVIIA, MVIIB, GVIA, GVIIA
 CC or RVIA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal
 CC damage caused by stroke. By delaying admin. for some time (compare
 CC US051403 where cpds. are given within 1 hr of the onset of ischaemia) a
 CC greater reduction in neuronal damage is achieved. (I) is admin. e.g. by
 CC intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also
 CC be given i.v. (opt. after treatment with antihistamines to minimise redn.
 CC in blood pressure caused by (I)). (I) is also at least as effective as
 CC the specified conotoxins for (I). (I) is also at least as effective as
 CC gated Ca currents in neuronal tissue and (2) selective inhibition of N-
 CC channel mediated neurotransmitter release in neuronal tissue. Primary
 CC sequences of omega-conopeptides are given in AAR37752-62. Several analog
 CC omega-conopeptides are given in AAR37763-76. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX Sequence 26 AA;

Query Match 44.1%; Score 71; DB 2; Length 26;

Best Local Similarity 42.3%; Pred. No. 0.62;
 Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNFNKC 26
 Db 1 CKLKGOSCRKTSYDCCSGSGRSGKC 26

RESULT 66

AAW19551

ID AAW19551 standard; peptide; 26 AA.

XX AAW19551;

DT 27-AUG-2003 (revised)

DT 13-OCT-1997 (first entry)

XX Natural omega-conopeptide SVIB/SNX-183 used for pain relief.

XX Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;

XX N-type voltage-sensitive calcium channel; block; Conus.

XX Conus.

XX Key Location/Qualifiers
 FH Modified-site 26
 FT /note= "optionally amidated"

XX WO9701351-A1.

XX 16-JAN-1997.

XX 26-JUN-1996; 96WO-US011041.

XX 27-JUN-1995; 95US-00496847.

XX 08-MAR-1996; 96US-00613400.

XX (NEUR-) NEUREX CORP.

XX Amstutz GA, Bowersox SS, Gohil K, Adriaenssens PI, Kristipati R;
 PI Gadbois T, Pettus MR, Luther RR;

XX WPI; 1997-100012/09.

XX Stable omega conopeptide compositions - for producing analgesia and for
 inhibiting progression of neuropathic pain disorders.

XX Disclosure; Fig 2, Fig 3; 47pp; English.

XX AAW19544-W19553 are naturally occurring omega conopeptides (OCs) isolated
 CC from Conus sp. (cone snails). The peptides and their analogues are used
 CC as analgesics acting by blocking N-type voltage-sensitive calcium
 CC channels. The OCs can be used to treat neuropathic pain as a result of
 CC e.g. insult to the spinal cord or peripheral nerves, cancer, bone
 CC degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes zoster
 CC neuropathy, diabetic neuropathy, hyperesthesia, allodynia or
 CC hyperalgesia. The OCs are preferably administered in a medicament via an
 CC epidural route in a continuous infusion or sustained release formulation.
 CC The OCs can provide pain relief when administered epidurally in the
 CC absence of a permeation enhancer, at doses that are comparable to
 CC effective analgesic doses using intrathecal administration. OC
 CC formulations comprising an OC and a carboxylic acid buffer anti-oxidant.
 CC they also confer stability to solutions containing them for prolonged.
 CC treatment methods and long-term storage. (Updated on 27-AUG-2003 to
 CC correct OS field.)

XX Sequence 26 AA;

Query Match 44.1%; Score 71; DB 2; Length 26;
 Best Local Similarity 42.3%; Pred. No. 0.62;
 Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNFNKC 26

XX PD 12-JAN-1999.
XX PF 03-JUL-1996; 96US-00675354.
XX PR 30-DEC-1991; 91US-00814759.
XX PR 15-APR-1993; 93US-00049794.
XX PA (NEUR-) NEUREX CORP.
XX PI Miljanich GP, Gohil KC, Valentino KL, Justice A, Singh T;
XX WPI; 1999-120002/10.
XX Production of analgesia in mammal - by administration of omega cono-
XX peptide(s).
XX Disclosure; Fig 1B; 59pp; English.
XX Sequences AAW95564-573 represent primary sequences of natural omega-
XX conopeptides. Omega-conopeptides are components of peptide toxins
XX produced by marine snails of the genus Conus, and which act as calcium
XX channel blockers. The invention relates to a method of producing
XX analgesia in a mammal that comprises administering an omega conopeptide
XX having activities in (a) inhibiting electrically stimulated contraction
XX of guinea pig ileum and (b) selectively binding to omega conopeptide
XX of MW18A binding sites in neuronal tissue, where these activities are within
XX the ranges of those of omega-conotoxins MW18A and TW1A. The method is
XX used for treating chronic pain, especially neuropathic pain
XX SQ Sequence 26 AA;
Query Match 44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.62;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 CRIXNQKCFQHLDDCCSRKCNKNC 26
DB 1 CKLKGQSCRKTSYDCCSGSGCRSGKC 26
RESULT 70
AA156480
ID AAY56480 standard; peptide; 26 AA.
XX AC AAY56480;
XX AC AAY56480;
XX DT 16-FEB-2000 (first entry)
XX DE Natural omega conopeptide SVIB/SNX-183.
XX KW Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin;
XX KW marine snail; peptide toxin; inflammation; binding;
XX KW voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline;
XX KW anti-inflammatory.
XX OS Conus sp.
XX PN US994305-A.
XX PD 30-NOV-1999.
XX PF 21-AUG-1998; 98US-00138439.
XX PR 30-DEC-1991; 91US-00814759.
XX PR 15-APR-1993; 93US-00049794.
XX PR 03-JUL-1996; 96US-00675354.
XX PR 01-NOV-1996; 96US-00742774.
XX PA (ELAN-) ELAN PHARM INC.
XX PI Justice A, Singh T, Valentino KL, Miljanich GP, Gohil KC;
XX

DR WPI; 2000-038270/03.
XX Measuring the activity of test compounds in blocking voltage-gated
XX PT calcium channels, binding to the omega conopeptide binding site and
XX PT inhibiting norepinephrine (noradrenaline) release for treating
XX inflammation.
XX PS Disclosure; Fig 1; 47pp; English.
XX CC A method has been developed of selecting a test compound for treating
XX CC inflammation. The method comprises measuring the activity of the test
XX CC compound in blocking voltage-gated calcium channels, binding to the omega
XX CC conopeptide binding site and inhibiting norepinephrine (noradrenaline)
XX CC release from nervous tissue. The method is useful for selecting compounds
XX CC for treating inflammation. The selected compounds are capable of
XX CC producing analgesia in a mammalian subject with chronic or intractable
XX CC pain. Analgesia caused by selected compounds may reduce the reliance on
XX CC opioid analgesic agents of the prior art which cause dependency and
XX CC tolerance, requiring potentially dangerous increases in opioid doses to
XX CC achieve the analgesic effect. The present sequence represents an omega
XX CC conopeptide given in the present invention
XX SQ Sequence 26 AA;
Query Match 44.1%; Score 71; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.62;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 CRIXNQKCFQHLDDCCSRKCNKNC 26
DB 1 CKLKGQSCRKTSYDCCSGSGCRSGKC 26
RESULT 71
AAB14359
ID AAB14359 standard; peptide; 26 AA.
XX AC AAB14359;
XX AC AAB14359;
XX DT 06-DEC-2000 (first entry)
XX DE Omega-conopeptide SVIB/SNX-183.
XX KW Marine snail; omega-conopeptide; calcium channel blocker; SVIB; SNX-183;
XX KW toxin; analgesic; anti-inflammatory; anticonvulsant; neuroleptic;
XX KW norepinephrine release inhibitor; schizophrenia; tardive dyskinesia;
XX KW acute dystonic reaction; inflammation; epilepsy.
XX OS Conus sp.
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 1..16
XX FT Disulfide-bond 8..20
XX FT Disulfide-bond 15..26
XX FT Modified-site 26
XX FT /notes "C-terminal amide"
XX PN US6087091-A.
XX PD 11-JUL-2000.
XX PF 23-APR-1999; 99US-00298017.
XX PR 30-DEC-1991; 91US-00814759.
XX PR 15-APR-1993; 93US-00049794.
XX PR 03-JUL-1996; 96US-00675354.
XX PR 01-NOV-1996; 96US-00742774.
XX PR 21-AUG-1998; 98US-00138439.
XX PA (ELAN-) ELAN PHARM INC.
XX PI Singh T, Gohil KC, Valentino KL, Miljanich GP, Justice A;
XX

DR WPI; 2000-490177/43.
 XX Selecting a compound for producing analgesia involves measuring activity
 PT of test compound in blocking voltage-gated calcium channels, binding to
 PT omega conopeptide binding site and inhibiting norepinephrine release.
 XX Example 4; Fig 1; 58pp; English.
 XX The present sequence is an omega-conopeptide from marine snails of the
 CC genus Conus. Omega-conopeptides are components of peptide toxins produced
 CC by the cone snails, and which act as calcium channel blockers. Natural
 CC omega-conopeptides and their derivatives may be useful for producing
 CC analgesia in nociceptive and neuropathic pain. The peptides bind to omega
 CC -conopeptide binding sites, which are present mainly in neuronal tissue,
 CC and inhibit norepinephrine release from nervous tissue. Conopeptides such
 CC as MWIIA and TWIA are effective as therapeutic agents for treating
 CC neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
 CC dystonic reactions, inflammation and epilepsy
 XX
 SQ Sequence 26 AA;
 Query Match 44.1%; Score 71; DB 3; Length 26;
 Best Local Similarity 42.3%; Pred. No. 0.62;
 Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
 Db 1 CKLKGQSCRKTSYDCSGSGRSGKC 26
 RESULT 72
 AAB92221
 ID AAB92221 standard; peptide; 26 AA.
 XX
 AC AAB92221;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Toxin peptide SEQ ID NO:1397.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013576.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 XX WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 653-654; 733pp; English.
 XX
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 26 AA;
 Query Match 44.1%; Score 71; DB 4; Length 26;
 Best Local Similarity 42.3%; Pred. No. 0.62;
 Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
 Db 1 CKLKGQSCRKTSYDCSGSGRSGKC 26
 RESULT 73
 AAB19449
 ID AAB19449 standard; peptide; 26 AA.
 XX
 AC AAB19449;
 XX
 DT 06-MAR-2001 (first entry)
 XX
 DE Primary sequence of a natural omega-conopeptide SVIB/SNX-183.
 XX
 KW Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic;
 KW peptide toxin; opiate; pain; neuronal damage; ischemic condition;
 KW schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
 KW epilepsy.
 XX
 OS Conus sp.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..15
 FT Disulfide-bond 8..19
 FT Disulfide-bond 15..26
 FT Modified-site 26
 FT /note= "amidated C-terminal"
 XX
 PN US6136786-A.
 XX
 PD 24-OCT-2000.
 XX
 PF 09-SEP-1999; 99US-00392979.
 XX
 PR 30-DEC-1991; 91US-00814759.
 PR 15-APR-1993; 93US-00049794.
 PR 23-JUN-1993; 93US-00081863.
 PR 03-JUL-1996; 96US-00675354.
 PR 01-NOV-1996; 96US-00742774.
 PR 21-AUG-1998; 98US-00138439.
 PR 23-APR-1999; 99US-00298017.
 XX
 PA (ELAN-) ELAN PHARM INC.
 XX
 PI Singh T, Gohl KC, Valentino KL, Miljanich GP, Justice A;
 XX
 XX WPI; 2001-030946/04.
 XX
 XX Enhancing analgesia produced by opiates by administering an omega-
 PT conopeptide that inhibits electrically stimulated contraction of guinea
 PT pig ilium and binds to omega-conopeptide MWIIA binding sites in neuronal
 PT tissues.
 XX

PS Disclosure; Fig 1; 58pp; English.

XX The present sequence represents an omega-conopeptide. Omega-conopeptides
CC are components of peptide toxins which act as voltage-gated calcium
CC channel inhibitors. The peptides are used to enhance the analgesic effect
CC produced by an opiate in a mammalian subject. The method comprises
CC administering to the subject an omega-conopeptide which is able to
CC inhibit electrically stimulated contraction of the guinea pig ileum and
CC bind to omega-conopeptide WIIIA binding sites present in neuronal tissue.
CC Omega-conopeptides are useful for enhancing the analgesic effect produced
CC by an opiate. Omega-conopeptides may also be used in the treatment of
CC pain, in reducing neuronal damage related to an ischemic condition in
CC mammals, and in treating schizophrenia, tardive dyskinesia and acute
CC dystonic reactions, inflammation and epilepsy
XX

SQ Sequence 26 AA;

Query Match 44.1%; Score 71; DB 4; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.62;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRIXNQKCFQHLDDCCSRKCNFNKC 25

DB 1 CLKKGQSCRKTSYDCCSGSGRSGKC 25

RESULT 74

AAO15126

ID AAO15126 standard; peptide; 26 AA.

AC AAO15126;

DT 22-AUG-2002 (first entry)

DE Cone snail w-conotoxin peptide SVIB.

KW Cone snail; venomous saliva; calcium channel blocking activity;
KW stenocardia; hypertension; myocarditis; arrhythmia; cerebral ischaemia;
KW w-conotoxin.

OS Conus sp.

XX JP2002080499-A.

XX 19-MAR-2002.

XX 01-SEP-2000; 2000JP-00266187.

XX 01-SEP-2000; 2000JP-00266187.

XX (SUNR) SUNTORY LTD.

XX WPI; 2002-421068/45.

XX A new peptide derived from venomous saliva of assassin bug, has calcium
XX channel blocking activity.

XX Disclosure; Page 4; 26pp; Japanese.

XX The invention comprises peptides having calcium channel blocking
XX activities which are derived from the venomous saliva of assassin bugs.
XX The calcium channel blocking peptides of the invention are useful for
XX treating stenocardia, hypertension, myocarditis, arrhythmia and cerebral
XX ischaemia. The present amino acid sequence represents a cone snail w-
XX conotoxin peptide
XX

SQ Sequence 26 AA;

Query Match 44.1%; Score 71; DB 5; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.62;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRIXNQKCFQHLDDCCSRKCNFNKC 26

DB 1 CLKKGQSCRKTSYDCCSGSGRSGKC 26

RESULT 75

ABB96876

ID ABB96876 standard; peptide; 27 AA.

XX ABB96876;

DT 12-JUL-2002 (first entry)

DE Omega-conopeptide P6.3 toxin sequence.

KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
KW stroke; cerebrovascular accident; brain trauma; spinal cord trauma;
KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
KW psychosis; anxiety; schizophrenia.

OS Conus purpurascens.

XX WO200207675-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023041.

XX 21-JUL-2000; 2000US-0219616P.

XX 05-FEB-2001; 2001US-0265888P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
XX Jacobsen R, Jones RM, Cartier GE;

XX WPI; 2002-257318/30.

XX New omega-conopeptides useful for treating disorders associated with
XX voltage gated ion channels e.g. pain, inflammation, neurologic or
XX cardiovascular disorders.

XX Claim 1(a); Page 72; 195pp; English.

XX The invention relates to isolated omega-conopeptides, nucleic acid
XX sequences encoding them, and propeptide sequences. The activity of the
XX peptides of the invention may be described as, analgesic, anticonvulsant,
XX vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
XX antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
XX antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
XX by modulating the activity of voltage gated ion channels. They may be
XX used for treating or preventing disorders associated with voltage gated
XX ion channels such as neurological disorders, e.g. seizure (associated
XX with epilepsy), neurotoxic injury associated with conditions of hypoxia,
XX anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
XX cord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
XX events; pain e.g. migraine; inflammation or cardiovascular disorders.
XX They may also be used for treating psychiatric disorders e.g. psychosis,
XX anxiety or schizophrenia. The analgesic agents of the invention show
XX diminished side effects and toxicity, and are non-addictive. The
XX sequences given in records ABB96807-ABB96905 represent omega-conopeptide
XX toxin sequences

XX Sequence 27 AA;

Query Match 44.1%; Score 71; DB 5; Length 27;
Best Local Similarity 50.0%; Pred. No. 0.64;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRIXNKCFOHLDCCSRKC 20
 | : : | | | | | | | |
 Db 2 CKKTGRKCFPHQKCCGRAC 21

RESULT 76
 ABB96668
 ID ABB96668 standard; peptide; 72 AA.
 XX
 AC ABB96668;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Omega-conopeptide P6.3 propeptide.
 XX
 KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.
 XX
 OS Conus purpurascens.
 XX
 PN W0200207675-A2.
 XX
 PD 31-JAN-2002.
 XX
 XX 23-JUL-2001; 2001WO-US023041.
 XX
 PF 21-JUL-2000; 2000US-0219616P.
 PR 05-FEB-2001; 2001US-0265888P.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX
 PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;
 XX
 DR WPI; 2002-257318/30.
 DR N-PSDB; ABL98927.
 XX
 PT New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.
 XX
 PS Claim 1(c); Page 56; 195pp; English.
 XX
 CC The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96595-ABB96697 represent omega-conopeptide
 CC propeptide sequences
 XX
 SQ Sequence 72 AA;

Query Match 44.1%; Score 71; DB 5; Length 72;
 Best Local Similarity 50.0%; Pred. No. 1.4;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRIXNKCFOHLDCCSRKC 20
 | : : | | | | | | | |
 Db 47 CKKTGRKCFPHQKCCGRAC 66

RESULT 77
 ABB96786
 ID ABB96786 standard; peptide; 26 AA.
 XX
 AC ABB96786;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Omega-conopeptide S6.2 generic toxin sequence.
 XX
 KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.
 XX
 OS Conus striatus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 13
 FT /label= OTHER
 FT /note= "OTHER is Tyr, 125I-Tyr, mono-iodo-Tyr or di-iodo-
 FT Tyr or O-sulpho-Tyr or O-Phospho-Tyr"
 XX
 PN W0200207675-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001WO-US023041.
 XX
 PR 21-JUL-2000; 2000US-0219616P.
 PR 05-FEB-2001; 2001US-0265888P.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX
 PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;
 XX
 DR WPI; 2002-257318/30.
 XX
 CC New omega-conopeptides useful for treating disorders associated with
 CC voltage gated ion channels e.g. pain, inflammation, neurologic or
 CC cardiovascular disorders.
 XX
 PS Example 2; Page 62; 195pp; English.
 CC
 CC The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.

The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiac, neuroprotective, cerebroprotective, cardiovascular, antiinflammatory, antimigraine, antidiabetic, tranquilliser vulnery,

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 XX Jacobsen R, Jones RM, Cartier GE;
 DR WPI; 2002-257318/30.
 XX
 PT New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.
 XX
 PS Example 2; Page 56; 195pp; English.
 XX
 CC The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96698-ABB96906 represent omega-conopeptide
 CC generic toxin sequences
 XX
 SQ Sequence 27 AA;
 Query Match 39.8%; Score 64; DB 5; Length 27;
 Best Local Similarity 55.0%; Pred. No. 3.7;
 Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CRXNOKCFQHLDDCCSRKC 20
 Db | : ||| | ||| |
 2 CKTXGRKCFXHQKCCGRAC 21
 RESULT 80
 ID ABB96874 standard; peptide; 27 AA.
 XX
 AC ABB96874;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE Omega-conopeptide P6.1 toxin sequence.
 XX
 KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.
 XX
 OS Conus purpurascens.
 XX
 PN WO200207675-A2.
 XX
 PD 31-JAN-2002.
 XX
 XX 23-JUL-2001; 2001WO-US023041.
 XX
 XX 21-JUL-2000; 2000US-0219616P.
 PR 05-FEB-2001; 2001US-0265888P.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 PA

PA (COGN-) COGNETIX INC.
 XX
 PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;
 XX
 DR WPI; 2002-257318/30.
 XX
 PT New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.
 XX
 PS Claim 1(a); Page 72; 195pp; English.
 XX
 CC The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96807-ABB96905 represent omega-conopeptide
 CC toxin sequences
 XX
 SQ Sequence 27 AA;
 Query Match 39.8%; Score 64; DB 5; Length 27;
 Best Local Similarity 55.0%; Pred. No. 3.7;
 Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CRXNOKCFQHLDDCCSRKC 20
 Db | : ||| | ||| |
 2 CKTXGRKCFXHQKCCGRAC 21
 RESULT 81
 ID ABB96842 standard; peptide; 27 AA.
 XX
 AC ABB96842;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Omega-conopeptide Cr6.3 toxin sequence.
 XX
 KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.
 XX
 OS Conus circumcissus.
 XX
 PN WO200207675-A2.
 XX
 PD 31-JAN-2002.
 XX
 XX 23-JUL-2001; 2001WO-US023041.
 XX
 XX 21-JUL-2000; 2000US-0219616P.
 PR 05-FEB-2001; 2001US-0265888P.
 PR


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PR 21-JUL-2000; 2000US-0219616P.
PR 05-FEB-2001; 2001US-0265888P.
XX
PA PA (UTAH ) UNIV UTAH RES FOUND.
PA PA (COGN-) COGNITEX INC.
XX
PI Ollivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
PI Jacobsen R, Jones RM, Cartier GE;
XX
DR WPI; 2002-257318/30.
DR N-PSDB; ABL98885.
XX
PT New omega-conopeptides useful for treating disorders associated with
PT voltage gated ion channels e.g. pain, inflammation, neurologic or
PT cardiovascular disorders.
XX
PS Claim 1(c); Page 36; 195pp; English.
XX
CC The invention relates to isolated omega-conopeptides, nucleic acid
CC sequences encoding them, and propeptide sequences. The activity of the
CC peptides of the invention may be described as, analgesic, anticonvulsant,
CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
CC antiinflammatory, antimigraine, antididiabetic, tranquiliser, vulnerary,
CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
CC by modulating the activity of voltage gated ion channels. They may be
CC used for treating or preventing disorders associated with voltage gated
CC ion channels such as neurological disorders, e.g. seizure (associated
CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
CC They may also be used for treating psychiatric disorders e.g. psychosis,
CC anxiety or schizophrenia. The analgesic agents of the invention show
CC diminished side effects and toxicity, and are non-addictive. The
CC sequences given in records ABB96595-ABB96697 represent omega-conopeptide
CC propeptide sequences
XX
SQ Sequence 73 AA;
    Query Match          39,4%; Score 63.5; DB 5; Length 73;
    Best Local Similarity 37.0%; Pred. No. 9.3;
    Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;
QY 1 CRXNQKCFQHLDCCSRKCNRFN-KC 26
   |: : ||| : |||| |:::|
Db 46 CKSGAKCSRLMYDCCSGSCRSYGRG 72
RESULT 83
AAW06589 ID AAW06589 standard; peptide; 38 AA.
XX AC AAW06589;
XX
DT 14-FEB-1997 (first entry)
DE Tyrosinase inhibitor peptide.
XX
KW Tyrosinase inhibitor; pupae; house fly; melanin; dermal medicine;
XX cosmetic; food preservative; insecticide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 32 /label= Tyr, OTHER
FT /note= "OTHER = 3,4-dihydroxyphenylalanine"
XX
JP08231592-A.
XX
DD 10-SEP-1996.
XX
KP 27-FEB-1995; 95JP-00038405.

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XX PR 27-FEB-1995; 95JP-00038405.
 XX PA (SIYA) SANSEI SEIYAKU KK.
 XX DR WPI; 1996-461344/46.
 XX PT Peptide inhibitor of tyrosinase - useful for dermal medicines, cosmetics,
 PT food preservatives, etc.
 XX PS Claim 1; Page 2; 9pp; Japanese.
 XX CC This sequence represents a tyrosinase inhibitor peptide which was
 CC isolated from the pupae of house flies. The peptide has a high inhibitory
 CC activity on tyrosinase, which catalyses biological production of melanin
 CC pigment, and is stable at ambient pH. The peptide can be used for dermal
 CC medicines, cosmetics, food preservatives and insecticides
 XX SQ Sequence 38 AA;
 Query Match 39.1%; Score 63; DB 2; Length 38;
 Best Local Similarity 39.3%; Pred. No. 6.3;
 Matches 11; Conservative 6; Mismatches 9; Indels 2; Gaps 2;
 QY 1 CRXNOKCFQHLDDCCSRKCNR-FNKCV 27
 Db 11 CLANGSKCYSH-DVCCTKRCHXAKCV 37
 RESULT 84
 ID ABB88797
 AC ABB88797;
 DT 22-MAY-2002 (first entry)
 DE Conus betulinus I-superfamily conotoxin type I peptide SEQ:369.
 XX Conotoxin; Conus; I-conotoxin; I-superfamily conotoxin; venom; antidote;
 KW cone snail; marine gastropod; neuroprotective; antiinflammatory;
 KW ophthalmological; antibacterial; anticonvulsant; muscular; antidiabetic;
 KW cardiovascular; antiarrhythmic; cardiant; immunosuppressive; nootropic;
 KW antidiabetic; cytostatic; cerebroprotective; antiaesthetic; vasotropic;
 KW analgesic; antimigraine; relaxant; antirheumatic; antiarthritic;
 KW dermatological; tranquilliser; neuroleptic; H-ATPase stimulator;
 KW potassium agonist; curare antagonist.
 XX Conus betulinus.
 OS WO200202590-A2.
 XX 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US020796.
 XX 30-JUN-2000; 2000US-0304166P.
 XX 27-OCT-2000; 2000US-0243410P.
 XX 08-NOV-2000; 2000US-0246581P.
 XX 14-NOV-2000; 2000US-0247714P.
 XX 29-JAN-2001; 2001US-0264256P.
 XX (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX Walker CS, Shetty R, Jimenez EC, McIntosh JM, Olivera BM;
 PI Watkins M, Jones RM, Shen GS;
 XX WPI; 2002-171634/22.
 XX Pure I-conotoxin peptides isolated from venom of cone snails, useful for
 PT the regulation of the flow of potassium through potassium channels in the
 PT treatment of e.g. multiple sclerosis.

XX Example 3; Page 81; 260pp; English.
 XX The present invention describes substantially pure I-conotoxin peptides
 CC of 30 -50 residues (I). (I) have neuroprotective, antiinflammatory,
 CC ophthalmological, antidote, antibacterial, anticonvulsant, muscular,
 CC cardiovascular, antiarrhythmic, cardiant, antidiabetic, antidiabetic,
 CC immunosuppressive, cytostatic, cerebroprotective, antirheumatic,
 CC antiaesthetic, vasotropic, analgesic, antimigraine, antirheumatic,
 CC antiarthritic, dermatological, tranquilliser and neuroleptic activities.
 CC (I) can be used as an H-ATPase stimulator, potassium agonist and curare
 CC antagonist. (I) are useful in the treatment of multiple sclerosis, acute
 CC disseminated encephalomyelitis, optic neuromyelitis, progressive
 CC multifocal leukoencephalopathy, adrenoleukodystrophy, acute transverse
 CC myelitis, subacute sclerosing panencephalomyelitis, metachromic
 CC botulinum toxin poisoning, Huntington's chorea, compression and
 CC entrapment neuropathies, cardiovascular disease, reactive gliosis,
 CC hyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive
 CC dysfunction, disorders resulting from the defects of neurotransmitter
 CC release and reversal of the actions curare and other neuromuscular
 CC blocking drugs. (I) can also be used to treat disorders associated with
 CC radical depolarisation of excitable membranes, and disorders associated
 CC with voltage gated ion channels, pain and a neuromuscular disorder. (I)
 CC are also useful for screening compounds that mimic the activity of an I-
 CC conotoxin. They are also useful for the treatment of autoimmune diseases,
 CC rheumatoid arthritis, systemic lupus erythematosus, Alzheimer's, anxiety
 CC and schizophrenia. ABL88662 to ABL88778 and ABB88546 to ABB88934
 CC represent sequences used in the exemplification of the present invention
 XX SQ Sequence 36 AA;
 Query Match 38.8%; Score 62.5; DB 5; Length 36;
 Best Local Similarity 40.7%; Pred. No. 6.8;
 Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;
 QY 1 CRXNOKCFQHLDDCCSRKCNRFNKCV 27
 Db 2 CLSLGQRCERH-SDCCGYLCCFYDKCV 27
 RESULT 85
 ID ABB88659
 ID ABB88659 standard; peptide; 73 AA.
 XX ABB88659;
 XX 22-MAY-2002 (first entry)
 XX Conus betulinus I-superfamily conotoxin peptide sequence SEQ:167.
 XX Conotoxin; Conus; I-conotoxin; I-superfamily conotoxin; venom; antidote;
 KW cone snail; marine gastropod; neuroprotective; antiinflammatory;
 KW ophthalmological; antibacterial; anticonvulsant; muscular; antidiabetic;
 KW cardiovascular; antiarrhythmic; cardiant; immunosuppressive; nootropic;
 KW antidiabetic; cytostatic; cerebroprotective; antiaesthetic; vasotropic;
 KW analgesic; antimigraine; relaxant; antirheumatic; antiarthritic;
 KW dermatological; tranquilliser; neuroleptic; H-ATPase stimulator;
 KW potassium agonist; curare antagonist.
 XX Conus betulinus.
 OS WO200202590-A2.
 XX 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US020796.
 XX 30-JUN-2000; 2000US-0304166P.
 XX 27-OCT-2000; 2000US-0243410P.
 XX 08-NOV-2000; 2000US-0246581P.
 XX 14-NOV-2000; 2000US-0247714P.
 XX 29-JAN-2001; 2001US-0264256P.

XX PA (UTAH) UNIV UTAH RES FOUND.
XX PA (COGN-) COGNETIX INC.
XX PI Walker CS, Shetty R, Jiminez EC, McIntosh JM, Olivera BM;
XX PI Watkins M, Jones RM, Shen GS;
XX PI WPI; 2002-171634/22.
XX PT Pure I-conotoxin peptides isolated from venom of cone snails, useful for
XX PT the regulation of the flow of potassium through potassium channels in the
XX PT treatment of e.g. multiple sclerosis.
XX PS Claim 2; Page 54; 260pp; English.
XX CC The present invention describes substantially pure I-conotoxin peptides
XX CC of 30 -50 residues (I). (I) have neuroprotective, antiinflammatory,
XX CC ophthalmological, antidote, antibacterial, anticonvulsant, muscular,
XX CC cardiovascular, antiarrhythmic, cardiac, antidiabetic, antitoxic, antitumor,
XX CC immunosuppressive, cytostatic, nootropic, cerebroprotective, relaxant,
XX CC antiasthmatic, vasotropic, analgesic, antimigraine, antirheumatic,
XX CC antiarthritic, dermatological, tranquilizer and neuroleptic activities.
XX CC (I) can be used as an H-ATPase stimulator, potassium agonist and cure
XX CC antagonist. (I) are useful in the treatment of multiple sclerosis, acute
XX CC disseminated encephalomyelitis, optic neuromyelitis, progressive
XX CC multifocal leukoencephalopathy, adrenoleukodystrophy, acute transverse
XX CC myelitis, subacute sclerosing panencephalomyelitis, metachromatic
XX CC leukodystrophy, Pelizaeus-Werzbacher disease, spinal cord injury,
XX CC botulinum toxin poisoning, Huntington's chorea, compression and
XX CC entrapment neuropathies, cardiovascular disease, cocaine addiction and
XX CC hyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive
XX CC dysfunction, disorders resulting from the defects of neurotransmitter
XX CC release and reversal of the actions of curare and other neuromuscular
XX CC blocking drugs. (I) can also be used to treat disorders associated with
XX CC radical depolarisation of excitable membranes, and disorders associated
XX CC with voltage gated ion channels, pain and a neuromuscular disorder. (I)
XX CC are also useful for screening compounds that mimic the activity of an I-
XX CC conotoxin. They are also useful for the treatment of autoimmune diseases,
XX CC rheumatoid arthritis, systemic lupus erythematosus, Alzheimer's, anxiety
XX CC and schizophrenia. ABL8662 to ABL88778 and ABB88546 to ABB88934
XX CC represent sequences used in the exemplification of the present invention
XX CC Sequence 73 AA;
XX CC
XX CC Query Match 38.8%; Score 62.5; DB 5; Length 73;
XX CC Best Local Similarity 40.7%; Pred. No. 12; Mismatches 1; Gaps 1;
XX CC Matches 11; Conservative 5;
XX CC
XX CC QY 1 CRXNKKCFQHLDDCCSRKNCV 27
XX CC 39 CLSLGQRCERH-SDCCGYLCCFYDKCV 64
XX CC
XX CC RESULT 86
XX CC ABB96774
XX CC ID ABB96774 standard; peptide; 27 AA.
XX CC AC ABB96774;
XX CC
XX CC 12-JUL-2002 (first entry)
XX CC
XX CC Omega-conopeptide P6.3 generic toxin sequence.
XX CC
XX CC Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiac;
XX CC neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
XX CC antimigraine; antidiabetic; tranquilizer; vulnary; antipsychotic;
XX CC anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
XX CC neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
XX CC stroke; cerebrovascular accident; brain trauma; spinal cord trauma;
XX CC drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
XX CC migraine; inflammation; cardiovascular disorder; psychiatric disorder;
XX CC psychosis; anxiety; schizophrenia.

OS Conus purpurascens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /label= OTHER
XX FT /note= "OTHER is Pro or Hydroxy Pro"
XX FT Misc-difference 11 /label= OTHER
XX FT /note= "OTHER is Pro or Hydroxy Pro"
XX FT Misc-difference 27 /label= OTHER
XX FT /note= "OTHER is Pro or Hydroxy Pro"
XX FT /label= OTHER
XX FT /note= "OTHER is Pro or Hydroxy Pro"
XX PN WO200207675-A2.
XX PD 31-JAN-2002.
XX XX 23-JUL-2001; 2001WO-US023041.
XX XX 21-JUL-2000; 2000US-0219616P.
XX PR 05-FEB-2001; 2001US-0265888P.
XX XX (UTAH) UNIV UTAH RES FOUND.
XX PA (COGN-) COGNETIX INC.
XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
XX PI Jacobsen R, Jones RM, Cartier GE;
XX XX WPI; 2002-257318/30.
XX PT New omega-conopeptides useful for treating disorders associated with
XX PT voltage gated ion channels e.g. pain, inflammation, neurologic or
XX PT cardiovascular disorders.
XX PS Example 2; Page 56; 195pp; English.
XX CC The invention relates to isolated omega-conopeptides, nucleic acid
XX CC sequences encoding them, and propeptide sequences. The activity of the
XX CC peptides of the invention may be described as, analgesic, anticonvulsant,
XX CC vasotropic, cardiac, neuroprotective, cerebroprotective, cardiovascular,
XX CC antiinflammatory, antimigraine, antidiabetic, tranquilizer, vulnary,
XX CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
XX CC by modulating the activity of voltage gated ion channels. They may be
XX CC used for treating or preventing disorders associated with voltage gated
XX CC ion channels such as neurological disorders, e.g. seizure (associated
XX CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
XX CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
XX CC cord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
XX CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
XX CC They may also be used for treating psychiatric disorders e.g. psychosis,
XX CC anxiety or schizophrenia. The analgesic agents of the invention show
XX CC diminished side effects and toxicity, and are non-addictive. The
XX CC sequences given in records ABB96698-ABB96806 represent omega-conopeptide
XX CC generic toxin sequences
XX CC Sequence 27 AA;
XX CC
XX CC Query Match 38.5%; Score 62; DB 5; Length 27;
XX CC Best Local Similarity 50.0%; Pred. No. 6.1;
XX CC Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
XX CC
XX CC QY 1 CRXNKKCFQHLDDCCSRKC 20
XX CC 2 CKKTGRKCFXHQKCCGRAC 21
XX CC
XX CC Db
XX CC
XX CC RESULT 87
XX CC AAU05927
XX CC ID AAU05927 standard; peptide; 76 AA.
XX CC AC AAU05927;
XX CC
XX CC 24-OCT-2001 (first entry)

XX DE Cone snail O-superfamily conotoxin propeptide, Di6.5.

XX KW Cone snail; O-superfamily conotoxin; sodium channel;

KW demyelinating disease; multiple sclerosis; Huntington's disease;

KW neuropathy; carpal tunnel syndrome; cardiovascular disorder;

KW congestive heart failure; cancer; immunosuppression; epilepsy; asthma;

KW ischaemia; stroke; pain.

XX OS Conus distans.

XX PN WO200149312-A2.

XX PD 12-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US035431.

XX PR 30-DEC-1999; 99US-0173754P.

PR 26-JUN-2000; 2000US-0214263P.

PR 20-JUL-2000; 2000US-0219440P.

PR 27-OCT-2000; 2000US-0243412P.

XX PA [UTAH] UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

XX PI Olivera BM, Cartier GE, Watkins M, Hillyard DR, McIntosh JM;

PI Layer RT, Jones RM;

XX DR WPI: 2001-418352/44.

DR N-PSDB; AAS10951.

XX PT New O-superfamily polypeptides useful for treating voltage gated ion

PT channel disorders, including demyelinating diseases i.e. multiple

PT sclerosis.

XX PS Claim 15; Page 60; 277pp; English.

XX CC The sequence is a cone snail O-superfamily conotoxin propeptide. The

CC peptides are useful for regulating the flow of sodium through sodium

CC channels in an individual and the treatment or prevention of disorders

CC associated with voltage gated ion channel disorders including

CC demyelinating diseases i.e. multiple sclerosis, optic neuromyelitis,

CC disseminated encephalomyelitis, adrenoleukodystrophy, acute transverse

CC myelitis, progressive multifocal leukoencephalopathy, sub acute

CC sclerosing panencephalomyelitis (SSPE), metachromatic leukodystrophy,

CC Pelizaeus-Merzbacher disease, spinal cord injury, botulinum toxin

CC poisoning, Huntington's, compression, entrapment neuropathies i.e. ulnar

CC nerve palsy, and carpal tunnel syndrome, cardiovascular disorders, i.e.

CC cardiac arrhythmias and congestive heart failure, reactive gliosis,

CC hyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive

CC dysfunction, neurotransmitter disorders (i.e. Eaton-Lambert syndrome) and

CC reversal of curare and other neuromuscular blocking drugs. The

CC neurological disorder is a seizure, preferably one associated with

CC epilepsy. The neurological disorder is a neurotoxic injury associated

CC with hypoxia, anoxia or ischaemia. The neurotoxic injury is associated

CC with stroke, cerebrovascular accident, brain or spinal cord trauma,

CC myocardial infarct, physical trauma, drownings, suffocation, perinatal

CC asphyxia or hypoglycaemic events. The disorder is pain i.e. migraine,

CC acute pain, persistent pain, neuropathic pain, nociceptive pain. The

CC disorder is inflammation or a cardiovascular disorder. A conotoxin

CC peptide of is useful to alleviate pain in a mammal in pain or about to be

CC subjected to a pain causing event, and to treat disorders associated with

CC radical depolarisation of excitable membranes by activating a KATP

CC channel, the disorders include cardiac, ocular and cerebral ischaemia and

CC asthma

XX SQ Sequence 76 AA;

Query Match 38.5%; Score 62; DB 4; Length 76;

Best Local Similarity 39.3%; Pred. No. 14;

Matches 11; Conservative 6; Mismatches 9; Indels 2; Gaps 2;

QY 1 CRXNOKCFQHLDDCCSRKCNRF-NKCV 27

DB 48 CNEAQEHCTQN-PDCCSECNKRFVGRCL 74

RESULT 88

ABB96741

ID ABB96741 standard; peptide; 27 AA.

XX AC ABB96741;

XX DT 12-JUL-2002 (first entry)

XX DE Omega-conopeptide E6.2 generic toxin sequence.

XX KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiac;

KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;

KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;

KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;

KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;

KW stroke; cerebrovascular accident; brain trauma; spinal cord trauma;

KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;

KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;

KW psychosis; anxiety; schizophrenia.

XX OS Conus ermineus.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /label= OTHER

FT /note= "OTHER is Pro or Hydroxy Pro"

FT Misc-difference 4 /label= OTHER

FT /note= "OTHER is Pro or Hydroxy Pro"

FT Misc-difference 11 /label= OTHER

FT /note= "OTHER is Pro or Hydroxy Pro"

FT Misc-difference 27 /label= OTHER

FT /note= "OTHER is Pro or Hydroxy Pro"

PN WO200207675-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023041.

XX 21-JUL-2000; 2000US-0219616P.

PR 05-FEB-2001; 2001US-0265888P.

XX (UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;

PI Jacobsen R, Jones RM, Cartier GE;

XX WPI: 2002-257318/30.

XX New omega-conopeptides useful for treating disorders associated with

PT voltage gated ion channels e.g. pain, inflammation, neurologic or

PT cardiovascular disorders.

XX Example 2; Page 42; 195pp; English.

XX The invention relates to isolated omega-conopeptides, nucleic acid

CC sequences encoding them, and propeptide sequences. The activity of the

CC peptides of the invention may be described as, analgesic, anticonvulsant,

CC vasotropic, cardiac, neuroprotective, cerebroprotective, cardiovascular,

CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,

CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act

CC by modulating the activity of voltage gated ion channels. They may be

CC used for treating or preventing disorders associated with voltage gated

CC ion channels such as neurological disorders, e.g. seizure (associated

CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,

CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB9698-ABB96806 represent omega-conopeptide
 CC generic toxin sequences
 XX Sequence 27 AA;
 SQ

Query Match 38.2%; Score 61.5; DB 5; Length 27;
 Best Local Similarity 47.8%; Pred. No. 6.9;
 Matches 11; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 4 XNKCQFQHLDDCCSRKCNRFNKC 26
 Db 5 KGRKCFXHQKCCNKTCR-SKC 26

RESULT 89
 AAR39616
 ID AAR39616 standard; peptide; 26 AA.
 XX
 AC AAR39616;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-DEC-1993 (first entry)
 XX
 DE MVIIC/SNX230.
 XX
 KW Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
 KW calcium channel; neurone; contraction; guinea pig; ileum; MWIIA;
 KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
 KW narcotics.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..16
 FT Disulfide-bond 8..20
 FT Disulfide-bond 15..26
 XX
 PN WO9313128-A1.
 XX
 PD 08-JUL-1993.
 XX
 PF 30-DEC-1992; 92WO-US011349.
 XX
 PR 30-DEC-1991; 91US-00814759.
 XX
 PA (NEUR-) NEUREX CORP.
 XX
 PI Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;
 XX
 DR WPI; 1993-227270/28.
 XX
 PT Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
 PT calcium channels - to induce analgesia, enhance opiate analgesics, treat
 PT pain etc.
 XX
 PS Claim 1; Fig 1; 90pp; English.
 XX
 CC The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
 CC derivatives of these, which may be used to produce analgesia in a mammal.
 CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
 CC tissue. This is shown by the peptides ability to stimulate contraction in
 CC guinea pig ileum and to bind to OCT MWIIA binding sites present in
 CC neuronal tissue. OCTs are components of peptide toxins derived from
 CC marine snails of the genus Conus, and act as calcium channel blockers.
 CC These OCTs may be used to replace opiods in the treatment of chronic pain
 CC or to reduce the opiod dosage required. This helps to reduce dependence
 CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct

CC PN field.)
 XX
 SQ Sequence 26 AA;
 Query Match 37.9%; Score 61; DB 2; Length 26;
 Best Local Similarity 38.5%; Pred. No. 7.6;
 Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
 Db 1 CKKGAPCRKTMVYDCSGSGRRGKC 26

RESULT 90
 AAR39617
 ID AAR39617 standard; peptide; 26 AA.
 XX
 AC AAR39617;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-DEC-1993 (first entry)
 XX
 DE SNX231.
 XX
 KW Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
 KW calcium channel; neurone; contraction; guinea pig; ileum; MWIIA;
 KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
 KW narcotics.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..16
 FT Modified-site 7 /note= "4Hyp"
 FT Disulfide-bond 8..20
 FT Disulfide-bond 15..26
 XX
 PN WO9313128-A1.
 XX
 PD 08-JUL-1993.
 XX
 PF 30-DEC-1992; 92WO-US011349.
 XX
 PR 30-DEC-1991; 91US-00814759.
 XX
 PA (NEUR-) NEUREX CORP.
 XX
 PI Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;
 XX
 DR WPI; 1993-227270/28.
 XX
 PT Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
 PT calcium channels - to induce analgesia, enhance opiate analgesics, treat
 PT pain etc.
 XX
 PS Claim 1; Fig 1; 90pp; English.
 XX
 CC The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
 CC derivatives of these, which may be used to produce analgesia in a mammal.
 CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
 CC tissue. This is shown by the peptides ability to stimulate contraction in
 CC guinea pig ileum and to bind to OCT MWIIA binding sites present in
 CC neuronal tissue. OCTs are components of peptide toxins derived from
 CC marine snails of the genus Conus, and act as calcium channel blockers.
 CC These OCTs may be used to replace opiods in the treatment of chronic pain
 CC or to reduce the opiod dosage required. This helps to reduce dependence
 CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX
 SQ Sequence 26 AA;
 Query Match 37.9%; Score 61; DB 2; Length 26;

Best Local Similarity 38.5%; Pred. No. 7.6; Mismatches 4; Indels 12; Gaps 0;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRENKC 26
| : : : : | | | | |
Db 1 CKKGAPCRKTMWDCCSGCGRRGKC 26

RESULT 91
AAR37762
ID AAR37762 standard; peptide; 26 AA.
XX
AC AAR37762;
XX
DT 25-MAR-2003 (revised)
DT 08-SEP-1993 (first entry)
XX
DE SNX-231.
XX
KW Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB;
KW GVIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment;
KW antihistamine; blood pressure; N-type voltage-gated Ca currents;
KW N-channel mediated neurotransmitter release.
XX
OS Synthetic.
XX
Key Location/Qualifiers
FH Disulfide-bond 1. .16
FT Modified-site 7 /note= "hydroxyproline"
FT Disulfide-bond 8. .20
FT Disulfide-bond 15. .26
PN WO9310145-A1.
XX
PD 27-MAY-1993.
XX
PF 12-NOV-1992; 92WO-US009766.
XX
PR 12-NOV-1991; 91US-00789913.
PR 17-JUL-1992; 92US-00916478.
XX
XX (NEUR-) NEUREX CORP.
PA
PI Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;
PI Yamashiro DH;
XX
DR WPI; 1993-182487/22.
XX
PT Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
PT bind specifically to omega-conotoxin MVIIA binding sites.
XX
PS Disclosure; Fig 1; 103pp; English.
XX
CC Ischaemia-related neuronal damage in mammals is reduced by admin.; 4-24
CC hr after onset of ischaemia, of a cpd. (I) which binds selectively to an
CC omega-conotoxin (OCT) MVIIA site in neuronal tissue. (I) has selectivity
CC at least 100 expressed as ratio of binding affinity for the MVIIA site to
CC that for the MVIIC site. (I) is one of the OCTs MVIIA, MVIIB, GVIA, GVIIA
CC or RVIA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal
CC damage caused by stroke. By delaying admin. for some time (compare
CC US5051403 where cpds. are given within 1 hr of the onset of ischaemia) a
CC greater redn. in neuronal damage is achieved. (I) is admin. e.g. by
CC intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also
CC be given i.v. (opt. after treatment with antihistamines to minimise redn.
CC in blood pressure caused by (I)). (I) is also at least as effective as
CC the specified conotoxins for (1) selective inhibition of N-type voltage-
CC gated Ca currents in neuronal tissue and (2) selective inhibition of N-
CC channel mediated neurotransmitter release in neuronal tissue. Primary
CC sequences of omega-conopeptides are given in AAR37752-62. Several analog
CC omega-conopeptides are given in AAR37763-76. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX

SO Sequence 26 AA;
Query Match 37.9%; Score 61; DB 2; Length 26;
Best Local Similarity 38.5%; Pred. No. 7.6;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRENKC 26
| : : : : | | | | |
Db 1 CKKGAPCRKTMWDCCSGCGRRGKC 26

RESULT 92
AAR37761
ID AAR37761 standard; peptide; 26 AA.
XX
AC AAR37761;
XX
DT 25-MAR-2003 (revised)
DT 08-SEP-1993 (first entry)
XX
DE MVIIC/SNX-230.
XX
KW Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB;
KW GVIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment;
KW antihistamine; blood pressure; N-type voltage-gated Ca currents;
KW N-channel mediated neurotransmitter release.
XX
OS Synthetic.
XX
Key Location/Qualifiers
FH Disulfide-bond 1. .16
FT Disulfide-bond 8. .20
FT Disulfide-bond 15. .26
PN WO9310145-A1.
XX
PD 27-MAY-1993.
XX
PF 12-NOV-1992; 92WO-US009766.
XX
PR 12-NOV-1991; 91US-00789913.
PR 17-JUL-1992; 92US-00916478.
XX
XX (NEUR-) NEUREX CORP.
PA
PI Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;
PI Yamashiro DH;
XX
DR WPI; 1993-182487/22.
XX
PT Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
PT bind specifically to omega-conotoxin MVIIA binding sites.
XX
PS Disclosure; Fig 1; 103pp; English.
XX
CC Ischaemia-related neuronal damage in mammals is reduced by admin.; 4-24
CC hr after onset of ischaemia, of a cpd. (I) which binds selectively to an
CC omega-conotoxin (OCT) MVIIA site in neuronal tissue. (I) has selectivity
CC at least 100 expressed as ratio of binding affinity for the MVIIA site to
CC that for the MVIIC site. (I) is one of the OCTs MVIIA, MVIIB, GVIA, GVIIA
CC or RVIA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal
CC damage caused by stroke. By delaying admin. for some time (compare
CC US5051403 where cpds. are given within 1 hr of the onset of ischaemia) a
CC greater redn. in neuronal damage is achieved. (I) is admin. e.g. by
CC intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also
CC be given i.v. (opt. after treatment with antihistamines to minimise redn.
CC in blood pressure caused by (I)). (I) is also at least as effective as
CC the specified conotoxins for (1) selective inhibition of N-type voltage-
CC gated Ca currents in neuronal tissue and (2) selective inhibition of N-
CC channel mediated neurotransmitter release in neuronal tissue. Primary
CC sequences of omega-conopeptides are given in AAR37752-62. Several analog
CC omega-conopeptides are given in AAR37763-76. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX

Db	1	CKGKGPCKRTWTVDCCSGCGRRGKC	26
RESULT 94			
AAW72614			
ID	AAW72614	standard; peptide; 26 AA.	
XX	AC	AAW72614,	
XX	AC	AAW72614,	
DT	27-AUG-2003	(revised)	
DT	06-JAN-1999	(first entry)	
XX			
DE	Conus genus natural omega-conopeptide M		
XX			
KW	Conus genus; marine snail; cone snail;		
KW	nociceptive pain; neuropathic pain; new		
KW	inflammation; schizophrenia; tardive dysk		
KW	rheumatoid arthritis; epilepsy.		
XX			
OS	Conus.		
XX			
PN	US5824645-A.		
XX			
PD	20-OCT-1998.		
XX			
PF	01-NOV-1996; 96US-00742774.		
XX			
PR	30-DEC-1991; 91US-00814759.		
PR	15-APR-1993; 93US-00049794.		
PR	03-JUL-1996; 96US-00675354.		
XX			
XX	(NEUR-) NEUREX CORP.		
XX			
PI	Miljanich GP, Valentino KL, Gohil KC,		
XX			
XX	WPI; 1998-582596/49.		
DR			
XX			
PT	Treatment of inflammation, comprises admin		
PT	- effective to block voltage-gated calc		
PT	affinity to omega-conopeptide binding s		
PT	release.		
XX			
PS	Disclosure; Fig 1; 58pp; English.		
XX			
CC	A method has been developed for the treat		
CC	subject. The method comprises admin		
CC	effective to: (i) block voltage-gated ca		
CC	high affinity to an omega-conopeptide bi		
CC	neurotransmitter release from nervous ti		
CC	inflammation and associated pain. The tr		
CC	produce analgesia (especially in subject		
CC	and to treat schizophrenia, tardive dysk		
CC	reactions, rheumatoid arthritis, and epi		
CC	represents a natural omega-conopeptide.		
CC	of peptide toxins produced by marine sna		
CC	act as calcium channel blockers. (Update		
CC	field.)		
XX			
SQ	Sequence 26 AA;		
	Query Match	37.9%;	Score 61;
	Best Local Similarity	38.5%;	Pred. No. 7
	Matches	10; Conservative	4; Mismatch
QY	1	CRIXNKCQFQHLDDCCSRKCNFNKC	26
Db	1	CKGKGPCKRTWTVDCCSGCGRRGKC	26
RESULT 95			
AAW72613			
ID	AAW72613	standard; peptide; 26 AA.	


```

PR 15-APR-1993; 93US-00049794.
PR 03-JUL-1996; 96US-00675354.
PR 01-NOV-1996; 96US-00742774.
XX
PA (ELAN-) ELAN PHARM INC.
XX
XX Justice A, Singh T, Valentino KL, Miljanich GP, Gohil KC;
XX WPI; 2000-038270/03.
XX
XX Measuring the activity of test compounds in blocking voltage-gated
XX calcium channels, binding to the omega conopeptide binding site and
XX inhibiting norepinephrine (noradrenaline) release for treating
XX inflammation.
XX
XX Disclosure; Fig 1; 47pp; English.
XX
XX A method has been developed of selecting a test compound for treating
XX inflammation. The method comprises measuring the activity of the test
XX compound in blocking voltage-gated calcium channels, binding to the omega
XX conopeptide binding site and inhibiting norepinephrine (noradrenaline)
XX release from nervous tissue. The method is useful for selecting compounds
XX for treating inflammation. The selected compounds are capable of
XX producing analgesia in a mammalian subject with chronic or intractable
XX pain. Analgesia caused by selected compounds may reduce the reliance on
XX opioid analgesic agents of the prior art which cause dependency and
XX tolerance, requiring potentially dangerous increases in opioid doses to
XX achieve the analgesic effect. The present sequence represents an omega
XX conopeptide given in the present invention
XX
XX Sequence 26 AA;
XX
XX Query Match 37.9%; Score 61; DB 3; Length 26;
XX Best Local Similarity 38.5%; Pred. NO. 7.6;
XX Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0
QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
Db |: : : : : : : : : : : : : : : :
1 CKGKGAPCRKTMVDCSGSCGRRGKC 26
RESULT 99
AAY43715
ID AAY43715 standard; peptide; 26 AA.
XX
XX AAY43715;
XX
XX 11-FEB-2000 (first entry)
XX
XX Amino acid sequence of an omega-conotoxin MWIIC.
XX
XX Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
XX neuronal damage reduction; ischemia; analgesia; opiate analgesia;
XX schizophrenia; stimulant induced psychosis; hypertension; inflammation;
XX bronchotension; neuropathic pain; voltage sensitive calcium channel.
XX
XX Conus magus.
XX
XX WO9954350-A1.
XX
XX 28-OCT-1999.
XX
XX 16-APR-1999; 99WO-AU000288.
XX
XX 16-APR-1998; 98AU-00002989.
XX
XX 01-FEB-1999; 99AU-00008419.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX WPI; 2000-013226/01.
XX

```


PT Novel peptides used for the treatment of disorders and diseases where
 XX blockage of the N-type calcium channels is required.
 PS Disclosure; Page 12; 81pp; English.
 CC The present sequence represents an omega-conotoxin. Omega-conotoxins are
 CC isolated from venoms of predatory marine snails, and have a selectivity
 CC for N-type calcium channels over P/Q type channels, and so block N-type
 CC calcium channels. The omega-conotoxins of the invention can be used in
 CC any disease or disorder where blockage of N-type calcium channels is
 CC required, e.g. in the reduction of neuronal damage following ischemia,
 CC production of analgesia, or enhancement of opiate analgesia, in the
 CC treatment of schizophrenia, stimulant induced psychoses, hypertension,
 CC inflammation, and diseases which cause bronchotension, and also in the
 CC inhibition of progression of neuropathic pain. They can also be used in a
 CC screen to identify compounds with activity at N-type voltage sensitive
 CC calcium channels
 XX Sequence 26 AA;
 SQ Query Match 37.9%; Score 61; DB 3; Length 26;
 Best Local Similarity 38.5%; Pred. No. 7.6;
 Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
 OY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 | : : : : |||||
 Db 1 CKGKGAPCRKTMWDCCSGSGRRGKC 26
 | : : : : |||||
 RESULT 100
 AAB14377
 ID AAB14377 standard; peptide; 26 AA.
 XX
 AC AAB14377;
 XX
 DT 06-DEC-2000 (first entry)
 XX
 DE Omega-conopeptide MVIIC/SNX-230.
 XX
 KW Marine snail; omega-conopeptide; calcium channel blocker; MVIIC; SNX-230;
 KW toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic;
 KW norepinephrine release inhibitor; schizophrenia; tardive dyskinesia;
 KW acute dystonic reaction; inflammation; epilepsy.
 XX
 OS Conus sp.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..16
 FT Disulfide-bond 8..20
 FT Disulfide-bond 15..26
 FT Modified-site 26
 FT /note= "C-terminal amide"
 XX
 PN US6087091-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 23-APR-1999; 99US-00298017.
 XX
 PR 30-DEC-1991; 91US-00814759.
 PR 15-APR-1993; 93US-00049794.
 PR 03-JUL-1996; 96US-00675354.
 PR 01-NOV-1996; 96US-00742774.
 PR 21-AUG-1998; 98US-00138439.
 XX
 PA (ELAN-) ELAN PHARM INC.
 XX
 PI Singh T, Gohil KC, Valentino KL, Miljanich GP, Justice A;
 XX
 DR WPI; 2000-490177/43.
 XX
 XX Selecting a compound for producing analgesia involves measuring activity
 PT of test compound in blocking voltage-gated calcium channels, binding to

PT omega conopeptide binding site and inhibiting norepinephrine release.
 XX Disclosure; Fig 1; 58pp; English.
 PS
 CC The present sequence is an omega-conopeptide from marine snails of the
 CC genus Conus. Omega-conopeptides are components of peptide toxins produced
 CC by the cone snails, and which act as calcium channel blockers. Natural
 CC omega-conopeptides and their derivatives may be useful for producing
 CC analgesia in nociceptive and neuropathic pain. The peptides bind to omega
 CC -conopeptide binding sites, which are present mainly in neuronal tissue,
 CC and inhibit norepinephrine release from nervous tissue. Conopeptides such
 CC as MVIIC and TVIIC are effective as therapeutic agents for treating
 CC neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
 CC dystonic reactions, inflammation and epilepsy
 XX Sequence 26 AA;
 SQ Query Match 37.9%; Score 61; DB 3; Length 26;
 Best Local Similarity 38.5%; Pred. No. 7.6;
 Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
 OY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 | : : : : |||||
 Db 1 CKGKGAPCRKTMWDCCSGSGRRGKC 26
 | : : : : |||||
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 Job time : 126.5 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:24:17 ; Search time 30.5 Seconds
(without alignments)
66.083 Million cell updates/sec

Title: US-10-627-685A-26

Perfect score: 161

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	161	100.0	27	1	US-08-619-936-1
2	75	46.6	26	1	US-07-789-913-19
3	75	46.6	26	1	US-08-049-794-19
4	75	46.6	26	1	US-08-496-847-19
5	75	46.6	26	2	US-08-742-774-19
6	75	46.6	26	2	US-08-675-354-19
7	75	46.6	26	2	US-08-965-918-19
8	75	46.6	26	2	US-09-138-439-19
9	75	46.6	26	3	US-08-613-400A-19
10	75	46.6	26	3	US-09-298-017-19
11	75	46.6	26	3	US-09-392-979A-19
12	71	44.1	26	1	US-07-789-913-8
13	71	44.1	26	1	US-08-049-794-8
14	71	44.1	26	1	US-08-496-847-8
15	71	44.1	26	2	US-08-742-774-8
16	71	44.1	26	2	US-08-675-354-8
17	71	44.1	26	2	US-08-965-918-8
18	71	44.1	26	2	US-09-138-439-8
19	71	44.1	26	3	US-08-613-400A-8
20	71	44.1	26	3	US-09-298-017-8
21	71	44.1	26	3	US-09-392-979A-8
22	62.5	38.8	36	4	US-09-894-882-369
23	62.5	38.8	73	4	US-09-894-882-167
24	62	38.5	76	4	US-09-749-637A-207
25	61	37.9	26	1	US-08-049-794-29
26	61	37.9	26	1	US-08-496-847-29
27	61	37.9	26	2	US-08-742-774-29

28	61	37.9	26	2	US-08-675-354-29	Sequence 29, Appl
29	61	37.9	26	2	US-08-965-918-29	Sequence 29, Appl
30	61	37.9	26	2	US-09-138-439-29	Sequence 29, Appl
31	61	37.9	26	3	US-08-613-400A-29	Sequence 29, Appl
32	61	37.9	26	3	US-09-298-017-29	Sequence 29, Appl
33	61	37.9	26	3	US-09-392-979A-29	Sequence 29, Appl
34	61	37.9	29	1	US-08-092-215-9	Sequence 9, Appl
35	59	36.6	735	3	US-09-191-647-9	Sequence 9, Appl
36	59	36.6	735	3	US-09-540-245A-9	Sequence 9, Appl
37	59	36.6	735	3	US-09-540-153-9	Sequence 9, Appl
38	57.5	35.7	36	4	US-09-894-882-365	Sequence 365, App
39	57.5	35.7	36	4	US-09-894-882-368	Sequence 368, App
40	57.5	35.7	36	4	US-09-894-882-371	Sequence 371, App
41	57.5	35.7	36	4	US-09-894-882-372	Sequence 372, App
42	57.5	35.7	73	4	US-09-894-882-155	Sequence 155, App
43	57.5	35.7	73	4	US-09-894-882-164	Sequence 164, App
44	57.5	35.7	73	4	US-09-894-882-173	Sequence 173, App
45	57.5	35.7	73	4	US-09-894-882-176	Sequence 176, App
46	57	35.4	2523	1	US-08-185-432-18	Sequence 18, Appl
47	57	35.4	2523	4	US-08-899-232-3	Sequence 3, Appl
48	57	35.4	2523	4	US-09-121-457-3	Sequence 3, Appl
49	56.5	35.1	1277	3	US-08-937-236-6	Sequence 6, Appl
50	56.5	35.1	1292	3	US-08-569-214-5	Sequence 5, Appl
51	56.5	35.1	1292	3	US-08-569-214-6	Sequence 6, Appl
52	56.5	35.1	1292	3	US-08-377-236-5	Sequence 5, Appl
53	56	34.8	585	4	US-09-641-612-5	Sequence 5, Appl
54	56	34.8	2703	1	US-08-185-432-19	Sequence 19, Appl
55	56	34.8	2703	4	US-08-899-232-4	Sequence 4, Appl
56	56	34.8	2703	4	US-09-121-457-4	Sequence 4, Appl
57	55.5	34.5	25	1	US-07-689-693B-2	Sequence 2, Appl
58	55.5	34.5	25	1	US-07-789-913-2	Sequence 2, Appl
59	55.5	34.5	25	1	US-08-049-794-2	Sequence 2, Appl
60	55.5	34.5	25	1	US-08-496-847-2	Sequence 2, Appl
61	55.5	34.5	25	2	US-08-742-774-2	Sequence 2, Appl
62	55.5	34.5	25	2	US-08-675-354-2	Sequence 2, Appl
63	55.5	34.5	25	2	US-08-965-918-2	Sequence 2, Appl
64	55.5	34.5	25	2	US-09-039-168-2	Sequence 2, Appl
65	55.5	34.5	25	2	US-09-138-439-2	Sequence 2, Appl
66	55.5	34.5	25	3	US-08-613-400A-2	Sequence 2, Appl
67	55.5	34.5	25	3	US-09-298-017-2	Sequence 2, Appl
68	55.5	34.5	25	3	US-09-392-979A-2	Sequence 2, Appl
69	55.5	34.5	25	6	5189020-1	Patent No. 5189020
70	55.5	34.5	25	6	5189020-2	Patent No. 5189020
71	55.5	34.5	25	6	5424218-2	Patent No. 5424218
72	55.5	34.5	25	6	5189020-1	Patent No. 5189020
73	55.5	34.5	25	6	5189020-2	Patent No. 5189020
74	55.5	34.5	25	6	5424218-2	Patent No. 5424218
75	55.5	34.5	71	1	US-07-689-693B-1	Sequence 1, Appl
76	55.5	34.5	1276	3	US-08-937-236-3	Sequence 3, Appl
77	55.5	34.5	1291	3	US-08-569-214-3	Sequence 3, Appl
78	55.5	34.5	1291	3	US-08-937-236-2	Sequence 2, Appl
79	55.5	34.5	1295	3	US-08-569-214-2	Sequence 2, Appl
80	55	34.2	26	1	US-08-049-794-21	Sequence 21, Appl
81	55	34.2	26	1	US-08-496-847-21	Sequence 21, Appl
82	55	34.2	26	2	US-08-742-774-21	Sequence 21, Appl
83	55	34.2	26	2	US-08-675-354-21	Sequence 21, Appl
84	55	34.2	26	2	US-08-965-918-21	Sequence 21, Appl
85	55	34.2	26	2	US-09-138-439-21	Sequence 21, Appl
86	55	34.2	26	3	US-08-613-400A-21	Sequence 21, Appl
87	55	34.2	26	3	US-09-298-017-21	Sequence 21, Appl
88	55	34.2	26	3	US-09-392-979A-21	Sequence 21, Appl
89	55	34.2	473	4	US-09-949-016-9481	Sequence 9481, Ap
90	55	34.2	583	4	US-09-641-612-2	Sequence 2, Appl
91	54.5	33.9	25	1	US-07-789-913-9	Sequence 9, Appl
92	54.5	33.9	25	1	US-07-789-913-9	Sequence 9, Appl
93	54.5	33.9	25	1	US-08-049-794-1	Sequence 1, Appl
94	54.5	33.9	25	1	US-08-496-847-1	Sequence 1, Appl
95	54.5	33.9	25	1	US-08-742-774-1	Sequence 1, Appl
96	54.5	33.9	25	1	US-08-496-847-9	Sequence 9, Appl
97	54.5	33.9	25	2	US-08-742-774-1	Sequence 1, Appl
98	54.5	33.9	25	2	US-08-742-774-9	Sequence 9, Appl
99	54.5	33.9	25	2	US-08-675-354-1	Sequence 1, Appl
100	54.5	33.9	25	2	US-08-675-354-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-08-619-936-1
; Sequence 1, Application US/08619936
; Patent No. 5672682
; GENERAL INFORMATION:
; APPLICANT: Terlau, Heinrich
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Grilley, Michelle
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Conotoxin Peptide PVIIA
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/619,936
; FILING DATE:
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 24260-107674-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus purpurascens

FEATURE:
; NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /product= "4Hyp"
; OTHER INFORMATION: /note= "Amino acid 4 may be 4-trans-hydroxyproline."

FEATURE:
; NAME/KEY: Disulfide-bond

LOCATION: 1..16

FEATURE:
; NAME/KEY: Disulfide-bond

LOCATION: 8..20

FEATURE:
; NAME/KEY: Disulfide-bond

LOCATION: 15..26

US-08-619-936-1

Query Match 100.0%; Score 161; DB 1; Length 27;

Best Local Similarity 100.0%; Pred. No. 3.9e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 27

DB 1 CRXNKKCFQHLDDCCSRKCNRFNKC 27

RESULT 2

US-07-789-913-19
; Sequence 19, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,913
; FILING DATE: 19911112
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0005.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: AMINO ACID

TOPOLOGY: both

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: SNX-202

US-07-789-913-19

Query Match 46.6%; Score 75; DB 1; Length 26;

Best Local Similarity 42.3%; Pred. No. 0.023;

Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26

DB 1 CKLKGQCSRLMYDCCSGCSGSGKC 26

RESULT 3

US-08-049-794-19
; Sequence 19, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C


```

; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/138,439
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
; US-09-138-439-19

Query Match 46.6%; Score 75; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNC 26
Db 1 CKLKGQCSRLMYDCCSGSGRSGKC 26

RESULT 9
US-08-613-400A-19
; Sequence 19, Application US/08613400A
; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pettus, Mark, R.
; APPLICANT: Luther, Robert, R.
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA

```

```

; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
; US-08-613-400A-19

Query Match 46.6%; Score 75; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNC 26
Db 1 CKLKGQCSRLMYDCCSGSGRSGKC 26

RESULT 10
US-09-298-017-19
; Sequence 19, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
;
US-09-298-017-19
;
Query Match 46.6%; Score 75; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 25
   |:::|:::|:::|:::|:::|:::|
Db 1 CKLKGQSCSRLMYDCCSGCSGRSGKC 25

RESULT 11
US-09-392-979A-19
; Sequence 19, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L.
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/392,979A
; APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-09-392-979A-19
;
Query Match 46.6%; Score 75; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 25
   |:::|:::|:::|:::|:::|:::|
Db 1 CKLKGQSCSRLMYDCCSGCSGRSGKC 25

RESULT 12
US-07-789-913-8
; Sequence 8, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/07/789,913
; APPLICATION DATA:
; FILING DATE: 19911112
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0005.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-183
;
US-07-789-913-8
;
Query Match 44.1%; Score 71; DB 1; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,774
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,354
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-08-742-774-8

Query Match 44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
|:::|:|:|:|:|:|:|:|:|:|
Db 1 CKLKQSCRKTSYDCSCGSGRSKC 26

RESULT 16
US-08-675-354-8
; Sequence 8, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Deklinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,354
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:

```

```

;
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-08-675-354-8

Query Match 44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
|:::|:|:|:|:|:|:|:|:|:|
Db 1 CKLKQSCRKTSYDCSCGSGRSKC 26

RESULT 17
US-08-965-918-8
; Sequence 8, Application US/08965918
; Patent No. 5891849
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,918
; FILING DATE: 07-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohr, Judy M.
; REGISTRATION NUMBER: 38,563
; REFERENCE/DOCKET NUMBER: 5865-0009.34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-08-965-918-8

```


Query Match 44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CRXNKCFOHLDCCSRKCNFNKC 26
Db 1 CKLGQSCRKTSYDCCSGSGRSKC 26

RESULT 18

US-09-138-439-8
; Sequence 8, Application US/09138439
; Patent No. 5994305
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,439
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-09-138-439-8

Query Match 44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CRXNKCFOHLDCCSRKCNFNKC 26
Db 1 CKLGQSCRKTSYDCCSGSGRSKC 26

RESULT 19

US-08-613-400A-8
; Sequence 8, Application US/08613400A

; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pettus, Mark R.
; APPLICANT: Luther, Robert, R.
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-613-400A-8

Query Match 44.1%; Score 71; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CRXNKCFOHLDCCSRKCNFNKC 26
Db 1 CKLGQSCRKTSYDCCSGSGRSKC 26

RESULT 20

US-09-298-017-8
; Sequence 8, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA

COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-09-298-017-8

Query Match 44.1%; Score 71; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
Oy 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
Db 1 CLKKGQSCRKTSYDCCSGSGRSGKC 26

RESULT 21
US-09-392-979A-8
Sequence 8, Application US/09392979A
Patent No. 6136786
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Deklinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15

APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-09-392-979A-8

Query Match 44.1%; Score 71; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
Oy 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
Db 1 CLKKGQSCRKTSYDCCSGSGRSGKC 26

RESULT 22
US-09-894-882-369
Sequence 369, Application US/09894882
Patent No. 676785
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Oliveira, Balomero M.
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patent in version 3.0
SEQ ID NO 369
LENGTH: 36
TYPE: PRT
ORGANISM: Conus betulinus
US-09-894-882-369

Query Match 38.8%; Score 62.5; DB 4; Length 36;
Best Local Similarity 40.7%; Pred. No. 0.8;
Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;
Oy 1 CRXNKKCFQHLDDCCSRKCNRFNKC 27
Db 2 CLSLGQRCERH-SDCCGYLCCFYDKCV 27


```

RESULT 23
US-09-894-882-167
; Sequence 167, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 167
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167

```

```

Query Match      38.8%; Score 62.5; DB 4; Length 73;
  Best Local Similarity 40.7%; Pred. No. 1.5;
Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY  1 CRIXNQKCFQHLDDCCSRKCNRFKCV 27
      | | | | | | | | | | | | | |
Db  39 CLSLGRCERH-SDCCGYLCCFYDKCV 64
      | | | | | | | | | | | | | |

```

RESULT 24
US-09-749-637A-207
; Sequence 207, Application US/09749637A
; Patent No. 6762165
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754

```

; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Conus distans
US-09-749-637A-207

Query Match          38.5%; Score 62; DB 4; Length 76;
Best Local Similarity 39.3%; Pred. No. 1.7;
Matches 11; Conservative 6; Mismatches 9; Indels

QY 1 CRXNQKCFQHLDDCCSRKCNRF-NKCV 27
   | : | : | | | | | | | : | :
DB 48 CNEAQEHCTQN-PDCCSECNKVGRCCL 74

RESULT 25
US-08-049-794-29
; Sequence 29, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-049-794-29

Query Match          37.9%; Score 61; DB 1; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.89;
Matches 10; Conservative 4; Mismatches 12; Indels

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26

```



```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,774
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,354
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/POCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
;
; US-08-742-774-29
;
; Query Match 37.9%; Score 61; DB 2; Length 26;
; Best Local Similarity 38.5%; Pred. No. 0.89;
; Matches 10; Conservative 4; Mismatches 12; Indels
;
; QY 1 CRXNQKCFOHLDDCCSRKCNRENKC 26
; : : : : :
;
; Db 1 CRKGAPCRKTMYYDCSGSGRGKC 26
; : : : : :
;
; RESULT 28
; US-08-675-354-29
; Sequence 29, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```


Query Match 37.9%; Score 61; DB 2; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.89;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
| : : : : ||| | | | |
Db 1 CKGKAPCRKTMWDCCSGCGRRGKC 26

RESULT 31
US-08-613-400A-29
; Sequence 29, Application US/08613400A
; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pettus, Mark, R.
; APPLICANT: Luther, Robert, R.
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-613-400A-29

Query Match 37.9%; Score 61; DB 3; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.89;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
| : : : : ||| | | | |
Db 1 CKGKAPCRKTMWDCCSGCGRRGKC 26

RESULT 32
US-09-298-017-29
; Sequence 29, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN

; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-09-298-017-29

Query Match 37.9%; Score 61; DB 3; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.89;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
| : : : : ||| | | | |
Db 1 CKGKAPCRKTMWDCCSGCGRRGKC 26

RESULT 33
US-09-392-979A-29
; Sequence 29, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306


```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
; US-09-392-979A-29

Query Match 37.9%; Score 61; DB 3; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.89;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
   | : | : | : | : | : | : | : |
Db 1 CKGKGAPCRKTMVDCSCGSGRRGKC 26

RESULT 34
US-08-092-215-9
; Sequence 9, Application US/08092215
; Patent No. 5591821
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hillyard, David R.
; APPLICANT: Imperial, Julita S.
; APPLICANT: Monje, Virginia D.
; TITLE OF INVENTION: w-Conotoxin Peptides
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/092,215
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107674
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
```

```
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-092-215-9

Query Match 37.9%; Score 61; DB 1; Length 29;
Best Local Similarity 38.5%; Pred. No. 0.97;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
   | : | : | : | : | : | : | : |
Db 3 CKGKGAPCRKTMVDCSCGSGRRGKC 28

RESULT 35
US-09-191-647-9
; Sequence 9, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brosse, Katja
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-191-647-9

Query Match 36.6%; Score 59; DB 3; Length 735;
Best Local Similarity 45.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKC 27
   | : | : | : | : | : | : | : |
Db 254 CEKNIDDCVNSKCGGKCV 273

RESULT 36
US-09-540-245A-9
; Sequence 9, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brosse, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 735
```



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; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-245A-9

Query Match      36.6%; Score 59; DB 3; Length 735;
Best Local Similarity 45.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 8 CFOHLDCCSRKCNRFNKCVCV 27
Db 254 CEKNIDCVNSKENGKVCV 273

RESULT 37
US-09-540-153-9
; Sequence 9, Application US/09540153
; Patent No. 6270995
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,153
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/191,647
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-153-9

Query Match      36.6%; Score 59; DB 3; Length 735;
Best Local Similarity 45.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 8 CFOHLDCCSRKCNRFNKCVCV 27
Db 254 CEKNIDCVNSKENGKVCV 273

RESULT 38
US-09-894-882-365
; Sequence 365, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 365
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-365

Query Match      35.7%; Score 57.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 2.9;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 2 CLSLGQRCGRH-SNCCGYLCCFYDKVCV 27

RESULT 40
US-09-894-882-371
; Sequence 371, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
```



```
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 371
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-371

Query Match      35.7%; Score 57.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 2.9;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNOKCFQHLDDCCSRKCNRFNKCVCV 27
Db 2 CLSLGQRCERH-SNCCGYLCCFYDKVCV 27

RESULT 41
US-09-894-882-372
; Sequence 372, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 372
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-372

Query Match      35.7%; Score 57.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 2.9;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNOKCFQHLDDCCSRKCNRFNKCVCV 27
Db 2 CLSLGQRCERH-SNCCGYLCCFYDKVCV 27

RESULT 41
US-09-894-882-372
; Sequence 372, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 372
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-372
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; ORGANISM: Conus betulinus
US-09-894-882-372

Query Match      35.7%; Score 57.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 2.9;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNOKCFQHLDDCCSRKCNRFNKCVCV 27
Db 2 CLSLGQRCERH-SNCCGYLCCFYDKVCV 27

RESULT 42
US-09-894-882-155
; Sequence 155, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 155
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-155

Query Match      35.7%; Score 57.5; DB 4; Length 73;
Best Local Similarity 37.0%; Pred. No. 5.5;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNOKCFQHLDDCCSRKCNRFNKCVCV 27
Db 39 CLSLGQRCERH-SNCCGYLCCFYDKVCV 64

RESULT 43
US-09-894-882-164
; Sequence 164, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
```


; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 164
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-164

Query Match 35.7%; Score 57.5; DB 4; Length 73;
Best Local Similarity 37.0%; Pred. No. 5.5;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27
DB 39 CLSLGQRCGRH-SNCCGYLCCFYDKCV 64

RESULT 44
US-09-894-882-173
; Sequence 173, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 173
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-173

Query Match 35.7%; Score 57.5; DB 4; Length 73;
Best Local Similarity 37.0%; Pred. No. 5.5;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27

Db 39 CLSLGQRCGRH-SNCCGYLCCFYDKCV 64

RESULT 45
US-09-894-882-176
; Sequence 176, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 176
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-176

Query Match 35.7%; Score 57.5; DB 4; Length 73;
Best Local Similarity 37.0%; Pred. No. 5.5;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27
DB 39 CLSLGQRCGRH-SNCCGYLCCFYDKCV 64

RESULT 46
US-08-185-432-18
; Sequence 18, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Buseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; NUMBER OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible


```
RESULT 50
US-08-569-214-5
; Sequence 5, Application US/08569214
; Patent No. 6165469
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 200006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,214
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06890
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9148-0006.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1292 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-569-214-5
; Query Match 35.1%; Score 56.5; DB 3; Length 1292;
; Best Local Similarity 43.3%; Pred. No. 88;
; Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
Db 718 CSMGTDNIITYHDDCNRSKQCGNFNGKCV 747

RESULT 51
US-08-569-214-6
; Sequence 6, Application US/08569214
; Patent No. 6165469
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 200006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,214
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06890
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9148-0006.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-569-214-5
; Query Match 35.1%; Score 56.5; DB 3; Length 1292;
; Best Local Similarity 43.3%; Pred. No. 88;
; Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
Db 718 CSMGTDNIITYHDDCNRSKQCGNFNGKCV 747

RESULT 52
US-08-937-236-5
; Sequence 5, Application US/08937236
; Patent No. 6187310
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; APPLICANT: PETRI, WILLIAM A.
; APPLICANT: DODSON, JAMES M.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 200006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,236
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/569,214
; FILING DATE: 16 SEPTEMBER 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: 291482000622
; TELECOMMUNICATION INFORMATION:
```



```
;
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-937-236-5

Query Match      35.1%; Score 56.5; DB 3; Length 1292;
Best Local Similarity 43.3%; Pred. No. 88;
Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
Db 718 CSMGTDNITVHDDCNSRKSCQGNFGKCV 747

RESULT 53
US-09-641-612-5
; Sequence 5, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641.612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(585)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-641-612-5

Query Match      34.8%; Score 56; DB 4; Length 585;
Best Local Similarity 37.9%; Pred. No. 50;
Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

QY 1 CR--IXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 377 CRAGFAGPRCEHLDLDCAGACANAGTCV 405

RESULT 54
US-08-185-432-19
; Sequence 19, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Buseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-3090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2703 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-185-432-19

Query Match      34.8%; Score 56; DB 1; Length 2703;
Best Local Similarity 33.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 822 TGQKCTNIDDCVTNPGNGGTCTI 845

RESULT 55
US-08-899-232-4
; Sequence 4, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2703
; TYPE: PRT
; ORGANISM: Drosophila sp.
; US-08-899-232-4

Query Match      34.8%; Score 56; DB 4; Length 2703;
Best Local Similarity 33.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 822 TGQKCTNIDDCVTNPGNGGTCTI 845

RESULT 56
US-09-121-457-4
; Sequence 4, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
```


EARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 2703
TYPE: PRT
ORGANISM: Drosophila sp.
US-09-121-457-4

Query Match 34.8%; Score 56; DB 4; Length 2703;
Best Local Similarity 33.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 4 XNKKCFHLDCCSRKCNRFKNCV 27
Db 822 TQCKETNIDCVTFPCNGGTCTI 845

RESULT 57
US-07-689-693B-2
Sequence 2, Application US/07689693B
Patent No. 5231011
GENERAL INFORMATION:

APPLICANT: David Hillyard
APPLICANT: Balomero M. Olivera
TITLE OF INVENTION: Segregated Folding Determinants
TITLE OF INVENTION: for Small Disulfide-Rich Peptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No. 5231011th & Western
STREET: 9035 South 700 East, Suite 200
CITY: Sandy
STATE: Utah
COUNTRY: USA
ZIP: 84070

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
COMPUTER: Compaq LTR/286
OPERATING SYSTEM: DOS 4.01
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/689,693B
FILING DATE: 19910418
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
FILING DATE: na

ATTORNEY/AGENT INFORMATION:
NAME: Western, M. Wayne
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: 9925
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 566-8633
TELEFAX: (801) 566-0750
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACIDS
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: MVIIB Omega conotoxin.
IDENTIFICATION METHOD: Direct peptide
IDENTIFICATION METHOD: sequencing of purified Conus magus venom
US-07-689-693B-2

Query Match 34.5%; Score 55.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 CRXNKKCFHLDCCSRKCNRFKNC 26
Db 1 CKGKGASCHRTSYDCTGSCNR-GKC 25

RESULT 58
US-07-789-913-2
Sequence 2, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:

APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Bitner, Robert S.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing
TITLE OF INVENTION: Ischemia-Related Neuronal Damage
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-159

US-07-789-913-2

Query Match 34.5%; Score 55.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 CRXNKKCFHLDCCSRKCNRFKNC 26
Db 1 CKGKGASCHRTSYDCTGSCNR-GKC 25

RESULT 59

US-08-049-794-2
Sequence 2, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER


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RESULT 60
US-08-496-847-2
; Sequence 2, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amatutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:

```

STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.

GENERAL INFORMATION:
APPLICANT: Pang, Lok-Hou; Kapin, Michael and Hellberg,
APPLICANT: Mark
TITLE OF INVENTION: The Use of w-Conotoxin Analogs For
TREATING RETINAL AND OPTIC NERVE HEAD DAMAGE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alcon Laboratories, Inc.
STREET: 6201 South Freeway, Patent Legal
CITY: Fort Worth
STATE: Texas
COUNTRY: USA

ZIP: 76134-2099
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.2 mg, 3.25" floppy disk
COMPUTER: Compaq Deskpro XE 560
OPERATING SYSTEM: Microsoft Windows for Workgroups,
OPERATING SYSTEM: Version 3.11
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,168
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,142
FILING DATE: NO. 5965534ember 22, 1995
ATTORNEY/AGENT INFORMATION:
NAME: MAYO, MICHAEL C.
REGISTRATION NUMBER: 39,545
REFERENCE/DOCKET NUMBER: 1462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (817) 551-4321
TELEFAX: (817) 551-4610
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
DESCRIPTION: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-09-039-168-2
Query Match 34.5%; Score 55.5; DB 2; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
QY 1 CRXKQCFQHLDDCCSRKCNRFNC 26
| : : : : : ||| : ||
Db 1 CKKGASCHRTSYDCCCTGSCNR-GKC 25
RESULT 65
US-09-138-439-2
Sequence 2, Application US/09138439
Patent No. 5994305
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
US-09-138-439-2

Query Match 34.5%; Score 55.5; DB 2; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
QY 1 CRXKQCFQHLDDCCSRKCNRFNC 26
| : : : : : ||| : ||
Db 1 CKKGASCHRTSYDCCCTGSCNR-GKC 25

RESULT 66
US-08-613-400A-2
Sequence 2, Application US/08613400A
Patent No. 6054429
GENERAL INFORMATION:
APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Pettus, Mark, R.
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US

ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:


```

; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
US-08-613-400A-2

Query Match      34.5%; Score 55.5; DB 3; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy      1 CRXNQKCFQHLDDCCSRKCNRFNC 26
      | : : : : : : : : : : : :
Db      1 CKKGASCHRTSYDCCGTGSCNR-GKC 25

RESULT 67
US-09-298-017-2
; Sequence 2, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

```

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; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
US-09-298-017-2

Query Match      34.5%; Score 55.5; DB 3; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy      1 CRXNQKCFQHLDDCCSRKCNRFNC 26
      | : : : : : : : : : : : :
Db      1 CKKGASCHRTSYDCCGTGSCNR-GKC 25

RESULT 68
US-09-392-979A-2
; Sequence 2, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
US-09-392-979A-2

Query Match      34.5%; Score 55.5; DB 3; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy      1 CRXNQKCFQHLDDCCSRKCNRFNC 26
      | : : : : : : : : : : : :
Db      1 CKKGASCHRTSYDCCGTGSCNR-GKC 25

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; FILING DATE: 22-NOV-1989
; SEQ ID NO:2:
; LENGTH: 25
5424218-2

Query Match      34.5%; Score 55.5; DB 6; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | : : : : | : : : : | : : : : |
Db 1 CKKGASCHRTSYDCCGTGSCNR-GKC 25

RESULT 72
5189020-1
; Patent No. 5189020
; APPLICANT: Milijanich, George P.; Bitner, Robert S.; Bowersox,
; Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald
; H.; Tsubokawa, Makoto
; TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING
; OMEGA CONOTOXIN PEPTIDES
; NUMBER OF SEQUENCES: 29
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,094
; FILING DATE: 22-NOV-1989
; SEQ ID NO:1:
; LENGTH: 25
5189020-1

Query Match      34.5%; Score 55.5; DB 6; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | : : : : | : : : : | : : : : |
Db 1 CKKGASCHRTSYDCCGTGSCNR-GKC 25

RESULT 70
5189020-2
; Patent No. 5189020
; APPLICANT: Milijanich, George P.; Bitner, Robert S.; Bowersox,
; Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald
; H.; Tsubokawa, Makoto
; TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING
; OMEGA CONOTOXIN PEPTIDES
; NUMBER OF SEQUENCES: 29
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,094
; FILING DATE: 22-NOV-1989
; SEQ ID NO:2:
; LENGTH: 25
5189020-2

Query Match      34.5%; Score 55.5; DB 6; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | : : : : | : : : : | : : : : |
Db 1 CKKGASCHRTSYDCCGTGSCNR-GKC 25

RESULT 71
5424218-2
; Patent No. 5424218
; APPLICANT: MILJANICH, GEORGE P.; BITNER, ROBERT S.; BOWERSOX,
; STEPHEN S.; FOX, JAMES A.; VALENTINO, KAREN L.; YAMASHIRO, DONALD H.
; TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,714
; FILING DATE: 04-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 855,269
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: 561,766
; FILING DATE: 02-AUG-1990
; APPLICATION NUMBER: 440,094

```


RESULT 77
S-08-569-214-3
Sequence 3, Application US/08569214
Patent No. 6165469
GENERAL INFORMATION:


```
; APPLICANT: MANN, BARBARA J.
; APPLICANT: PETRI, WILLIAM A.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/569,214
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06890
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9148-0006.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1291 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-569-214-3

Query Match 34.5%; Score 55.5; DB 3; Length 1291;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNREN-KCV 27
Db 717 CSMGTNIITYHDDCNRSKQCGNFGKCI 746

RESULT 78
US-08-937-236-2
; Sequence 2, Application US/08937236
; Patent No. 6187310
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; APPLICANT: PETRI, WILLIAM A.
; APPLICANT: DODSON, JAMES M.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/569,214
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06890
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9148-0006.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1291 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-569-214-3

Query Match 34.5%; Score 55.5; DB 3; Length 1291;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNREN-KCV 27
Db 717 CSMGTNIITYHDDCNRSKQCGNFGKCI 746

RESULT 79
US-08-569-214-2
; Sequence 2, Application US/08569214
; Patent No. 6165469
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; APPLICANT: PETRI, WILLIAM A.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/569,214
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06890
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9148-0006.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-937-236-2

Query Match 34.5%; Score 55.5; DB 3; Length 1291;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNREN-KCV 27
Db 717 CSMGTNIITYHDDCNRSKQCGNFGKCI 746
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,236
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/569,214
; FILING DATE: 16 SEPTEMBER 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: 291482000622
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-937-236-2

Query Match 34.5%; Score 55.5; DB 3; Length 1291;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNREN-KCV 27
Db 717 CSMGTNIITYHDDCNRSKQCGNFGKCI 746

RESULT 79
US-08-569-214-2
; Sequence 2, Application US/08569214
; Patent No. 6165469
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; APPLICANT: PETRI, WILLIAM A.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,214
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06890
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9148-0006.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1295 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-569-214-2

Query Match 34.5%; Score 55.5; DB 3; Length 1295;
 Best Local Similarity 40.0%; Pred. No. 1.1e+02;
 Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

Qy 1 CRXKQCFQHLDDCCSRK--CNRFN-KCV 27
 Db 717 CSMGTDNIITHDDCNSRKSQCNGFRGKI 746

RESULT 80

; US-08-049-794-21
 ; Sequence 21, Application US/08049794
 ; Patent No. 5587454
 ; GENERAL INFORMATION:
 ; APPLICANT: JUSTICE, ALAN
 ; APPLICANT: SINGH, TEJINDER
 ; APPLICANT: GOHIL, KISHOR C
 ; APPLICANT: VALENTINO, KAREN L
 ; APPLICANT: MILJANICH, GEORGE P
 ; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
 ; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Peter Dehlinger
 ; STREET: 350 Cambridge Avenue, Suite 300
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/049,794
 ; FILING DATE: 19930415
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/814,759
 ; FILING DATE: 30-DEC-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stratford, Carol A.
 ; REGISTRATION NUMBER: 34,444
 ; REFERENCE/DOCKET NUMBER: 5865-0009.30
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 7
 ; OTHER INFORMATION: /note= "where X is hydroxyproline"
 US-08-049-794-21

Query Match 34.2%; Score 55; DB 1; Length 26;
 Best Local Similarity 47.4%; Pred. No. 4.3;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 8 CFQHLDDCCSRKCNRFNKC 26
 Db 8 CRKTMVDCSGSGCGRRGKC 26

RESULT 81

; US-08-496-847-21
 ; Sequence 21, Application US/08496847
 ; Patent No. 5795864
 ; GENERAL INFORMATION:
 ; APPLICANT: Amstutz, Gary A.
 ; APPLICANT: Bowersox, Stephen S.
 ; APPLICANT: Gohil, Kishorchandra
 ; APPLICANT: Adriaenssens, Peter I.
 ; APPLICANT: Kristipati, Ramasharma
 ; TITLE OF INVENTION: METHODS AND
 ; TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94306-1546
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/496,847
 ; FILING DATE: 27-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stratford, Carol A.
 ; REGISTRATION NUMBER: 34,444
 ; REFERENCE/DOCKET NUMBER: 5865-0009.31
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-324-0880
 ; TELEFAX: 650-324-0960
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 7
 ; OTHER INFORMATION: /note= "where X is hydroxyproline"
 US-08-496-847-21

Query Match 34.2%; Score 55; DB 1; Length 26;
 Best Local Similarity 47.4%; Pred. No. 4.3;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 8 CFQHLDDCCSRKCNRFNKC 26
 Db 8 CRKTMVDCSGSGCGRRGKC 26

RESULT 82

; US-08-742-774-21
 ; Sequence 21, Application US/08742774
 ; Patent No. 5824645
 ; GENERAL INFORMATION:
 ; APPLICANT: JUSTICE, ALAN
 ; APPLICANT: SINGH, TEJINDER
 ; APPLICANT: GOHIL, KISHOR C


```

; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,774
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,354
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-08-742-774-21

```

```

Query Match 34.2%; Score 55; DB 2; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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```

QY 8 CFQHLDDCCSRKCNRENKC 26
Db 8 CRKTYDCCSGCGRRGKC 26

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RESULT 83
US-08-675-354-21
; Sequence 21, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,354
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-08-675-354-21

```

```

Query Match 34.2%; Score 55; DB 2; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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```

QY 8 CFQHLDDCCSRKCNRENKC 26
Db 8 CRKTYDCCSGCGRRGKC 26

```

```

RESULT 84
US-08-965-918-21
; Sequence 21, Application US/08965918
; Patent No. 5891849
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```


COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-965-918-21

Query Match 34.2%; Score 55; DB 2; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 8 CFQHLDDCCSRKCNRFNKC 26
Db 8 CRKTYDCCSGSGRRGKC 26

RESULT 85
US-09-138-439-21
Sequence 21, Application US/09138439
Patent No. 5994305
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
US-09-138-439-21

Query Match 34.2%; Score 55; DB 2; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 8 CFQHLDDCCSRKCNRFNKC 26
Db 8 CRKTYDCCSGSGRRGKC 26

RESULT 86
US-08-613-400A-21
Sequence 21, Application US/08613400A
Patent No. 6054429
GENERAL INFORMATION:
APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Pettus, Mark, R.
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear

; MOLECULE TYPE: 'protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 1
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-08-613-400A-21

Query Match 34.2%; Score 55; DB 3; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKC 26
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Db 8 CRKTYDCCSGCGRRGKC 26

RESULT 87
US-09-298-017-21
; Sequence 21, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-09-298-017-21

Query Match 34.2%; Score 55; DB 3; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKC 26
| : ||||| ||
Db 8 CRKTYDCCSGCGRRGKC 26

RESULT 88
US-09-392-979A-21
; Sequence 21, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-09-392-979A-21

Query Match 34.2%; Score 55; DB 3; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKC 26
| : ||||| ||
Db 8 CRKTYDCCSGCGRRGKC 26


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RESULT 89
US-09-949-016-9481
; Sequence 9481, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9481
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9481

Query Match 34.2%; Score 55; DB 4; Length 473;
Best Local Similarity 44.0%; Pred. No. 54;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

Qy 2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
Db 89 RAWVKCVQ-----CCECKCNLTKEC 109

RESULT 90
US-09-641-612-2
; Sequence 2, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.458
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-2

Query Match 34.2%; Score 55; DB 4; Length 583;
Best Local Similarity 37.9%; Pred. No. 65;
Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

Qy 1 CR--IXNQKCFQHLDDCCSRKCNRFNKC 27
Db 375 CRAGFAGPRCEHLDLDDCAGACANGTCV 403

RESULT 91
US-07-789-913-1
; Sequence 1, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
```

```
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,913
; FILING DATE: 19911112
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0005.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-111
US-07-789-913-1

Query Match 33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
Db 1 CKGKGAKCSRLMYDCTGSC-RSGKC 25

RESULT 92
US-07-789-913-9
; Sequence 9, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
```



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
; US-08-049-794-1

Query Match 33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | : | : | : | : | : | : |
DB 1 CRGKGAKCSRLMYDCTGSC-RSGKC 25

RESULT 94
US-08-049-794-9
; Sequence 9, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID

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RESULT 96

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30


```

:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (415) 324-0880
:
: TELEFAX: (415) 324-0960
:
: INFORMATION FOR SEQ ID NO: 1:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 25 amino acids
:
: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: HYPOTHETICAL: NO
:
: ORIGINAL SOURCE:
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: INDIVIDUAL ISOLATE: MVIIA/S/
:
: US-08-675-354-1

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Query Match      . 33.9%;   Score 54.5;   DB 2;   Length 25;
Best Local Similarity 38.5%;   Pred. No. 4.7;
Matches 10;   Conservative 5;   Mismatches 10;   Indels

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Db  1  CKGKGAKCSRLMYDCCCTGSC-RSGKC 25

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RESULT 100
US-08-675-354-9
; Sequence 9, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MITJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
;

US-08-675-354-9

Query Match 33.9%; Score 54.5; DB 2; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels

Qy	1	CRIXNQCFQHLDDCCSRKCNRENKC	26
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Db	1	CKGAGAKCSRLMYDCCGTGSC-RSGKC	25

Search completed: April 18, 2005, 20:39:52
Job time : 31.5 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:29:42 ; Search time 91.5 Seconds
(without alignments)

98.077 Million cell updates/sec

Title: US-10-627-685A-26

Perfect score: 161

Sequence: 1 CR1XNQKCFQHLDDCCSKRCNRFNKC 27

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Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	161	100.0	27	15	US-10-352-254-24
2	161	100.0	27	15	US-10-627-685-24
3	158	98.1	27	15	US-10-352-254-9
4	158	98.1	27	15	US-10-352-254-12
5	158	98.1	27	15	US-10-352-254-18
6	158	98.1	27	15	US-10-627-685-9
7	158	98.1	27	15	US-10-627-685-12
8	158	98.1	27	15	US-10-627-685-18
9	157	97.5	27	15	US-10-352-254-13
10	157	97.5	27	15	US-10-352-254-23
11	157	97.5	27	15	US-10-627-685-13
12	157	97.5	27	15	US-10-627-685-23
13	156	96.9	27	15	US-10-352-254-4

14	156	96.9	27	15	US-10-352-254-20	Sequence 20, Appl
15	156	96.9	27	15	US-10-627-685-4	Sequence 4, Appl
16	156	96.9	27	15	US-10-627-685-20	Sequence 20, Appl
17	155	96.3	27	15	US-10-352-254-2	Sequence 2, Appl
18	155	96.3	27	15	US-10-352-254-3	Sequence 3, Appl
19	155	96.3	27	15	US-10-352-254-5	Sequence 5, Appl
20	155	96.3	27	15	US-10-352-254-6	Sequence 6, Appl
21	155	96.3	27	15	US-10-352-254-8	Sequence 8, Appl
22	155	96.3	27	15	US-10-352-254-10	Sequence 10, Appl
23	155	96.3	27	15	US-10-352-254-11	Sequence 11, Appl
24	155	96.3	27	15	US-10-352-254-16	Sequence 16, Appl
25	155	96.3	27	15	US-10-352-254-22	Sequence 22, Appl
26	155	96.3	27	15	US-10-627-685-2	Sequence 2, Appl
27	155	96.3	27	15	US-10-627-685-3	Sequence 3, Appl
28	155	96.3	27	15	US-10-627-685-5	Sequence 5, Appl
29	155	96.3	27	15	US-10-627-685-6	Sequence 6, Appl
30	155	96.3	27	15	US-10-627-685-8	Sequence 8, Appl
31	155	96.3	27	15	US-10-627-685-10	Sequence 10, Appl
32	155	96.3	27	15	US-10-627-685-11	Sequence 11, Appl
33	155	96.3	27	15	US-10-627-685-16	Sequence 16, Appl
34	155	96.3	27	15	US-10-627-685-22	Sequence 22, Appl
35	153	95.0	27	15	US-10-352-254-7	Sequence 7, Appl
36	153	95.0	27	15	US-10-352-254-15	Sequence 15, Appl
37	153	95.0	27	15	US-10-352-254-17	Sequence 17, Appl
38	153	95.0	27	15	US-10-352-254-19	Sequence 19, Appl
39	153	95.0	27	15	US-10-352-254-21	Sequence 21, Appl
40	153	95.0	27	15	US-10-352-254-25	Sequence 25, Appl
41	153	95.0	27	15	US-10-627-685-7	Sequence 7, Appl
42	153	95.0	27	15	US-10-627-685-15	Sequence 15, Appl
43	153	95.0	27	15	US-10-627-685-17	Sequence 17, Appl
44	153	95.0	27	15	US-10-627-685-19	Sequence 19, Appl
45	153	95.0	27	15	US-10-627-685-21	Sequence 21, Appl
46	153	95.0	27	15	US-10-627-685-25	Sequence 25, Appl
47	151	93.8	27	15	US-10-352-254-14	Sequence 14, Appl
48	151	93.8	27	15	US-10-627-685-14	Sequence 14, Appl
49	78.5	48.8	27	16	US-09-910-082A-354	Sequence 354, App
50	78.5	48.8	27	16	US-10-765-926-354	Sequence 354, App
51	78.5	48.8	72	10	US-09-910-082A-130	Sequence 130, App
52	78.5	48.8	72	16	US-10-765-926-130	Sequence 130, App
53	74	46.0	26	10	US-09-910-082A-395	Sequence 395, App
54	74	46.0	26	16	US-10-765-926-395	Sequence 395, App
55	74	46.0	30	10	US-09-910-082A-257	Sequence 257, App
56	74	46.0	30	16	US-10-765-926-257	Sequence 257, App
57	73	45.3	72	10	US-09-910-082A-217	Sequence 217, App
58	73	45.3	72	16	US-10-765-926-217	Sequence 217, App
59	71	44.1	27	16	US-09-910-082A-384	Sequence 384, App
60	71	44.1	27	16	US-10-765-926-384	Sequence 384, App
61	71	44.1	72	10	US-09-910-082A-223	Sequence 223, App
62	71	44.1	72	16	US-10-765-926-223	Sequence 223, App
63	67	41.6	26	10	US-09-910-082A-258	Sequence 258, App
64	67	41.6	26	16	US-10-765-926-258	Sequence 258, App
65	64	39.8	26	10	US-09-910-082A-268	Sequence 268, App
66	64	39.8	26	16	US-10-765-926-268	Sequence 268, App
67	64	39.8	27	10	US-09-910-082A-218	Sequence 218, App
68	64	39.8	27	16	US-09-910-082A-382	Sequence 382, App
69	64	39.8	27	16	US-10-765-926-218	Sequence 218, App
70	64	39.8	27	16	US-10-765-926-382	Sequence 382, App
71	63.5	39.4	27	10	US-09-910-082A-350	Sequence 350, App
72	63.5	39.4	27	16	US-10-765-926-350	Sequence 350, App
73	63.5	39.4	73	10	US-09-910-082A-94	Sequence 94, Appl
74	63.5	39.4	73	16	US-10-765-926-94	Sequence 94, Appl
75	62.5	38.8	36	9	US-09-894-882-369	Sequence 369, App
76	62.5	38.8	36	9	US-09-894-882-167	Sequence 167, App
77	62	38.5	27	10	US-09-910-082A-224	Sequence 224, App
78	62	38.5	27	16	US-10-765-926-224	Sequence 224, App
79	62	38.5	76	9	US-09-749-637A-207	Sequence 207, App
80	61.5	38.2	27	10	US-09-910-082A-131	Sequence 131, App
81	61.5	38.2	27	16	US-10-765-926-131	Sequence 131, App
82	61	37.9	27	10	US-09-910-082A-359	Sequence 359, App
83	61	37.9	27	16	US-10-765-926-359	Sequence 359, App
84	61	37.9	74	10	US-09-910-082A-5	Sequence 5, Appl
85	61	37.9	74	16	US-10-765-926-5	Sequence 5, Appl
86	59.5	37.0	27	10	US-09-910-082A-236	Sequence 236, App

87	59.5	37.0	27	10	US-09-910-082A-390	Sequence 390, App
88	59.5	37.0	27	16	US-10-765-926-236	Sequence 236, App
89	59.5	37.0	27	16	US-10-765-926-390	Sequence 390, App
90	59.5	37.0	74	10	US-09-910-082A-235	Sequence 235, App
91	59.5	37.0	74	16	US-10-765-926-235	Sequence 235, App
92	59	36.6	601	15	US-10-369-493-6999	Sequence 6999, App
93	59	36.6	735	14	US-10-289-776-9	Sequence 9, Appli
94	58.5	36.3	27	10	US-09-910-082A-391	Sequence 391, App
95	58.5	36.3	27	10	US-09-910-082A-392	Sequence 392, App
96	58.5	36.3	27	16	US-10-765-926-391	Sequence 391, App
97	58.5	36.3	27	16	US-10-765-926-392	Sequence 392, App
98	58.5	36.3	74	10	US-09-910-082A-238	Sequence 238, App
99	58.5	36.3	74	10	US-09-910-082A-241	Sequence 241, App
100	58.5	36.3	74	16	US-10-765-926-238	Sequence 238, App

ALIGNMENTS

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RESULT 1
US-10-352-254-24
; Sequence 24, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-352-254-24

```

Query Match 100.0%; Score 161; DB 15; Length 27;
Best Local Similarity 96.3%; pred. No. 1.2e-12;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRIXNQKCFQHLDDCCSRKCNRENKCV 27
|||:|||||

Db 1 CRIANQKCFQHLDDCCSRKCNRENKCV 27

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RESULT 2
US/10-627-685-24
; Sequence 24, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438

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; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-627-685-24

```

Query Match 100.0%; Score 161; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. NO. 1.2e-12;
Matches 26; Conservative 1; Mismatches 0; Indels

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Qy 1 CRIXNQCFQHLDDCCSRKCNFKCV 27
    |||:|||||
Db 1 CRIANQCFQHLDDCCSRKCNFKCV 27
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RESULT 3
US-10-352-254-9
; Sequence 9, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-9

Query Match 98.1%; Score 158; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 2.8e-12;
Matches 26; Conservative 1; Mismatches 0; Indels

QY	1 CRIXNQKCFQHLDCCSRKCNRNFKCV 27 :
Db	1 CKIXNQKCFQHLDCCSRKCNRNFKCV 27

RESULT 4
US-10-352-254-12
; Sequence 12, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254


```
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-9

Query Match          98.1%; Score 158; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 2.8e-12;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRIXNQKCFQHLLDDCCSRKCNRFNKCIV 27
Db       |::|::|::|::|::|::|::|::|::|::|::|::|::|
         1 CRIXNQKCFQHLLDDCCSRKCNRFNKCIV 27

RESULT 7
US-10-627-685-12
; Sequence 12, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-12

Query Match          98.1%; Score 158; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 2.8e-12;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-13

Query Match
Best Local Similarity 97.5%; Score 157; DB 15; Length 27;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27
Db 1 CQIXNQKCFQHLDDCCSRKCNRFNKC 27

RESULT 12
US-10-627-685-23
; Sequence 23, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornelli-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Leyer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-23

Query Match
Best Local Similarity 97.5%; Score 157; DB 15; Length 27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26

RESULT 13
US-10-352-254-4
; Sequence 4, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
US-10-627-685-4

Query Match
Best Local Similarity 96.3%; Score 156; DB 15; Length 27;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27

RESULT 14
US-10-352-254-20
; Sequence 20, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-20

Query Match
Best Local Similarity 96.9%; Score 156; DB 15; Length 27;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27

RESULT 15
US-10-627-685-4
; Sequence 4, Application US/10627685
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Publication No. US20040092447A1
 GENERAL INFORMATION:
 APPLICANT: Cornell-Bell, Ann H.
 APPLICANT: Pemberton, Karen E.
 APPLICANT: Temple Jr., Davis L.
 APPLICANT: Layer, Richard T.
 APPLICANT: McCabe, R. Tyler
 APPLICANT: Jones, Robert M.
 APPLICANT: Cognetix, Inc.
 TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
 FILE REFERENCE: Kappa-PVIIA
 CURRENT APPLICATION NUMBER: US/10/627,685
 PRIOR FILING DATE: 2003-07-28
 PRIOR APPLICATION NUMBER: US/09/666,837
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 60/219,438
 PRIOR FILING DATE: 2000-07-20
 PRIOR APPLICATION NUMBER: US 60/155,135
 PRIOR FILING DATE: 1999-09-22
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 4
 LENGTH: 27
 TYPE: PRT
 ORGANISM: Conus purpurascens
 FEATURE:
 NAME/KEY: PEPTIDE
 LOCATION: (1)..(27)
 OTHER INFORMATION: Xaa is Hyp
 US-10-627-685-4

Query Match 96.9%; Score 156; DB 15; Length 27;
 Best Local Similarity 96.3%; Pred. No. 4.9e-12;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRXNKKCFQHLDDCCSRKCNRFNKCV 27
 |||||
 Db 1 CRXNKKCFQHLDDCCSRKCNRFNKCV 27

RESULT 16
 US-10-627-685-20
 Sequence 20, Application US/10627685
 Publication No. US20040092447A1
 GENERAL INFORMATION:
 APPLICANT: Cornell-Bell, Ann H.
 APPLICANT: Pemberton, Karen E.
 APPLICANT: Temple Jr., Davis L.
 APPLICANT: Layer, Richard T.
 APPLICANT: McCabe, R. Tyler
 APPLICANT: Jones, Robert M.
 APPLICANT: Cognetix, Inc.
 TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
 FILE REFERENCE: Kappa-PVIIA
 CURRENT APPLICATION NUMBER: US/10/627,685
 PRIOR FILING DATE: 2003-07-28
 PRIOR APPLICATION NUMBER: US/09/666,837
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 60/219,438
 PRIOR FILING DATE: 2000-07-20
 PRIOR APPLICATION NUMBER: US 60/155,135
 PRIOR FILING DATE: 1999-09-22
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 20
 LENGTH: 27
 TYPE: PRT
 ORGANISM: Conus purpurascens
 FEATURE:
 NAME/KEY: PEPTIDE
 LOCATION: (1)..(27)
 OTHER INFORMATION: Xaa is Hyp
 US-10-627-685-20

Query Match 96.9%; Score 156; DB 15; Length 27;
 Best Local Similarity 96.3%; Pred. No. 4.9e-12;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CRXNKKCFQHLDDCCSRKCNRFNKCV 27
 |||||
 Db 1 CRXNKKCFQHLDDCCSRKCNRFNKCV 27

RESULT 17
 US-10-352-254-2
 Sequence 2, Application US/10352254
 Publication No. US20030224343A1
 GENERAL INFORMATION:
 APPLICANT: Cognetix, Inc.
 APPLICANT: University of Utah Research Foundation
 APPLICANT: Pemberton-Goodman, Karen
 APPLICANT: Jones, Robert M.
 APPLICANT: Temple, Davis
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Olivera, Baldomero M.
 TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
 FILE REFERENCE: 2314-254
 CURRENT APPLICATION NUMBER: US/10/352,254
 CURRENT FILING DATE: 2003-01-28
 PRIOR APPLICATION NUMBER: US 60/352,219
 PRIOR FILING DATE: 2002-01-29
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 27
 TYPE: PRT
 ORGANISM: Conus purpurascens
 FEATURE:
 NAME/KEY: PEPTIDE
 LOCATION: (1)..(27)
 OTHER INFORMATION: Xaa is Hyp
 US-10-352-254-2

Query Match 96.3%; Score 155; DB 15; Length 27;
 Best Local Similarity 96.3%; Pred. No. 6.5e-12;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CRXNKKCFQHLDDCCSRKCNRFNKCV 27
 |||||
 Db 1 CRXNKKCFQHLDDCCSAKCNRFNKCV 27

RESULT 18
 US-10-352-254-3
 Sequence 3, Application US/10352254
 Publication No. US20030224343A1
 GENERAL INFORMATION:
 APPLICANT: Cognetix, Inc.
 APPLICANT: University of Utah Research Foundation
 APPLICANT: Pemberton-Goodman, Karen
 APPLICANT: Jones, Robert M.
 APPLICANT: Temple, Davis
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Olivera, Baldomero M.
 TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
 FILE REFERENCE: 2314-254
 CURRENT APPLICATION NUMBER: US/10/352,254
 CURRENT FILING DATE: 2003-01-28
 PRIOR APPLICATION NUMBER: US 60/352,219
 PRIOR FILING DATE: 2002-01-29
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 3
 LENGTH: 27
 TYPE: PRT
 ORGANISM: Conus purpurascens


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; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-3

Query Match          96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 19
US-10-352-254-5
; Sequence 5, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-5

Query Match          96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 20
US-10-352-254-6
; Sequence 6, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
```

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-6

Query Match          96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CAIXNKKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 21
US-10-352-254-8
; Sequence 8, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-8

Query Match          96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 22
US-10-352-254-10
; Sequence 10, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
```


; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-10

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQACFQHLDDCCSRKCNRFNKCVCV 27

RESULT 23

US-10-352-254-11
; Sequence 11, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:

; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-11

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQACFQHLDDCCSRKCNRFNKCVCV 27

RESULT 24

US-10-352-254-16
; Sequence 16, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:

; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.

; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-16

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQACFQHLDDCCSRKCNRFNKCVCV 27

RESULT 25

US-10-352-254-22
; Sequence 22, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:

; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-22

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQACFQHLDDCCSRKCNRFNKCVCV 27

RESULT 26

US-10-627-685-2
; Sequence 2, Application US/10627685
; Publication No. US20040092447A1

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp

US-10-627-685-2

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNFNKCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNFNKCV 27
|||||

RESULT 27
US-10-627-685-3
; Sequence 3, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp

US-10-627-685-3

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNFNKCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNFNKCV 27
|||||

RESULT 28
US-10-627-685-5
; Sequence 5, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp

US-10-627-685-5

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNFNKCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNFNKCV 27
|||||

RESULT 29
US-10-627-685-6
; Sequence 6, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135

; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-6

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CAIXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 30

US-10-627-685-8
; Sequence 8, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp

US-10-627-685-8

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CRXNQKCFQHLDDCCSRKCNRFNACVCV 27

RESULT 31

US-10-627-685-10
; Sequence 10, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.

; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-10

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 32

US-10-627-685-11
; Sequence 11, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp

US-10-627-685-11

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-15

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 37

US-10-352-254-17
; Sequence 17, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-17

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 38

US-10-352-254-19
; Sequence 19, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael

; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-19

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 39

US-10-352-254-21
; Sequence 21, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-21

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 40

US-10-352-254-25
; Sequence 25, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-352-254-25

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27
|||||
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27

RESULT 41
US-10-627-685-7
Sequence 7, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-7

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27
|||||
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27

RESULT 42
US-10-627-685-15
Sequence 15, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-15

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27
|||||
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27

RESULT 43
US-10-627-685-17
Sequence 17, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-17

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27
|||||
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27

; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: xaa is Hyp
US-10-627-685-17

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 44

US-10-627-685-19
; Sequence 19, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: xaa is Hyp
US-10-627-685-19

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 45

US-10-627-685-21
; Sequence 21, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA

; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: xaa is Hyp
US-10-627-685-21

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 46

US-10-627-685-25
; Sequence 25, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: xaa is Hyp
US-10-627-685-25

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 47


```

Best Local Similarity 96.3%; Pred. No. 2e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 27
   ||||| ||||| ||||| ||||| |||||
Db 1 CRXNOKCFQALDDCCSRKCNRFNKC 27

RESULT 49
US-09-910-082A-354
; Sequence 354, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 354
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus ermineus
US-09-910-082A-354

Query Match 48.8%; Score 78.5; DB 10; Length 27;
Best Local Similarity 46.2%; Pred. No. 0.011;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
   ||: |||| ||||: ||||: ||||
Db 2 CRPKGRKCFPHQKDCCKTCTR-SKC 26

RESULT 50
US-10-765-926-354
; Sequence 354, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05

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RESULT 54
US-10-765-926-395
; Sequence 395, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.

US-09-910-082A-217

Query Match 45.3%; Score 73; DB 10; Length 72;
Best Local Similarity 50.0%; Pred. No. 0.12;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKC 20
| : : ||| | ||| |
Db 47 CKTPGRKCFPHQKDCGRAC 66

RESULT 58

US-10-765-926-217
; Sequence 217, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 217
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-765-926-217

Query Match 45.3%; Score 73; DB 16; Length 72;
Best Local Similarity 50.0%; Pred. No. 0.12;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKC 20
| : : ||| | ||| |
Db 47 CKTPGRKCFPHQKDCGRAC 66

RESULT 59

US-09-910-082A-384
; Sequence 384, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616

; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 384
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-09-910-082A-384

Query Match 44.1%; Score 71; DB 10; Length 27;
Best Local Similarity 50.0%; Pred. No. 0.087;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKC 20
| : : ||| | ||| |
Db 2 CKKTGRKCFPHQKDCGRAC 21

RESULT 60

US-10-765-926-384
; Sequence 384, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 384
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-765-926-384

Query Match 44.1%; Score 71; DB 16; Length 27;
Best Local Similarity 50.0%; Pred. No. 0.087;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKC 20
| : : ||| | ||| |
Db 2 CKKTGRKCFPHQKDCGRAC 21

RESULT 61

US-09-910-082A-223
; Sequence 223, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.

; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR FILING DATE: 2000-07-21
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 223
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-09-910-082A-223

Query Match 44.1%; Score 71; DB 10; Length 72;
Best Local Similarity 50.0%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKC 20
| : : | | | | | | | |
DB 47 CKXGRKCFPHQKCCGRAC 66

RESULT 62

US-10-765-926-223
; Sequence 223, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR FILING DATE: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 223
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-765-926-223

Query Match 44.1%; Score 71; DB 16; Length 72;
Best Local Similarity 50.0%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKC 20
| : : | | | | | | | |
DB 47 CKXGRKCFPHQKCCGRAC 66

RESULT 63

US-09-910-082A-258

; Sequence 258, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR FILING DATE: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 258
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Conus striatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(26)
; OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O

Query Match 41.6%; Score 67; DB 10; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.26;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNC 26
| : : | | | | | | | |
DB 1 CKXGQSCRRRTMXDCSGSGRRGKC 26

RESULT 64

US-10-765-926-258
; Sequence 258, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR FILING DATE: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 258
; LENGTH: 26
; TYPE: PRT


```
/ ORGANISM: Conus striatus
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(26)
/ OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
/ O-sulpho-Tyr or O-phospho-Tyr
US-10-765-926-258
```

```
Query Match          41.6%; Score 67; DB 16; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.26;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
   |::|::|::|::|::|::|::|::|
Db 1 CKLKGQSCRRTWXDCSGSGRSGKC 26
```

RESULT 65

```
US-09-910-082A-268
/ Sequence 268, Application US/09910082A
/ Publication No. US20030119731A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ APPLICANT: Olivera, Baldomero M.
/ APPLICANT: McIntosh, J. Michael
/ APPLICANT: Watkins, Maren
/ APPLICANT: Garrett, James E.
/ APPLICANT: Shon, Ki-Joon
/ APPLICANT: Jacobsen, Richard
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Cartier, G. Edward
```

```
/ TITLE OF INVENTION: Omega-Conopeptides
/ FILE REFERENCE: 2314-241
/ CURRENT APPLICATION NUMBER: US/09/910,082A
/ PRIOR FILING DATE: 2001-07-23
/ PRIOR FILING DATE: 2001-07-23
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 413
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 268
```

```
/ LENGTH: 26
```

```
/ TYPE: PRT
```

```
/ ORGANISM: Conus striatus
```

```
/ FEATURE:
```

```
/ NAME/KEY: PEPTIDE
```

```
/ LOCATION: (1)..(26)
```

```
/ OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
US-09-910-082A-268
```

```
Query Match          39.8%; Score 64; DB 10; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.59;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
   |::|::|::|::|::|::|::|::|
Db 1 CKLKGQSCRRTWXDCSGSGRSGKC 26
```

RESULT 66

```
US-10-765-926-268
/ Sequence 268, Application US/10765926
/ Publication No. US20040132663A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ APPLICANT: Olivera, Baldomero M.
/ APPLICANT: McIntosh, J. Michael
/ APPLICANT: Watkins, Maren
/ APPLICANT: Garrett, James E.
```

```
/ APPLICANT: Shon, Ki-Joon
/ APPLICANT: Jacobsen, Richard
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Cartier, G. Edward
/ TITLE OF INVENTION: Omega-Conopeptides
/ FILE REFERENCE: 2314-241
/ CURRENT APPLICATION NUMBER: US/10/765,926
/ CURRENT FILING DATE: 2004-01-29
/ PRIOR FILING DATE: 2001-07-23
/ PRIOR FILING DATE: 2001-07-23
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 413
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 268
/ LENGTH: 26
/ TYPE: PRT
/ ORGANISM: Conus striatus
/ FEATURE:
```

```
/ NAME/KEY: PEPTIDE
```

```
/ LOCATION: (1)..(26)
```

```
/ OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
/ O-sulpho-Tyr or O-phospho-Tyr
US-10-765-926-268
```

```
Query Match          39.8%; Score 64; DB 16; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.59;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
   |::|::|::|::|::|::|::|::|
Db 1 CKLKGQSCRRTWXDCSGSGRSGKC 26
```

RESULT 67

```
US-09-910-082A-218
/ Sequence 218, Application US/09910082A
/ Publication No. US20030119731A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ APPLICANT: Olivera, Baldomero M.
/ APPLICANT: McIntosh, J. Michael
/ APPLICANT: Watkins, Maren
/ APPLICANT: Garrett, James E.
/ APPLICANT: Shon, Ki-Joon
/ APPLICANT: Jacobsen, Richard
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Cartier, G. Edward
```

```
/ TITLE OF INVENTION: Omega-Conopeptides
```

```
/ FILE REFERENCE: 2314-241
```

```
/ CURRENT APPLICATION NUMBER: US/09/910,082A
```

```
/ PRIOR FILING DATE: 2001-07-23
```

```
/ PRIOR FILING DATE: 2001-07-23
```

```
/ PRIOR FILING DATE: 2000-07-21
```

```
/ PRIOR FILING DATE: 2000-07-21
```

```
/ NUMBER OF SEQ ID NOS: 413
```

```
/ SOFTWARE: PatentIn version 3.0
```

```
/ SEQ ID NO 218
```

```
/ LENGTH: 27
```

```
/ TYPE: PRT
```

```
/ ORGANISM: Conus purpurascens
```

```
/ FEATURE:
```

```
/ NAME/KEY: PEPTIDE
```

```
/ LOCATION: (1)..(27)
```

```
/ OTHER INFORMATION: Xaa at residue 1, 5, 11 and 27 is Pro or Hyp
US-09-910-082A-218
```

```
Query Match          39.8%; Score 64; DB 10; Length 27;
Best Local Similarity 55.0%; Pred. No. 0.61;
```


US-09-910-082A-350
; Sequence 350, Application US/09910082A


```

; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; PRIOR FILING DATE: 2001-07-23
; PRIOR FILING DATE: 2000-07-21
; PRIOR FILING DATE: 2000-07-21
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 350
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus circumciscus
US-09-910-082A-350

```

```

Query Match      39.4%; Score 63.5; DB 10; Length 27;
Best Local Similarity 37.0%; Pred. No. 0.7;
Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

```

```

Qy 1 CRXNQKCFQHLDDCCSRKKNRFN-KC 26
| : : | : : | : : | : : | : : |
Db 1 CKSGAKCSRLMYDCCSGCSRYSGRC 27

```

```

RESULT 72
US-10-765-926-350
; Sequence 350, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR FILING DATE: 2004-01-29
; PRIOR FILING DATE: 2001-07-23
; PRIOR FILING DATE: 2001-07-23
; PRIOR FILING DATE: 2000-07-21
; PRIOR FILING DATE: 2000-07-21
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 350
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus circumciscus
US-10-765-926-350

```

```

Query Match      39.4%; Score 63.5; DB 16; Length 27;
Best Local Similarity 37.0%; Pred. No. 0.7;
Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

```

```

Qy 1 CRXNQKCFQHLDDCCSRKKNRFN-KC 26
| : : | : : | : : | : : | : : |
Db 1 CKSGAKCSRLMYDCCSGCSRYSGRC 27

RESULT 73
US-09-910-082A-94
; Sequence 94, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR FILING DATE: 2000-07-21
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 94
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus circumciscus
US-09-910-082A-94

```

```

Query Match      39.4%; Score 63.5; DB 10; Length 73;
Best Local Similarity 37.0%; Pred. No. 1.7;
Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

```

```

Qy 1 CRXNQKCFQHLDDCCSRKKNRFN-KC 26
| : : | : : | : : | : : | : : |
Db 46 CKSGAKCSRLMYDCCSGCSRYSGRC 72

```

```

RESULT 74
US-10-765-926-94
; Sequence 94, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR FILING DATE: 2004-01-29
; PRIOR FILING DATE: 2001-07-23
; PRIOR FILING DATE: 2001-07-23
; PRIOR FILING DATE: 2000-07-21
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0

```



```
; SEQ ID NO 94
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus circumcinctus
US-10-765-926-94

Query Match
Best Local Similarity 39.4%; Score 63.5; DB 16; Length 73;
Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 CRXNKCFOHLDCCSRKCNRFN-KC 26
Db 46 CKSGAKCSRLMYDCCSGCSRYSGRC 72

RESULT 75
US-09-894-882-369
; Sequence 369, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 369
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-369

Query Match
Best Local Similarity 38.8%; Score 62.5; DB 9; Length 36;
Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNKCFOHLDCCSRKCNRFN-KCV 27
Db 2 CLSLGQRCERH-SDCCGYLCCFYDKCV 27

RESULT 76
US-09-894-882-167
; Sequence 167, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
```

```
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 167
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167

Query Match
Best Local Similarity 38.8%; Score 62.5; DB 9; Length 73;
Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNKCFOHLDCCSRKCNRFN-KCV 27
Db 39 CLSLGQRCERH-SDCCGYLCCFYDKCV 64

RESULT 77
US-09-910-082A-224
; Sequence 224, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 224
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa at residue 1, 11 and 27 is Pro or Hyp
US-09-910-082A-224

Query Match
Best Local Similarity 38.5%; Score 62; DB 10; Length 27;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```


QY 1 CRXNOKCFQHLDDCCSRKC 20
| : : ||| | ||| |
Db 2 CKTKGRKCFXHQKDCGRAC 21

RESULT 78

US-10-765-926-224
; Sequence 224, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 224
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa at residue 1, 11 and 27 is Pro or Hyp
US-10-765-926-224

Query Match 38.5%; Score 62; DB 16; Length 27;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKC 20
| : : ||| | ||| |
Db 2 CKTKGRKCFXHQKDCGRAC 21

RESULT 79

US-09-749-637A-207
; Sequence 207, Application US/09749637A
; Patent No. US20020173449A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20

; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 207
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Conus distans
US-09-749-637A-207

Query Match 38.5%; Score 62; DB 9; Length 76;
Best Local Similarity 39.3%; Pred. No. 2.6;
Matches 11; Conservative 6; Mismatches 9; Indels 2; Gaps 2;

QY 1 CRXNOKCFQHLDDCCSRKCNRP-NKCV 27
| : : ||| | ||| |
Db 48 CNEAQEHCTQN-PDCCSCKNFVGRCL 74

RESULT 80

US-09-910-082A-131
; Sequence 131, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 131
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus ermineus
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa at residue 1, 4, 11 and 27 is Pro or Hyp
US-09-910-082A-131

Query Match 38.2%; Score 61.5; DB 10; Length 27;
Best Local Similarity 47.8%; Pred. No. 1.2;
Matches 11; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 4 XNOKCFQHLDDCCSRKCNRPNC 26
| : : ||| | ||| |
Db 5 KGRKCFXHQKDCNCTCTR-SKC 26

RESULT 81

US-10-765-926-131
; Sequence 131, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael

US-10-765-926-236

US-10-765-926-236


```
; Sequence 236, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 236
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-236

Query Match      37.0%; Score 59.5; DB 16; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY      1 CRXNKKCFQHLDDCCSRKCN 22
DB      1 CNARNDGCSQH-SQCCSGSCNK 21

RESULT 90
US-09-910-082A-235
; Sequence 235, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Conus rattus
US-09-910-082A-235

Query Match      37.0%; Score 59.5; DB 10; Length 74;
Best Local Similarity 45.5%; Pred. No. 5.1;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY      1 CRXNKKCFQHLDDCCSRKCN 22
DB      48 CNARNDGCSQH-SQCCSGSCNK 68

RESULT 91
US-10-765-926-235
; Sequence 235, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 239
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-390

; Sequence 390, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 390
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-390
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; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent version 3.0
; SEQ ID NO 235
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-235

Query Match
Best Local Similarity 37.0%; Score 59.5; DB 16; Length 74;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRXNKCFOHLDCCSRKCNK 27
Db 48 CNARNDGCSQH-SQCCSGSCNK 68

RESULT 92
US-10-369-493-6999
; Sequence 6999, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6999
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6999

Query Match
Best Local Similarity 36.8%; Score 59; DB 15; Length 601;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNKRNKCV 27
Db 120 CERNIDCVNKCENGKCV 139

RESULT 93
US-10-289-776-9
; Sequence 9, Application US/10289776
; Publication No. US20030170727A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/10/289,776
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US/09/540,245
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 9
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; LENGTH: 735
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-289-776-9
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Query Match
Best Local Similarity 36.6%; Score 59; DB 14; Length 735;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNKRNKCV 27
Db 254 CERNIDCVNKCENGKCV 273
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RESULT 94
US-09-910-082A-391
; Sequence 391, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent version 3.0
; SEQ ID NO 391
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-09-910-082A-391
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Query Match
Best Local Similarity 36.3%; Score 58.5; DB 10; Length 27;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
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```
QY 1 CRXNKCFOHLDCCSRKCNK 22
Db 1 CNARNSGCSQH-POCCSGSCNK 21
```

```
RESULT 95
US-09-910-082A-392
; Sequence 392, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
```



```

; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 392
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-392

Query Match          36.3%; Score 58.5; DB 16; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.8;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY      1 CRXNQKCFQHLDDCCSRKCNR 22
      | : | | | | | | | | :
Db      1 CNARNSGCSQH-PQCCSGSCNK 21

RESULT 98
US-09-910-082A-238
; Sequence 238, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 238
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Conus rattus
US-09-910-082A-238

Query Match          36.3%; Score 58.5; DB 10; Length 74;
Best Local Similarity 45.5%; Pred. No. 6.7;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY      1 CRXNQKCFQHLDDCCSRKCNR 22
      | : | | | | | | | | :
Db      48 CNARNSGCSQH-PQCCSGSCNK 68

RESULT 99

```


US-09-910-082A-241
; Sequence 241, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 241
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Conus rattus
US-09-910-082A-241

Query Match 36.3%; Score 58.5; DB 10; Length 74;
Best Local Similarity 45.5%; Pred. No. 6.7;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
Qy 1 CRIXNKCFOHLDCCSRKCNR 22
Db 48 CNARNSGCSQH-PQCCSGSCNK 68

RESULT 100
US-10-765-926-238
; Sequence 238, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 238
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-238

Query Match 36.3%; Score 58.5; DB 16; Length 74;

Best Local Similarity 45.5%; Pred. No. 6.7;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
Qy 1 CRIXNKCFOHLDCCSRKCNR 22
Db 48 CNARNSGCSQH-PQCCSGSCNK 68

Search completed: April 18, 2005, 20:43:01
Job time : 92.5 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:23:04 ; Search time 26.5 Seconds
(without alignments)
98.032 Million cell updates/sec

Title: US-10-627-685A-26

Perfect score: 161

Sequence: 1 CRXNQKCFQHLDDCCSKRKNRKNVCV 27

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	161	100.0	27	2 A58997	kappa-conotoxin sv
2	71	44.1	26	2 C43379	omega-conotoxin pv
3	61	37.9	29	2 JH0699	omega-conotoxin mv
4	59	36.6	601	2 T22025	hypothetical prote
5	58	35.4	2524	2 A35844	protein F40E10.4 [
6	57	35.4	194	2 S70563	lectin heavy chain
7	56.5	35.1	1292	2 T09229	galactose binding
8	56.5	35.1	1292	2 T09229	notch protein - fr
9	56	34.8	2703	1 A24420	omega-conotoxin mv
10	55.5	34.5	25	2 JH0701	lectin heavy chain
11	55.5	34.5	194	2 S70664	homeotic protein l
12	55	34.2	403	1 S23802	LIM domain transcr
13	55	34.2	404	2 G01507	homeotic protein l
14	55	34.2	406	1 I58187	homeotic protein l
15	55	34.2	406	1 I48186	homeotic protein l
16	55	34.2	406	1 I48637	homeotic protein l
17	55	34.2	406	1 I50375	homeotic protein l
18	54.5	33.9	25	2 JH0700	hypothetical prote
19	54.5	33.9	239	2 T24619	glycosyltransferas
20	54.5	33.9	252	2 H97189	hypothetical prote
21	54	33.5	1372	2 T25933	hypothetical prote
22	53.5	33.2	572	2 T20764	hypothetical prote
23	53	32.9	277	2 B71406	notch homolog - se
24	53	32.9	2531	2 T31070	notch protein homo
25	53	32.9	2555	2 A40043	hydroxymethylgluta
26	52.5	32.6	474	2 T09588	170K lectin precu
27	52.5	32.6	1280	2 A39117	hypothetical prote
28	52	32.3	293	2 B26637	
29	52	32.3	354	2 T22274	

30	52	32.3	2139	2 A35672	crumbs protein - f
31	52	32.3	2471	2 A49128	cell-fate determin
32	52	32.3	2531	2 S18188	notch protein homo
33	52	32.3	2531	2 A46019	notch-1 protein -
34	51.5	32.0	29	2 A58537	omega-conotoxin mv
35	51.5	32.0	113	2 JCI088	propionyl acylase
36	51.5	32.0	1984	2 T13171	probable vitellog
37	51	31.7	29	2 A43620	omega-conotoxin gv
38	51	31.7	29	2 B43620	omega-conotoxin gv
39	51	31.7	53	2 T10405	conotoxin-like pro
40	51	31.7	53	2 T30499	conotoxin-like pro
41	51	31.7	100	2 S01348	acetylcholinester
42	51	31.7	358	2 E84452	protein F6N18.15 [
43	51	31.7	1687	2 T30176	EGF repeat transme
44	50.5	31.4	131	2 T25924	hypothetical prote
45	50.5	31.4	371	2 T23369	hypothetical prote
46	50.5	31.4	389	2 T46722	conserved hypotet
47	50.5	31.4	1208	2 T27822	hypothetical prote
48	50	31.1	53	2 C72850	conotoxin homolog
49	50	31.1	403	2 T28551	hypothetical prote
50	50	31.1	1474	2 T18281	hypothetical prote
51	50	31.1	1810	1 A32230	tenascin precursor
52	50	31.1	3623	2 T08618	intrinsic factor-B
53	49.5	30.7	37	2 A59457	I-superfamily cono
54	49.5	30.7	268	1 A30584	interleukin-1 beta
55	49.5	30.7	1282	2 JE0120	glycoprotein A - m
56	49.5	30.7	1516	2 T01055	hypothetical prote
57	49	30.4	194	2 T16556	hypothetical prote
58	49	30.4	395	2 T40102	conserved hypotet
59	49	30.4	427	2 G88492	protein T07E3.4 [i
60	49	30.4	833	2 T32289	hypothetical prote
61	49	30.4	846	2 A30889	integrin beta chal
62	49	30.4	1064	2 A40136	fibropellin Ia - s
63	49	30.4	1203	2 A49175	Notch B protein -
64	49	30.4	1291	2 T06692	hypothetical prote
65	49	30.4	1528	2 T08694	hypothetical prote
66	49	30.4	2318	2 S45306	notch 3 protein -
67	49	30.4	2437	2 S42612	transmembrane prot
68	48.5	30.1	124	1 NRCB	pancreatic ribonuc
69	48.5	30.1	128	2 JQ1739	hypothetical 14.7K
70	48.5	30.1	328	2 G89152	protein C24B5.5 [i
71	48.5	30.1	400	2 A45545	major merozoite su
72	48.5	30.1	461	2 T09341	hydroxymethylgluta
73	48.5	30.1	651	2 S47282	merozoite surface
74	48.5	30.1	1631	1 SA2QK1	major merozoite su
75	48.5	30.1	1639	2 S05603	major merozoite su
76	48.5	30.1	1701	2 A54498	major merozoite su
77	48.5	30.1	1726	1 SA2QGM	major merozoite su
78	48.5	30.1	1726	2 A45948	major merozoite su
79	48	29.8	49	2 S02007	protamine I - rabb
80	48	29.8	296	2 T26875	hypothetical prote
81	48	29.8	644	2 S64135	hypothetical prote
82	48	29.8	832	2 A31246	neurogenic protein
83	48	29.8	833	2 S15087	gene Delta protein
84	48	29.8	880	2 S06670	neurogenic repetit
85	48	29.8	1429	2 S06434	homeotic protein l
86	48	29.8	2321	2 T78549	notch3 protein - h
87	48	29.8	3006	2 T28625	variant-specific s
88	48	29.8	4544	1 S02392	alpha-2-macroglobu
89	48	29.8	4545	1 S25111	alpha-2-macroglobu
90	47.5	29.5	124	1 NRDEN	pancreatic ribonuc
91	47.5	29.5	196	2 A39384	finger protein HPP
92	47.5	29.5	249	2 H72858	apoptosis inhibito
93	47.5	29.5	249	2 T41814	IAP2 orf71 - Bomby
94	47.5	29.5	253	2 A49371	repB protein - Cam
95	47.5	29.5	595	2 G02075	transcription repr
96	47	29.2	285	2 T20506	hypothetical prote
97	47	29.2	295	2 AG3129	transcription regu
98	47	29.2	295	2 B98158	agpt protein (AF23
99	47	29.2	351	2 B71604	rRNA methylase (Sp
100	47	29.2	365	2 T26564	hypothetical prote

ALIGNMENTS

```

RESULT 1
A58997
kappa-conotoxin PVIIA - cone shell (Conus purpurascens)
N:Alternate names: fin-popping peptide
C:Species: Conus purpurascens (purple cone)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: A58997
E:Terlau, H.; Shon, K.J.; Grilley, M.; Stocker, M.; Stuehmer, W.; Olivera, B.M.
Nature 381, 148-151, 1996
A:Title: Strategy for rapid immobilization of prey by a fish-hunting marine snail.
A:Reference number: A58997
A:Accession: A58997
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-27 <TER>
A:Cross-references: UNIPROT:P56633
C:Comment: This conotoxin blocks conductance of the Shaker potassium channel.
C:Keywords: hydroxyproline; neurotoxin; venom
F:4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match      100.0%; Score 161; DB 2; Length 27;
Best Local Similarity 96.3%; Pred. No.5.2e-12;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CRINXQKCFQHLDDCCSRKCNRFNKCV 27
    |||:|||||
Db 1 CRIPNOKCFQHLDDCCSRKCNRFNKCV 27
    |||:|||||

```

RESULT 2
C44379
omega-conotoxin SVIB [validated] - cone shell (Conus striatus)
N;Alternate names: SNX-183
C;Species: Conus striatus (striated cone)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000
C;Accession: C44379
R;Ramilo, C.A.; Zafaralla, G.C.; Nadaasdi, J.; Hammerland, L.G.; Yoshikami, D.; Gray, W.R.
Biochemistry 31, 9919-9926, 1992
A;Title: Novel alpha- and omega-conotoxins from Conus striatus venom.
A;Reference number: A44379; PMID:93003172; PMID:1390774
A;Accession: C44379
A;Molecule type: protein
A;Residues: 1-26 <RAM>
A;Cross-references: CAS:143306-19-8
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:116002); structure confirmed by che
R.Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A67649; PDB:1MVJ
A;Contents: annotation; conformation by (1)H-NMR, residues 1-26
R.Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
J. Mol. Biol. 263, 297-310, 1996
A;Title: A consensus structure for omega-conotoxins with different selectivities for vol
A;Reference number: A58619; PMID:97070382; PMID:8913308
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: This omega-conotoxin blocks presynaptic calcium channels.
C;Superfamily: omega-conotoxin
C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh
F.1-16, 8-20.15-26/disulfide bonds: #status predicted
F.26/Modified site: amidated carboxyl end (Cys) #status experimental

```

Query Match          .44.11%; Score 71; DB 2; Length 267.
Best Local Similarity 42.33%; Pred. No. 0.074;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 CRXNQKCFQHLDDCCSRKCNRFNK 26
      .:.|.|.|.|.|.|.|.|
DB 1 CKLKGOSCRKTSYDCCSGSCGSGRC 26

```

RESULT 3

JH0599
 omega-conotoxin MVIIIC precursor [validated] - cone shell (Conus magus) (fragment)
 C/Species: Conus magus (magus cone)
 C/Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
 C/Accession: JH0699; PC2380
 R/Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; M.
 Neuron 9, 69-77, 1992
 A/Title: A new cone peptide ligand for mammalian presynaptic Ca2+ channels.
 A/Reference number: JH0699; MUID:92337922; PMID:1352986
 A/Accession: JH0699
 A/Molecule type: mRNA
 A/Residues: 1-29 <HIL>
 A/Cross-references: UNIPROT:P37300; GB:S40826; NID:9252126; PIDN:AAB22674.1; PID:G252127
 R/Nemoto, N.; Kubo, S.; Yoshida, T.; Chino, N.; Kimura, T.; Sakakibara, S.; Kyogoku, Y.;
 Biochem. Biophys. Res. Commun. 207, 695-700, 1995
 A/Title: Solution structure of omega-conotoxin MVIIIC determined by NMR.
 A/Reference number: PC2380; MUID:95169113; PMID:7864862

A;Accession: P02180
 A;Molecule type: protein
 A;Residues: 3-28 <NEM>
 A;R:Fair-Jones, S.; Basus, V.J.
 submitted to the Brookhaven Protein Data Bank, December 1994
 A;Reference number: A66297; PDB:1OMN
 A;Contents: annotation; conformation by (1)H-NMR, residues 3-28
 R;Fair-Jones, S.; Miljanich, G.P.; Nadaesi, L.; Ramachandran, J.; Basus, V.J.
 J. Mol. Biol. 248, 106-124, 1995
 A;Title: Solution structure of omega-conotoxin MV1IC, a high affinity of P-type calcium C
 A;Reference number: A58582; MUID:95248539; PMID:7731037
 A;Contents: annotation; conformation by (1)H-NMR
 C;Superfamily: omega-conotoxin
 C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh;
 F;3-28/Product: omega-conotoxin MV1IC #status experimental <NAT>
 F;3-18,10-22,17-28/Disulfide bonds: #status experimental
 F;F;28/Modified site: amidated carboxyl end (Cys) (amide in mature form from following glyc

Query Match 37.9%; Score 61; DB 2; Length 29;
 Best Local Similarity 38.5%; Pred: NO. 1.1;
 Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
 | : : : |||||
 3 CKGGAPCRKTMVDCSGSCGRRGKC 28

```

RESULT 4
T22025
#Name: Hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
#Species: Caenorhabditis elegans
#Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
#Accession: T22025
#Author: Smey, R.
#Submitted to the EMBL Data Library, February 1996
#Reference number: Z19503
#Accession: T22025
#Status: preliminary; translated from GB/EMBL/DBDJ
#Molecule type: DNA
#Residues: 1-601 <WIL>
#Cross-references: UNIPROT:Q20204; EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F4(
#Experimental source: clone F40E10
#Genetics:
#Gene: CESP:F40E10.4
#Map position: X

```

	Query Match	36.6%	Score 59	DB 2	Length 601
	Best Local Similarity	45.0%	Pred. NO. 13		
	Matches	9	Conservative	4	Mismatches 7
					Indels 0
					Gaps 0
1	8	CFQHLDDCCSRKCNRFNKCV	27		
		: : : : :			
		: : : : :			
2	120	CERNIDDCVNSKCGGKCV	139		


```
RESULT 5
D89711
Protein F40E10.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89711
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gac/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999
A:Accession: D89711
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-601 <STO>
A:Cross-references: UNIPROT:Q20204; GB:chr_X; PIDN:CAA93668.1; PID:g3877014; GSPDB:GN000000000
C:Genetics:
A:Gene: F40E10.4
A:Map position: X

Query Match 36.6%; Score 59; DB 2; Length 601;
Best Local Similarity 45.0%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRRNKCV 27
Db 120 CEKNIDDCVNSKCGNGKCV 139
| : : : | : : : |
| : : : | : : : |

RESULT 6
A35844
Xotch protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004
C:Accession: A35844
R:Coffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
A:Title: Xotch, the Xenopus homolog of Drosophila notch.
A:Reference number: A35844; MUID:90385285; PMID:2402639
A:Accession: A35844
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2524 <COF>
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
C:Keywords: transmembrane protein
F:146-177/Domain: EGF homology <EGX1>
F:184-215/Domain: EGF homology <EGF1>
F:222-254/Domain: EGF homology <EGF>
F:456-487/Domain: EGF homology <EGX2>
F:757-788/Domain: EGF homology <EGF3>
F:1025-1056/Domain: EGF homology <EGX3>
F:1924-1956/Domain: ankyrin repeat homology <AN1>
F:1957-1989/Domain: ankyrin repeat homology <AN2>
F:1991-2033/Domain: ankyrin repeat homology <AN3>
F:2024-2056/Domain: ankyrin repeat homology <AN4>
F:2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match 35.4%; Score 57; DB 2; Length 2524;
Best Local Similarity 37.5%; Pred. No. 58;
Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNQKCFQHLDDCCSRKCNRRNKCV 27
Db 250 SGQNCENIDDCFSNNCRNGTCV 273
| : : : | : : : |
| : : : | : : : |

RESULT 7
S70663
lectin heavy chain, N-acetylglactosamine-specific - Entamoeba histolytica (fragment)
C:Species: Entamoeba histolytica
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S70663
```

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R;Ramakrishnan, G.; Regland, B.D.; Purdy, J.E.; Mann, B.J.
Mol. Microbiol. 19, 91-100, 1996
A:Title: Physical mapping and expression of gene families encoding the N-acetyl D-galactose-4-epimerase
A:Reference number: S70662; MUID:96419166; PMID:8821939
A:Accession: S70663
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-194 <RAM>
A:Cross-references: UNIPROT:Q24821; EMBL:U33443; NID:g993052; PID:g993053
C:Genetics:
A:Gene: bg14

Query Match 35.1%; Score 56.5; DB 2; Length 194;
Best Local Similarity 43.3%; Pred. No. 12;
Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRRN-KCV 27
Db 119 CSMGTDTNIIYHDDCNRSKSCGNGKCV 148
| : : | : : |
| : : | : : |

RESULT 8
T09229
galactose binding adhesin heavy chain - Entamoeba histolytica
C:Species: Entamoeba histolytica
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09229
R:Purdy, J.E.; Mann, B.J.; Shugart, E.C.; Petri, W.A.
Mol. Biochem. Parasitol. 62, 53-59, 1993
A:Title: Analysis of the gene family encoding the Entamoeba histolytica galactose-specific lectin
A:Reference number: Z16622; MUID:94158976; PMID:8114826
A:Accession: T09229
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1292 <PUR>
A:Cross-references: UNIPROT:Q24835; EMBL:L14815; NID:g290648; PID:g290649
C:Genetics:
A:Gene: Hgl3
C:Keywords: lectin

Query Match 35.1%; Score 56.5; DB 2; Length 1292;
Best Local Similarity 43.3%; Pred. No. 43;
Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRRN-KCV 27
Db 718 CSMGTDTNIIYHDDCNRSKSCGNGKCV 747
| : : | : : |
| : : | : : |

RESULT 9
A24420
notch protein - fruit fly (Drosophila melanogaster)
N:Alternate names: neurogenic repetitive locus protein
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C:Accession: A24420; A24768; S09358; A05267
R:Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A:Reference number: A24420; MUID:87064624; PMID:3097517
A:Accession: A24420
A:Molecule type: DNA
A:Residues: 1-2703 <KID>
A:Cross-references: UNIPROT:P07207; GB:K03508; NID:g157991; PID:AA28725.1; PID:g157993
R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
A:Reference number: A24768; MUID:86079539; PMID:3935325
A:Accession: A24768
A:Molecule type: mRNA
A:Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958, 'I'
A>Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
R:Tautz, D.
Nucleic Acids Res. 17, 6463-6471, 1989
A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA markers
```


A:Reference number: S09358; MUID:89385974; PMID:2780284

A:Accession: S09358

A:Molecule type: DNA

A:Residues: 2505-2551, 'QQQ', 2552-2576, 'E', 2578-2604 <TAU>

R:Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Taakonas, S.

Cell 40, 55-62, 1985

A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and other

A:Reference number: A05267; MUID:85099329; PMID:2981631

A:Accession: A05267

A:Molecule type: DNA

A:Residues: 2504-2576, 'E', 2578-2611 <WHA2>

C:Genetics:

A:Gene: notch; opa

A:Cross-references: FlyBase:FBgn0004647

A:Map position: 8.96-9.36

A:Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3

C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology

C:Keywords: Differentiation; tandem repeat; transmembrane protein

F:27-43/Domain: transmembrane #status predicted <TM1>

F:297-328/Domain: EGF homology <EGX1>

F:530-561/Domain: EGF homology <EGF1>

F:568-599/Domain: EGF homology <EGF>

F:988-1019/Domain: EGF homology <EGX2>

F:1064-1095/Domain: EGF homology <EGF3>

F:1187-1218/Domain: EGF homology <EGX3>

F:1746-1762/Domain: transmembrane #status predicted <TMW2>

F:1950-1982/Domain: ankyrin repeat homology <AN1>

F:1983-2015/Domain: ankyrin repeat homology <AN2>

F:1988-2004/Domain: transmembrane #status predicted <TMW3>

F:2017-2049/Domain: ankyrin repeat homology <AN3>

F:2050-2082/Domain: ankyrin repeat homology <AN4>

F:2083-2115/Domain: ankyrin repeat homology <AN5>

F:2538-2568/Region: glutamine-rich

F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match

Best Local Similarity 34.8%; Score 56; DB 1; Length 2703;

Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKCNRFKCV 27

DB 822 TQKCTETNDDCVNPGNGGTCT 845

RESULT 10

JH0701

omega-conotoxin MVIIB - cone shell (Conus magus)

C:Species: Conus magus (magus cone)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C:Accession: JH0701; B34115

R:Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; M

Neuron 9, 69-77, 1992

A:Title: A new conus peptide ligand for mammalian presynaptic Ca²⁺ channels.

A:Reference number: JH0699; MUID:92337922; PMID:1352986

A:Accession: JH0701

A:Molecule type: nucleic acid

A:Status: nucleic acid sequence not shown

A:Residues: 1-25 <HIL>

A:Cross-references: UNIPROT:P05485

R:Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.;

Biochemistry 26, 2086-2090, 1987

A:Title: Neuronal calcium channel antagonists. Discrimination between calcium channel su

A:Reference number: A34115; MUID:87299637; PMID:2441741

A:Accession: B34115

A:Molecule type: protein

A:Residues: 1-25 <OLI>

C:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh

F:1-16, 8-20, 15-45/disulfide bonds: #status predicted

F:25/Modified site: amidated carboxyl end (Cys) #status predicted

Query Match

Best Local Similarity 34.5%; Score 55.5; DB 2; Length 25;

Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKCNRFKCV 27

DB 822 TQKCTETNDDCVNPGNGGTCT 845

RESULT 10

JH0701

omega-conotoxin MVIIB - cone shell (Conus magus)

C:Species: Conus magus (magus cone)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 CRXNOKCFQHLDDCCSRKCNRFKCV 26

DB 1 CRXNOKCFQHLDDCCSRKCNRFKCV 26

RESULT 11

S70664

lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)

C:Species: Entamoeba histolytica

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S70664

R:Ramakrishnan, G.; Ragland, B.D.; Purdy, J.E.; Mann, B.J.

Mol. Microbiol. 19, 91-100, 1996

A:Title: Physical mapping and expression of gene families encoding the N-acetyl D-galact

A:Reference number: S70662; MUID:96419166; PMID:8821939

A:Accession: S70664

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-194 <RAM>

A:Cross-references: UNIPROT:Q24822; EMBL:U33444; NID:g993054; PID:g993055

C:Genetics:

A:Gene: hgl5

Query Match

Best Local Similarity 34.5%; Score 55.5; DB 2; Length 194;

Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNOKCFQHLDDCCSRK--CNRFN-KCV 27

DB 119 CSWGTDNVITYHDDCNRSKSCQCNFNKCI 148

RESULT 12

S23802

homeotic protein lim-1 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S23802

R:Taira, M.; Jamrich, M.; Good, P.J.; Dawid, I.B.

Genes Dev. 6, 356-366, 1992

A:Title: The LIM domain-containing homeo box gene Xlim-1 is expressed specifically in the

A:Reference number: S23802; MUID:92192449; PMID:1347750

A:Accession: S23802

A:Molecule type: mRNA

A:Residues: 1-403 <TAI>

A:Cross-references: UNIPROT:P29674; EMBL:X63889; NID:g64829; PIDN:CAA45353.1; PID:g64830

C:Genetics:

A:Gene: lim-1

C:Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homol

C:Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation

F:4-54/Domain: LIM metal-binding repeat homology <LIM1>

F:63-117/Domain: LIM metal-binding repeat homology <LIM2>

F:180-236/Domain: homeobox homology <HOX>

Query Match

Best Local Similarity 34.2%; Score 55; DB 1; Length 403;

Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNOKCFQHLDDCCSRKCNRFKCV 26

DB 22 RAWHKVCVQ---CCECKNLTEKC 42

RESULT 13

G01507

LIM domain transcription factor LIM-1 - human

N:Alternate names: homeotic protein lim-1

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C:Accession: G01507

R:Dong, W.

submitted to the EMBL Data Library, September 1994

A;Reference number: G07570
A;Accession: G01507
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-404 <DON>
A;Cross-references: UNIPROT:P48742; EMBL:U14755; NID:G549845; PIDN:AAA21644.1; PID:G549845
C;Genetics:

A;Gene: hLim-1
C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation
F;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;181-237/Domain: homeobox homology <HOX>

Query Match 34.2%; Score 55; DB 2; Length 404;
Best Local Similarity 44.0%; Pred. No. 29;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

Qy 2 RIXNOKCFQHLDDCCSRKCNRFNKC 26
| : : | | | | | | | |
Db 22 RAWHVKCVQ-----CCECKCNLTETC 42

RESULT 14

I58187
homeotic protein lim-1 - rat
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I58187

R;Furuyama, T.; Inagaki, S.; Iwahashi, Y.; Takagi, H.
Neurosci. Lett. 170, 266-268, 1994
A;Title: Distribution of Rlim, an LIM homeodomain gene, in the rat brain.
A;Reference number: I58187; MUID:94336075; PMID:7914684
A;Accession: I58187
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-406 <RES>
A;Cross-references: GB:S71523; NID:G559635; PIDN:AAC60696.1; PID:G559636
C;Genetics:

A;Gene: lim-1
C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation
F;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;181-237/Domain: homeobox homology <HOX>

Query Match 34.2%; Score 55; DB 1; Length 406;
Best Local Similarity 44.0%; Pred. No. 29;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

Qy 2 RIXNOKCFQHLDDCCSRKCNRFNKC 26
| : : | | | | | | | |
Db 22 RAWHVKCVQ-----CCECKCNLTETC 42

RESULT 15

I48186
homeotic protein lim-1 - golden hamster
N;Alternate names: homeotic protein lmx2
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48186
R;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, W.J.; German, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
A;Title: Panceratic beta cells express a diverse set of homeobox genes.
A;Reference number: I48186; MUID:95083670; PMID:7991607
A;Accession: I48186
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-406 <RES>
A;Cross-references: UNIPROT:P36199; EMBL:X81407; NID:G587462; PIDN:CAA57164.1; PID:G587462
C;Genetics:

A;Gene: lmx2
C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation
F;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;181-237/Domain: homeobox homology <HOX>

Query Match 34.2%; Score 55; DB 1; Length 406;
Best Local Similarity 44.0%; Pred. No. 29;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

Qy 2 RIXNOKCFQHLDDCCSRKCNRFNKC 26
| : : | | | | | | | |
Db 22 RAWHVKCVQ-----CCECKCNLTETC 42

RESULT 16

I48637
homeotic protein lim-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48637; S42788
R;Fujii, T.; Pichel, J.G.; Taira, M.; Toyama, R.; David, I.B.; Westphal, H.
Dev. Dyn. 199, 73-83, 1994

A;Title: Expression patterns of the murine LIM class homeobox gene lim1 in the developing
A;Reference number: I48637; MUID:94220754; PMID:7909459
A;Accession: I48637
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-406 <RES>

A;Cross-references: UNIPROT:P36199; EMBL:Z27410; NID:G425216; PIDN:CAA81797.1; PID:G425217
R;Fujii, T.
submitted to the EMBL Data Library, November 1993
A;Reference number: S42788
A;Accession: S42788
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-406 <FUP>
A;Cross-references: EMBL:Z27410; NID:G425216; PIDN:CAA81797.1; PID:G425217
C;Genetics:

A;Gene: lhx1
C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation
F;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;181-237/Domain: homeobox homology <HOX>

Query Match 34.2%; Score 55; DB 1; Length 406;
Best Local Similarity 44.0%; Pred. No. 29;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

Qy 2 RIXNOKCFQHLDDCCSRKCNRFNKC 26
| : : | | | | | | | |
Db 22 RAWHVKCVQ-----CCECKCNLTETC 42

RESULT 17

I50375
homeotic protein lim-1 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50375
R;Tsushima, T.; Ensign, M.; Morton, S.B.; Baldassare, M.; Edlund, T.; Jessell, T.M.; Pfa.
Cell 79, 957-970, 1994
A;Title: Topographic organization of embryonic motor neurons defined by expression of LIM
A;Reference number: A55198; MUID:95094281; PMID:7528105
A;Accession: I50375
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-406 <TSU>
A;Cross-references: UNIPROT:P53411; GB:I35569; NID:G531182; PIDN:AAA62173.1; PID:G531183
C;Genetics:

A;Gene: lim-1

QY

1 CRIXNQKCFQHLLDCCSRKCNRFNKC 26
| : | : | : ||
Db

1 CKGKGAKCSRMLMYDCCTGSC-RSGKC 25

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

A;Residues: 1-1372 <MUR>
A;Cross-references: UNIPROT:P91526; EMBL:U08015; PIDN:AAB37995.1; GSPDB:GN00022; CESP:WMO
A;Experimental source: strain Bristol N2; clone W02C12
C;Genetics:
A;Gene: CESP:W02C12.1
A;Map position: 4
A;Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1

Query Match 33.5%; Score 54; DB 2; Length 1372;
Best Local Similarity 29.2%; Pred.No. 85;
Matches 7; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKCNRFNKCV 27
 : : | : | : | : | :
DB 95 TGENCDQNIDECAASPQONDAKCI 118

RESULT 22
T20764
hypothetical protein Fl1c1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20764
R;Palmer, S.
submitted to the EMBL Data Library, September 1995
A;Reference number: Z19321
A;Accession: T20764
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-572 <WIL>
A;Cross-references: UNIPROT:Q19345; EMBL:Z54270; PIDN:CAA91028.1; GSPDB:GN00028; CESP:F1
A;Experimental source: clone Fl1C1
C;Genetics:
A;Gene: CESP:Fl1C1.6
A;Map position: X
A;Introns: 39/3; 50/3; 87/1; 148/2; 190/1; 286/1; 377/3; 417/2; 499/2
C;Superfamily: steroid hormone receptor Ad4BP; erBA transforming protein homology

Query Match 33.2%; Score 53.5; DB 2; Length 572;
Best Local Similarity 32.4%; Pred.No. 54;
Matches 11; Conservative 8; Mismatches 6; Indels 9; Gaps 2;

QY 3 IXNOKCFQ-----HLDCCSKRCN--RPNKCVCV 27
 : : | : | : | : | :
DB 46 VQNKQYQCSAEANCHVDTRCKRCPCSRFQKCL 79

RESULT 23
B71406
hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: B71406
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitenegger, T.; Pohl, T.M.; Terry, N.; Giel
anavah, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C.; Chalmatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis tha
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: B71406
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-277 <BEV>
A;Cross-references: UNIPROT:O23297; GB:Z97336; NID:g2244788; PID:e327451; PID:g2244797
C;Genetics:
A;Map position: 4COP9-4G3845

Query Match 32.9%; Score 53; DB 2; Length 277;
Best Local Similarity 58.8%; Pred.No. 38;

N:Alternate names: 3-hydroxy-3-methylglutaryl-coenzyme A synthase
 C:Species: Pinus sylvestris (Scotch pine)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T09688
 R:Wegener, A.; Gimbel, W.; Werner, T.; Hani, J.; Ernst, D.; Sandermann, H.
 Biochim. Biophys. Acta 1350, 247-252, 1997
 A>Title: Molecular cloning of ozone-inducible protein from Pinus sylvestris L. with high
 A:Reference number: Z16823; MUID:97214637; PMID:9061017
 A:Accession: T09688
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-474 <WEG>
 A:Cross-references: UNIPROT:P93773; EMBL:X96386; NID:G1655678; PIDN:CAA65250.1; PID:G165
 A:Experimental source: tissue-type needles
 C:Function:
 A:Description: catalyzes the condensation of acetyl coenzyme A (Ac-CoA) with acetoacetyl
 tase
 C:Superfamily: hydroxymethylglutaryl-CoA synthase
 C:Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase

Query Match 32.6%; Score 52.5; DB 2; Length 474;
 Best Local Similarity 43.5%; Pred. No. 62;
 Matches 10; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 XNOKCF-OHLDDCCSRKCNRFNK 25
 DB 211 LSOTCYLMALDSCYKRFNCFEK 233

RESULT 27
 A39117
 170K lectin precursor - Entamoeba histolytica (fragment)
 C:Species: Entamoeba histolytica
 C>Date: 30-Aug-1991 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
 C:Accession: A39117
 R:Tannich, E.; Ebert, F.; Horstmann, R.D.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1849-1853, 1991
 A>Title: Primary structure of the 170-kDa surface lectin of pathogenic Entamoeba histoly
 A:Reference number: A39117; MUID:91156704; PMID:2000392
 A:Accession: A39117
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1280 <TAN>
 A:Cross-references: GB:M60498; NID:G158958; PID:G158959
 C:Keywords: transmembrane protein

Query Match 32.6%; Score 52.5; DB 2; Length 1280;
 Best Local Similarity 41.4%; Pred. No. 1.2e+02;
 Matches 12; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNKCFOHLDCCSRK--CNRFN-KC 26
 DB 705 CSMGTDNVITYHDDCCSRKSCQGNFNGKC 733

RESULT 28
 B26637
 neurogenic repetitive locus 95F protein - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
 C:Accession: B26637
 R:Knust, E.; Dietrich, U.; Tepass, U.; Brenner, K.A.; Weigel, D.; Vaessin, H.; Campos-Ord
 EMO J. 6, 761-766, 1987
 A>Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and
 A:Reference number: A91081; MUID:87218537; PMID:3107986
 A:Accession: B26637
 A:Molecule type: mRNA
 A:Residues: 1-293 <KNU>
 A:Cross-references: UNIPROT:P10040; GB:X05144; NID:G7519; PIDN:CAA28793.1; PID:G929536
 C:Genetics:
 A:Gene: FlyBase:crb
 A:Cross-references: FlyBase:FBgn0000368
 C:Keywords: transmembrane protein

F:139-170/Domain: EGF homology <EGX1>
 F:177-208/Domain: EGF homology <EGF1>
 F:216-252/Domain: EGF homology <EGF>

Query Match 32.3%; Score 52; DB 2; Length 293;
 Best Local Similarity 30.4%; Pred. No. 52;
 Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKCNRFNK 26
 DB 166 EGQHCQNIDECADQPCNGNC 188

RESULT 29
 T22274
 hypothetical protein F46B3.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22274
 R:Ainscough, R.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19541
 A:Accession: T22274
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-354 <WIL>
 A:Cross-references: UNIPROT:Q9XV21; EMBL:Z81540; PIDN:CAB04398.1; GSPDB:GN00023; CESP:F46B3
 A:Experimental source: clone F46B3
 C:Genetics:
 A:Gene: CESP:F46B3.9
 A:Map position: 5
 A:Introns: 23/1; 55/1; 82/1; 112/1; 142/1; 170/1; 193/1; 223/1; 299/1

Query Match 32.3%; Score 52; DB 2; Length 354;
 Best Local Similarity 35.7%; Pred. No. 58;
 Matches 10; Conservative 5; Mismatches 11; Indels 2; Gaps 1;

QY 1 CRXN--OKCFQHLDDCCSRKCNRFNK 26
 DB 158 CLKVNGSPKCVPELDQCCKSHIKCSIGSHC 185

RESULT 30
 A35672
 crumbs protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
 C:Accession: A35672
 R:Tepass, U.; Theres, C.; Knust, E.
 Cell 61, 787-799, 1990
 A>Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila e
 A:Reference number: A35672; MUID:90263104; PMID:2344615
 A:Accession: A35672
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2139 <TEP>
 A:Cross-references: UNIPROT:P10040; GB:M33753
 A>Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue
 C:Genetics:
 A:Gene: FlyBase:crb
 A:Cross-references: FlyBase:FBgn0000368
 C:Keywords: transmembrane protein
 F:352-385/Domain: EGF homology <EGX1>
 F:392-424/Domain: EGF homology <EGF1>
 F:691-722/Domain: EGF homology <EGF>
 F:767-799/Domain: EGF homology <EGF3>
 F:1878-1914/Domain: EGF homology <EGX2>

Query Match 32.3%; Score 52; DB 2; Length 2139;
 Best Local Similarity 30.4%; Pred. No. 1.9e+02;
 Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKCNRFNK 26

F:987-1018/Domain: EGF homology <EG14>
 F:1025-1056/Domain: EGF homology <EG15>
 F:1063-1094/Domain: EGF homology <EG16>
 F:1149-1180/Domain: EGF homology <EG17>
 F:1187-1218/Domain: EGF homology <EG18>
 F:1233-1264/Domain: EGF homology <EGF4>
 F:1352-1383/Domain: EGF homology <EGF4>
 F:1391-1425/Domain: EGF homology <EGF4>
 F:1917-1948/Domain: ankyrin repeat homology <AN1>
 F:1949-1981/Domain: ankyrin repeat homology <AN2>
 F:1983-2015/Domain: ankyrin repeat homology <AN3>
 F:2016-2048/Domain: ankyrin repeat homology <AN4>
 F:2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 32.3%; Score 52; DB 2; Length 2531;
 Best Local Similarity 33.3%; Pred. No. 2.1e+02;

Matches 8; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 4 XNQCFOHLDCCSRKCNRFNKC 27
 : : : : :
 Db 250 AQGNCENVDCPGNCKNGGACV 273

RESULT 34

A58537

omega-conotoxin MVIID precursor - cone shell (Conus magus) (fragment)

C:Species: Conus magus (magus cone)

C>Date: 27-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004

C:Accession: A58537

R:Monje, V.D.; Haack, J.A.; Naebitt, S.R.; Miljanich, G.; Ramachandran, J.; Naedaei, I.

Neuropharmacology 32, 1141-1149, 1993

A:Title: A new Conus peptide ligand for Ca channel subtypes.

A:Reference number: A58537; MUID:94150815; PMID:8107968

A:Accession: A58537

A:Molecule type: mRNA

A:Residues: 1-29 <MON>

A:Cross-references: UNIPROT:Q26350; GB:S69322; NID:G545399; PIDN:AAB29902.1; PID:G545400

A>Note: the predicted peptide was chemically synthesized and alternative disulfide bonds

C:Superfamily: omega-conotoxin

C:Keywords: toxin; venom

F:4-19,11-23,18-28/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 32.0%; Score 51.5; DB 2; Length 29;

Matches 9; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQCFOHLDCCSRKCNRFNKC 26
 : : : : :
 Db 4 CQGRGASCKTMYNCCSGSNR-GRC 28

RESULT 35

JC1088

propionyl acylase (EC 3.5.1.-) - Streptomyces mycarofaciens

C:Species: Streptomyces mycarofaciens

C>Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: JC1088

R:Cui, L.W.; Li, Y.; Liu, B.Y.

Acta Genet. Sin. 20, 561-570, 1993

A:Title: Localization and nucleotide sequence of propionyl acylase gene of Streptomyces

A:Reference number: JC1088; MUID:94235344; PMID:8179938

A:Accession: JC1088

A:Molecule type: DNA

A:Residues: 1-113 <CUI>

A:Cross-references: UNIPROT:Q53419; GB:S70840; NID:G546751; PIDN:AAB30769.1; PID:G546752

C:Superfamily: Streptomyces mycarofaciens propionyl acylase

C:Keywords: hydrolase

Query Match

Best Local Similarity 32.0%; Score 51.5; DB 2; Length 113;

Matches 10; Conservative 7; Mismatches 8; Indels 5; Gaps 2;

QY 1 CRXNQCFOHLDCCSRKC---NRENKCV 27
 : : : : :
 Db 17 CRESRRCMQR--DVCAARRRRMOQCV 44

RESULT 36

T13171

probable vitellogenin receptor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T13171

R:Schonbaum, C.P.; Lee, S.; Mahowald, A.P.

Proc. Natl. Acad. Sci. U.S.A. 92, 1485-1489, 1995

A:Title: The Drosophila yolkless gene encodes a vitellogenin receptor belonging to the

A:Reference number: Z17627; MUID:95183450; PMID:7878005

A:Accession: T13171

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1984 <SCH>

A:Cross-references: UNIPROT:P98163; EMBL:U13637; NID:G535345; PID:G535346; PIDN:AAB60217

C:Genetics:

A:Gene: Y1

A:Cross-references: FlyBase:FBgn0004649

A:Map position: 1

F:90-124/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F:129-166/Domain: LDL receptor ligand-binding repeat homology <LDL8>

F:184-220/Domain: LDL receptor ligand-binding repeat homology <LDL10>

F:227-262/Domain: LDL receptor ligand-binding repeat homology <LDL11>

F:266-304/Domain: LDL receptor ligand-binding repeat homology <LDL12>

F:1025-1062/Domain: LDL receptor ligand-binding repeat homology <LDL14>

F:1074-1109/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F:1118-1152/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F:1158-1193/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F:1198-1232/Domain: LDL receptor ligand-binding repeat homology <LDL5>

F:1243-1279/Domain: LDL receptor ligand-binding repeat homology <LDL6>

F:1283-1318/Domain: LDL receptor ligand-binding repeat homology <LDL7>

F:1340-1375/Domain: LDL receptor ligand-binding repeat homology <LDL9>

Query Match

Best Local Similarity 32.0%; Score 51.5; DB 2; Length 1984;

Matches 11; Conservative 3; Mismatches 9; Indels 7; Gaps 1;

QY 4 XNQCFOHLDCC---CSRKCNRFNKC 26
 : : : : :
 Db 1336 SSRSCRPHLDCQDQGEVDLSRVNPNFDC 1365

RESULT 37

A43620

omega-conotoxin GVIIA - cone shell (Conus geographus)

N:Alternate names: shaker peptide GVIIA

C:Species: Conus geographus (geography cone)

C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004

C:Accession: A43620

R:Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santos

Science 230, 1338-1343, 1985

A:Title: Peptide neurotoxins from fish-hunting cone snails.

A:Reference number: A43620; MUID:86070213; PMID:4071055

A:Accession: A43620

A:Molecule type: protein

A:Residues: 1-29 <OLI>

A:Cross-references: UNIPROT:P05483

C:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;

F:1-16,8-19,15-26/Disulfide bonds: #status predicted

F:4,7/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match

Best Local Similarity 31.7%; Score 51; DB 2; Length 29;

Matches 9; Conservative 5; Mismatches 9; Indels 6; Gaps 1;

QY 1 CRXNQCFOHLDCC---SRKCNRF 23
 : : : : :
 : : : : :

EGF repeat transmembrane protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30176
R:Sell, C.; Hoff III, H.B.
submitted to the EMBL Data Library, May 1996
A:Description: Cloning of a novel mRNA regulated by the insulin like growth factor type
A:Reference number: Z20762
A:Accession: T30176
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-1687 <SEL>
A:Cross-references: UNIPROT:Q61204; EMBL:U57368; NID:gl336627; PID:gl336628; PIDN:AAB013
A:Experimental source: strain C57BL/6J; clone DBI-1; whole embryo

Query Match 31.7%; Score 51; DB 2; Length 1687;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 8 CFQHLDDCCSRKCNRFKNCV 27
DB 486 CERNIDCPNHCQNGGVCV 505
:::|||||:|

RESULT 44
T25924
hypothetical protein T27E4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25924
R:Bradehaw, H.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid T27E4.
A:Reference number: Z20111
A:Accession: T25924
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-131 <BRA>
A:Cross-references: UNIPROT:Q23053; EMBL:U64837; PIDN:AAB04836.1; GSPDB:GN00023; CESP:T2
A:Experimental source: strain Bristol N2; clone T27E4
C:Genetics:
A:Gene: CESP:T27E4.5
A:Map position: 5
A:Introns: 40/1; 53/2; 98/1; 118/3

Query Match 31.4%; Score 50.5; DB 2; Length 131;
Best Local Similarity 33.3%; Pred. No. 45;
Matches 9; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 1 CRXNKCFOHLDCCSRKCNRFKNCV 27
DB 80 CKTDQCMFSNVQKCCDAGCG-FNVCV 105
:::|||||:|

RESULT 45
T23369
hypothetical protein K06B4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23369
R:Lloyd, C.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z19732
A:Accession: T23369
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-371 <WIL>
A:Cross-references: UNIPROT:O17932; EMBL:Z83233; PIDN:CAB05765.1; GSPDB:GN00023; CESP:K0
A:Experimental source: clone K06B4
C:Genetics:
A:Gene: CESP:K06B4.5
A:Map position: 5
A:Introns: 8/3; 120/3; 242/1

Query Match 31.4%; Score 50.5; DB 2; Length 371;
Best Local Similarity 42.3%; Pred. No. 89;
Matches 11; Conservative 4; Mismatches 10; Indels 1; Gaps 1;
QY 1 CRXNKCFOHLDCCSRKCNRFKNCV 26
DB 31 CRNINQ-CFQVNSPIKCRACRPRKC 55
:::|||||:|

RESULT 46
T46722
conserved hypothetical protein [imported] - Leishmania major
N:Alternate names: probable proline synthetase associated protein
C:Species: Leishmania major
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46722
R:Volckaert, G.; Ivens, A.C.; Lawson, D.; Quail, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1999
A:Reference number: Z23137
A:Accession: T46722
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-389 <VOL>
A:Cross-references: UNIPROT:Q9U147; EMBL:AL121861; PIDN:CAB58387.1
A:Experimental source: strain Friedlin
C:Genetics:
A:Note: L4326.11

Query Match 31.4%; Score 50.5; DB 2; Length 389;
Best Local Similarity 60.0%; Pred. No. 92;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
QY 8 CFQHLDDCCSRKCNRFKNCV 22
DB 84 CLCHV-DCCSRRCFR 97
:::|||||:|

RESULT 47
T27822
hypothetical protein ZK287.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27822
R:McMurray, A.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z20425
A:Accession: T27822
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1208 <WIL>
A:Cross-references: UNIPROT:Q23456; EMBL:Z70757; PIDN:CAA94800.1; GSPDB:GN00023; CESP:ZK
A:Experimental source: clone ZK287
C:Genetics:
A:Gene: CESP:ZK287.4
A:Map position: 5
A:Introns: 44/1; 131/3; 167/1; 259/1; 319/1; 355/1; 484/3; 713/3; 765/1; 840/2; 1036/1; 1
Query Match 31.4%; Score 50.5; DB 2; Length 1208;
Best Local Similarity 47.8%; Pred. No. 1.9e+02;
Matches 11; Conservative 1; Mismatches 10; Indels 1; Gaps 1;
QY 4 XNKCFOHLDCCSRKCNRFKNCV 26
DB 804 GNQNNFQFDS-CSRACGATNVC 825
:::|||||:|

RESULT 48
C72850
conotoxin homolog - Autographa californica nuclear polyhedrosis virus
C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A:Note: dsDNA virus
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004

F;773-857/Domain: fibronectin type III repeat homology <FN3C>
 F;865-949/Domain: fibronectin type III repeat homology <FN3D>
 F;957-1037/Domain: fibronectin type III repeat homology <FN3E>
 F;1046-1128/Domain: fibronectin type III repeat homology <FN3F>
 F;1137-1219/Domain: fibronectin type III repeat homology <FN3G>
 F;1228-1310/Domain: fibronectin type III repeat homology <FN3H>
 F;1318-1399/Domain: fibronectin type III repeat homology <FN3I>
 F;1407-1487/Domain: fibronectin type III repeat homology <FN3J>
 F;1495-1575/Domain: fibronectin type III repeat homology <FN3K>
 F;1590-1798/Domain: fibronectin type III repeat homology <FN3L>
 F;1734-1747/Domain: fibronectin type III repeat homology <FN3M>
 F;1734-1747/Domain: calcium binding #status predicted <CAB>

Query Match 31.1%; Score 50; DB 1; Length 1810;
 Best Local Similarity 35.3%; Pred. No. 2.9e+02;
 Matches 12; Conservative 3; Mismatches 11; Indels 8; Gaps 2;

QY 2 RIXNKCQFHL-----DDC-----CSRKNRFRNKC 27
 Db 356 RCENGLCVCHGFGVDDCSQRCPKTCNNRGCV 389

RESULT 52

T08618
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T08618
 F;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998
 A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
 A;Reference number: 216459; MUID:98148073; PMID:9478979
 A;Accession: T08618
 A;Status: preliminary; translated from GE/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-3623 <MOE>
 A;Cross-references: UNIPROT:O70244; EMBL:AF022247; NID:G3834379; PIDN:AACT1661.1; PID:G3834379
 C;Genetics:
 A;Gene: CUBILIN
 C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
 C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
 F;133-164/Domain: EGF homology <EGF1>
 F;436-467/Domain: EGF homology <EGF>

Query Match 31.1%; Score 50; DB 2; Length 3623;
 Best Local Similarity 29.2%; Pred. No. 4.6e+02;
 Matches 7; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCSRKNRFRNKC 27
 Db 425 SGQNCENINDCSSNPCLNGGTCI 448

RESULT 53

A59457
 I-superfamily conotoxin rille - Conus radiatus
 C;Species: Conus radiatus
 C;Date: 20-Jan-2003 #sequence_revision 20-Jan-2003 #text_change 09-Jul-2004
 C;Accession: A59457
 R;Olivera, B.
 submitted to the Protein Sequence Database, January 2003
 A;Description: Novel Excitatory Conus Peptides Define a New Conotoxin Superfamily.
 A;Reference number: A59457

A;Accession: A59457
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-37 <OLI>
 A;Cross-references: UNIPROT:Q7M4K5
 A;Note: Injection of rille in 13- to 15-day-old mice caused hyperactivity, circular motile
 ward swimming or swimming in a vertical direction and death.
 F;13/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
 F;14/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted

F;34/Modified site: 6-bromotryptophan (Trp) #status predicted
 Query Match 30.7%; Score 49.5; DB 2; Length 37;
 Best Local Similarity 30.8%; Pred. No. 25;
 Matches 8; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 CRXNKCQFHLDDCSRKNRFRNKC 26
 Db 2 CKTNKMSCSLH-EECCFRCCFHGKC 26

RESULT 54

A30584
 Interleukin-1 beta precursor - rabbit
 N;Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating factor
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 25-May-1989 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
 C;Accession: A27714; A30584; J00082; A32166
 R;Wori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
 Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
 A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiating
 A;Reference number: A27714; MUID:88134238; PMID:2449207
 A;Accession: A27714
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-268 <MOR>
 A;Cross-references: UNIPROT:P14628
 R;Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello, C.
 J. Immunol. 142, 2299-2306, 1989
 A;Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
 A;Reference number: A30584; MUID:89176242; PMID:2784458
 A;Accession: A30584
 A;Molecule type: mRNA
 A;Residues: 1-268 <CAN>
 A;Cross-references: GB:M26295; NID:G516632; PIDN:AAA1373.1; PID:G516633
 R;Young, P.R.; Sylvester, D.
 Protein Eng. 2, 545-551, 1989
 A;Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and beta
 A;Reference number: A94230; MUID:89315718; PMID:2787507
 A;Accession: J00082
 A;Molecule type: mRNA
 A;Residues: 1-268 <YOU>
 C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 ved form of interleukin-1 beta, unlike interleukin 1-alpha, is inactive.
 C;Comment: Interleukin-1 beta precursor is less heavily myristoylated than interleukin-1
 C;Superfamily: interleukin-1
 C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F;117-268/Product: interleukin-1 beta #status predicted <ILB>

Query Match 30.7%; Score 49.5; DB 1; Length 268;
 Best Local Similarity 37.0%; Pred. No. 93;
 Matches 10; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

QY 6 QKCFQHLDDCSRK-----CNRFRNKC 25
 Db 33 KSCFQDLDCPDGEGIQLRISCPYK 59

RESULT 55

JE0120
 Glycoprotein A - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 15-Jun-2001
 C;Accession: JE0120
 R;Haidaris, C.G.; Medzhradsky, O.F.; Gagliotti, F.; Simpson-haidaris, P.J.
 DNA Res. 5, 77-85, 1998
 A;Title: Molecular characterization of mouse Pneumocystis carinii surface glycoprotein A.
 A;Reference number: JE0120; MUID:98344138; PMID:9679195
 A;Accession: JE0120
 A;Molecule type: mRNA
 A;Residues: 1-1282 <HAI>
 A;Cross-references: GB:AF143102
 C;Comment: This protein is a surface antigen of pneumonia.

C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C;Keywords: Glycoprotein
F;248,612,717,779,1063/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.7%; Score 49.5; DB 2; Length 1282;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
Matches 9; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNKKCFQHLDDCCSRKCNRF-NKC 26
| : : : : | : : : : |
Db 366 QCEVLEKCYFVGSSCKDKCDKVNKC 392

RESULT 56
T01055
hypothetical protein YUP8H12R.38 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01055
R;Theologis, A.; Vysotskaia, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwan, P.; Davis, R.W.
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.
A;Reference number: Z14227
A;Accession: T01055
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1516 <THE>
A;Cross-references: UNIPROT:O64548; EMBL:AC002986; NID:g2494106; PID:g3152587; GSPDB:GN000066; SPDB:15
C;Genetics:
A;Gene: ATSP:YUP8H12R.38
A;Map position: 1
A;Introns: 59/2; 97/3; 185/1; 319/1; 379/1; 809/3; 908/3; 1001/3; 1044/3; 1111/3; 1159/2

Query Match 30.7%; Score 49.5; DB 2; Length 1516;
Best Local Similarity 28.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

QY 3 IXNKKCFQHLDDCCSRKCNRFNKC 27
| : : : : | : : : : | : : : : |
Db 543 VTQKLWKHNSCAAPQCS-YPRCL 566

RESULT 57
T16556
hypothetical protein K04C2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C;Accession: T16556
R;Pauley, A.
submitted to the EMBL Data Library, April 1994
A;Description: The sequence of C. elegans cosmid K04C2.
A;Reference number: Z18534
A;Accession: T16556
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-194 <PAU>
A;Cross-references: EMBL:U00044; NID:g470346; PID:g470348; PIDN:AAA50676.1; CESP:K04C2.1
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:K04C2.1
A;Introns: 26/2; 85/3; 131/3
C;Superfamily: Caenorhabditis elegans hypothetical protein K04C2.1

Query Match 30.4%; Score 49; DB 2; Length 194;
Best Local Similarity 33.3%; Pred. No. 86;
Matches 12; Conservative 6; Mismatches 8; Indels 10; Gaps 1;

QY 2 RIXNKKCFQHLDDCCS-----RKCNRNKC 27
| : : : : | : : : : | : : : : |
Db 86 RIPNEILFEILENCKSTEPSTVLAARLSRRFNACM 121

RESULT 58
T40102
conserved hypothetical protein SPBC2A9.11c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40102
R;Barrell, B.G.; Rajandream, M.A.; Lyne, M.; Skelton, J.; Churcher, C.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21905
A;Accession: T40102
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-395 <BAR>
A;Cross-references: UNIPROT:Q9UUM3; EMBL:AL049495; PIDN:CAB39853.1; GSPDB:GN000066; SPDB:15
A;Experimental source: strain 972h; cosmid c2A9_3p
C;Genetics:
A;Gene: SPDB:SPBC2A9.11c
A;Map position: 1
A;Introns: 216/3; 260/1

Query Match 30.4%; Score 49; DB 2; Length 395;
Best Local Similarity 24.4%; Pred. No. 1.4e+02;
Matches 11; Conservative 7; Mismatches 7; Indels 20; Gaps 2;

QY 3 IXNKKCFQHLDDCCS--RKC-----RPNKCV 27
| : : : : | : : : : | : : : : |
Db 339 LANTLAFEEEMDCVNFRCNAVYDSKPNRLMKESTDRFEKCM 383

RESULT 59
G88492
protein T07E3.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G88492
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G88492
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-427 <STO>
A;Cross-references: UNIPROT:Q22310; GB:chr.III; PIDN:AAA21083.1; PID:G532471; GSPDB:GN00
A;Note: weak similarity to glycosyl branching enzyme
C;Genetics:
A;Gene: T07E3.4
A;Map position: 3

Query Match 30.4%; Score 49; DB 2; Length 427;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 6; Mismatches 8; Indels 10; Gaps 1;

QY 2 RIXNKKCFQHLDDCCS-----RKCNRNKC 27
| : : : : | : : : : | : : : : |
Db 86 RIPNEILFEILENCKSTEPSTVLAARLSRRFNACM 121

RESULT 60
T32289
hypothetical protein F42G2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32289
R;Scheet, P.; Maggi, L.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F42G2.
A;Reference number: Z21146
A;Accession: T32289
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA

A:Residues: 1-833 <SCH>
A:Cross-references: UNIPROT:O17102; EMBL:AF024499; PIDN:AAB70358.1; GSPDB:GN00020; CESP:
A:Experimental source: strain Bristol N2; clone F42G2
C:Genetics:
A:Gene: CESP:F42G2.6
A:Map position: 2
A:Introns: 317/1; 335/1; 362/3; 781/1

Query Match 30.4%; Score 49; DB 2; Length 833;
Best Local Similarity 26.9%; Pred. No. 2.2e+02;
Matches 7; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 2 RIXNQKFQHLDDCCSRKCNFNKCV 27
::: ||||| : : :
Db 87 QVQNNCFQHLSPYSKFCHEYGHMI 112
::: ||||| : : :

RESULT 61
A30889
Integrin beta chain precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 16-Aug-2004
C:Accession: A30889
R:Mackrell, A.J.; Blumberg, B.; Haynes, S.R.; Fessler, J.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 2633-2637, 1988
A:Title: The lethal myospheroid gene of *Drosophila* encodes a membrane protein homologous
A:Reference number: A30889; MUID:88190122; PMID:3128792
A:Molecule type: mRNA
A:Residues: 1-846 <MAC>
A:Cross-references: UNIPROT:P11584; GB:J03251; NID:G157954; PIDN:AAA28714.1; PID:G157955
C:Genetics:
A:Gene: FlyBase:mys
A:Cross-references: FlyBase:FBgn0004657
C:Superfamily: Integrin beta chain; laminin-type EGF-like homology
C:Keywords: cell adhesion; cytoskeleton; transmembrane protein

Query Match 30.4%; Score 49; DB 2; Length 846;
Best Local Similarity 32.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 6; Mismatches 11; Indels 4; Gaps 2;

Qy 1 CRXNQKCF--QHLDDC--CSRKCNFNKCV 27
::: ||||| : : :
Db 669 CTVNDQGRFSGRHCEKPTCSGRCKQLKOCV 699
::: ||||| : : :

RESULT 62
A40136
fibropellin Ia - sea urchin (*Strongylocentrotus purpuratus*)
N:Alternate names: epidermal growth factor homolog precursor
N:Contains: alternatively spliced fibropellin Ib (EGFI)
C:Species: *Strongylocentrotus purpuratus* (purple urchin)
C:Date: 13-May-1992 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: A40136; B40136; A29316; A43131
R:Delgadillo-Reynosio, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A:Title: Structural analysis of the uEGF gene in the sea urchin *Strongylocentrotus purpuratus*
A:Reference number: A40136; MUID:90112459; PMID:2514273
A:Accession: A40136
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114
A:Cross-references: UNIPROT:P10079; GB:X17530; NID:G10225; PID:G667061
A:Accession: B40136
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>
A:Accession: C40136
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 'K',747-821,898-978 <DE3>
R:Hursh, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987

A:Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A:Reference number: A29316; MUID:87319677; PMID:3498216
A:Accession: A29316
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'S',280-481,786-1064 <HUR>
A:Cross-references: GB:M17421; NID:G161474; PIDN:AAA30050.1; PID:G552260
R:Hunt, L.T.; Barker, W.C.
FASEB J. 3, 1760-1764, 1989
A:Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.
A:Reference number: A43131; MUID:89196806; PMID:2784773
A:Contents: annotation
C:Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1064/Product: fibropellin I #status predicted <FIB>
F:23-54/Domain: EGF homology <EG01>
F:57-175/Domain: C1r/C1s repeat homology <C1R>
F:180-211/Domain: EGF homology <EG02>
F:218-249/Domain: EGF homology <EG03>
F:256-287/Domain: EGF homology <EG04>
F:294-325/Domain: EGF homology <EG05>
F:332-363/Domain: EGF homology <EG06>
F:370-401/Domain: EGF homology <EG07>
F:408-439/Domain: EGF homology <EG08>
F:446-477/Domain: EGF homology <EG09>
F:484-515/Domain: EGF homology <EG10>
F:522-553/Domain: EGF homology <EG11>
F:560-591/Domain: EGF homology <EG12>
F:598-629/Domain: EGF homology <EG13>
F:636-667/Domain: EGF homology <EG14>
F:674-705/Domain: EGF homology <EG15>
F:712-743/Domain: EGF homology <EG16>
F:750-781/Domain: EGF homology <EG17>
F:788-819/Domain: EGF homology <EG18>
F:826-857/Domain: EGF homology <EG19>
F:864-895/Domain: EGF homology <EG20>
F:902-933/Domain: EGF homology <EG21>
F:936-1064/Region: avidin-like
F:23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-271
57,451-466,468-477,484-495/Dissulfide bonds: #status predicted
F:489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-621
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Dissulfide bonds: #status predicted

Query Match 30.4%; Score 49; DB 2; Length 1064;
Best Local Similarity 40.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 8 CFQHLDDCCSRKCNFNKCV 27
::: ||||| : : :
Db 439 CENNIDECASRPCQNGAVCV 458
::: ||||| : : :

RESULT 63
A49175
Notch B protein - mouse (fragment)
N:Alternate names: Notch homolog
C:Species: *Mus musculus* (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004
C:Accession: A49175; PH1570; S32113
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: A49175
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1203 <LAR>
A:Cross-references: UNIPROT:O35516; EMBL:X68279; NID:G287989; PIDN:CAA48340.1; PID:G287989
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:126158)
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C:Comment: This protein is one of the neurogenic proteins controlling the decision between
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology

C;Accession: A00820
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coryu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00820
A;Molecule type: protein
A;Residues: 1-124 <VAN>
A;Cross-references: UNIPROT:P00675
A;Note: a second component of chinchilla ribonuclease has 32-Asp
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12.41.119/Active site: His, Lys, His #status predicted
F;26-84.40-95.58-110.65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 30.1%; Score 48.5; DB 1; Length 124;
Best Local Similarity 27.5%; Pred. NC. 72;
Matches 11; Conservative 6; Mismatches 8; Indels 15; Gaps 2;

Qy 1 CRXNKCFOHLDCC-----HLDDC-----CSRKNRPNK 25
Db 65 CKNGSQNCYQSNWNIHTDCLRTNSKYPNCSYRTSRENK 104

RESULT 69
JQ1739
N;Altername names: ORF6 protein
C;Species: shallot virus X
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
A;Accession: JQ1739
F;Kanyuka, K.V.; Vishnichenko, V.K.; Levay, K.E.; Kondrikov, D.V.; Ryabov, E.V.; Zavriv
J. Gen. Virol. 73, 2553-2560, 1992
A;Title: Nucleotide sequence of shallot virus X RNA reveals a 5'-proximal ciatron closed
A;Reference number: JQ1734; MUID:93019008; PMID:1339468
A;Accession: JQ1739
A;Molecule type: mRNA
A;Residues: 1-128 <KAN>
A;Cross-references: UNIPROT:Q04580
A;Experimental source: strain X

Query Match 30.1%; Score 48.5; DB 2; Length 128;
Best Local Similarity 34.6%; Pred. NC. 74;
Matches 9; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 2 RIXNKCFOHLDCCS-RKCNRFNK 26
Db 40 RLDDNPFQGTSCAKERRAKRYNC 65

RESULT 70
G89152
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
A;Accession: G89152
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G89152
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <STO>
A;Cross-references: UNIPROT:Q9TY01; GB:chr_V; PID:94883503; GSPDB:GN00023; CESP:C24B5.5
C;Genetics:
A;Gene: C24B5.5
A;Map position: 5

Query Match 30.1%; Score 48.5; DB 2; Length 328;
Best Local Similarity 39.1%; Pred. NC. 1.7e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

Best Local Similarity 30.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 7; Mismatches 9; Indels 9; Gaps 2;

Qy 1 CRXNKCFOHLDCC-----CSRKC-----NRFNKC 27
Db 170 CASONKTNQCANECNNQNCANSCSPSSQTSYSKCV 205

RESULT 71
A45545
major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
A;Accession: A45545
R;Blackman, M.J.; Ling, I.T.; Nicholls, S.C.; Holder, A.A.
Mol. Biochem. Parasitol. 49, 29-33, 1991
A;Title: Proteolytic processing of the Plasmodium falciparum merozoite surface protein-1
A;Reference number: A45545; MUID:92131048; PMID:1775158
A;Accession: A45545
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <BLA>
A;Cross-references: UNIPROT:Q03999
A;Note: sequence extracted from NCBI backbone (NCBIN:77612, NCBIIP:77621)
C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat

Query Match 30.1%; Score 48.5; DB 2; Length 400;
Best Local Similarity 37.9%; Pred. No. 1.6e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 5; Gaps 1;

Qy 4 XNQCFOHLDCCSRKC-----NRFNKC 27
Db 300 QNSGCFRHLDERECKCLLYNQEGDKCV 328

RESULT 72
T09341
hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana
N;Alternate names: 3-Hydroxy-3-methylglutaryl-coenzyme A synthase; protein T26M18.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
A;Accession: T09341; JC4567
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16650
A;Accession: T09341
A;Molecule type: DNA
A;Residues: 1-461 <BEV>
A;Cross-references: UNIPROT:P54873; EMBL:AL078606
A;Experimental source: cultivar Columbia; BAC clone T26M18
R;Montamat, F.; Guilloton, M.; Karst, F.; Delrot, S.
Gene 167, 197-201, 1995
A;Title: Isolation and characterization of a cDNA encoding Arabidopsis thaliana 3-hydroxy
A;Reference number: JC4567; MUID:96144274; PMID:8566777
A;Accession: JC4567
A;Molecule type: mRNA
A;Residues: 1-307 'S', 307-341 'N', 343-461 <MON>
A;Cross-references: EMBL:X83882; MID:G1143389; PIDN:CAA58763.1; PID:G1143390
C;Comment: This enzyme mediates the conversion of three acetyl-CoA molecules to one molec
ivity, and uptakes amino acids.
C;Genetics:
A;Gene: ATSP:T26M18.30
A;Map position: 4
A;Introns: 21/3; 57/2; 101/3; 149/3; 202/3; 227/2; 252/3; 271/2; 300/3; 347/3; 397/3
C;Superfamily: hydroxymethylglutaryl-CoA synthase
C;Keywords: carbon-carbon lyase; coenzyme A; glycoprotein; oxo-acid-lyase
F;117/Active site: Cys (covalent substrate-binding) #status predicted
F;269/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.1%; Score 48.5; DB 2; Length 461;
Best Local Similarity 39.1%; Pred. No. 1.7e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

A;Title: Merozoite surface protein sequence from the Camp strain of the human malaria parasite
A;Reference number: S06361; MUID:88143999; PMID:3278296
A;Accession: S06361
A;Molecule type: DNA
A;Residues: 1104-1726 <WEB2>
A;Cross-references: EMBL:X03831
C;Comment: The merozoite stages of different strains have strain-specific surface antigens
C;Superfamily: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The merozoite stage is the most abundant in the blood.
C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1726/Product: major merozoite surface antigen #status predicted <SIG>
F;67-87,91-96,100-105,109-120/Region: 3-residue repeats (S-G-T)
F;1757-765/Region: 3-residue repeats (T-E-E)
F;133,272,501,567,638,827,839,924,944,990,1016,1114,1221,1613,1658/Binding site: carboxy-terminal
Query Match 30.1%; Score 48.5; DB 1; Length 1726;
Best Local Similarity 37.9%; Pred. No. 4.1e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 5; Gaps 1;
QY 4 XNOKCFQHLDDCCSRKNC-----NRFNKCV 27
Db 1626 ENSGCFRHLDERECKLLNYKQEGDKCV 1654
RESULT 78
A45948
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (strain 3D7)
C;Species: Plasmodium falciparum
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A45948
R;Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A.
Exp. Parasitol. 67, 1-11, 1988
A;Title: Plasmodium falciparum: Gene structure and hydrophobic profile of the major merozoite surface antigen
A;Reference number: A45948; MUID:89005525; PMID:3049134
A;Accession: A45948
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-1726 <CHA>
A;Cross-references: UNIPROT:Q25922; GB:M37213
C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen
Query Match 30.1%; Score 48.5; DB 2; Length 1726;
Best Local Similarity 37.9%; Pred. No. 4.1e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 5; Gaps 1;
QY 4 XNOKCFQHLDDCCSRKNC-----NRFNKCV 27
Db 1626 ENSGCFRHLDERECKLLNYKQEGDKCV 1654
RESULT 79
S02007
protamine I - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S02007
R;Ammer, H.; Henschen, A.
FEBS Lett. 242, 111-116, 1988
A;Title: Primary structure of rabbit sperm protamine, the first protamine of its type with a conserved cysteine
A;Reference number: S02007; MUID:89078594; PMID:3060372
A;Accession: S02007
A;Molecule type: protein
A;Residues: 1-49 <AMM>
A;Cross-references: UNIPROT:P10119
C;Superfamily: sperm histone
C;Keywords: DNA binding; nucleus
Query Match 29.8%; Score 48; DB 2; Length 49;
Best Local Similarity 34.6%; Pred. No. 45;
Matches 9; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 1 CRXNOKCFQHLDDCCSRKNCNRKNC 26
Db 14 CRRRRRCRRRRRCRRRCRRRCRRRC 37

RESULT 80

T26875
hypothetical protein Y43F8C.16 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26875
R;Ainscough, R.
Submitted to the EMBL Data Library, October 1998
A;Reference number: Z20279
A;Accession: T26875
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-296 <WIL>
A;Cross-references: UNIPROT:Q9XWN5; EMBL:AL032637; PIDN:CAA21616.1; CESP:Y43F8C.16
A;Experimental source: clone Y43F8C
C;Genetics:
A;Gene: CESP:Y43F8C.16
A;Introns: 31/1; 53/2; 127/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Y43F8C.16
Query Match 29.8%; Score 48; DB 2; Length 296;
Best Local Similarity 37.5%; Pred. No. 1.5e+02;
Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 3 IXNOKCFQHLDDCCSRKNCNRKNC 26
Db 177 VIYHKCSTIHDDCRTYKYNFHC 200

RESULT 81

S64135
hypothetical protein YGL124C - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G2889
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64135; S72027
R;Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cadahia, J.L.; Cerdan, E.
Submitted to the Protein Sequence Database, May 1996
A;Reference number: S64134
A;Accession: S64135
A;Molecule type: DNA
A;Residues: 1-644 <CER>
A;Cross-references: UNIPROT:P53129; EMBL:Z72646; NID:gl322684; PIDN:CAA96832.1; PID:e243;
A;Experimental source: strain S288C
R;Tizon, B.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Cadahia, J.L.; Cerdan, E.
Yeast 12, 1047-1051, 1996
A;Title: Identification of a putative methyltetrahydrofolate reductase by sequence analysis
A;Reference number: S72026; MUID:97051592; PMID:8896269
A;Accession: S72027
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-644 <TIZ>
A;Cross-references: EMBL:X94106; NID:gl628448; PIDN:CAA63834.1; PID:e214776; PID:gl62845C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C;Genetics:
A;Gene: SGD:MON1
A;Cross-references: SGD:S0003092
A;Map position: 7L
A;Note: YGL124C

Query Match 29.8%; Score 48; DB 2; Length 644;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 FOHLDDCCSRKNCNR 22
Db 302 FENLDDCCSRKNCNR 315

EMBO J. 6, 3431-3440, 1987
A;Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic
A;Reference number: S00670
A;Accession: S00670
A;Molecule type: mRNA
A;Residues: 1-880 <VAE>
A;Cross-references: UNIPROT:P10041; EMBL:X06289; NID:g7852; PID:g7853
R;Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ortega
EMBO J. 6, 761-766, 1987
A;Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and t
A;Reference number: A91081; MUID:87218537; PMID:3107986
A;Accession: A26337
A;Molecule type: mRNA
A;Residues: 422-436, 'ET', 439-458, 'A', 460-489, 'T', 491-621 <KNU>
A;Cross-references: GB:X05140; NID:g7851; PIDN:CAA28786.1; PID:g929563
C;Genetics:
A;Gene: Delta; DL
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
C;Keywords: transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;13-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
F;457-488/Domain: EGF homology <EGF1>
F;533-564/Domain: EGF homology <EGF2>

Query Match 29.8%; Score 48; DB 2; Length 880;
Best Local Similarity 28.6%; Pred. No. 3e+02;
Matches 6; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 7 KCFQHLDDCCSRKCNRFNKCV 27
DB 449 RCETNIDDDCLGHQCENGGTCTI 469

RESULT 85
S06434
homeotic protein lin-12 precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Jan-1993 #revision 29-Jan-1993 #text_change 16-Aug-2004
C;Accession: S06434; A24769
R;Yochem, J.; Weston, K.; Greenwald, I.
Nature 335, 547-550, 1988
A;Title: The Caenorhabditis elegans lin-12 gene encodes a transmembrane protein with over
A;Reference number: S06434; MUID:88334747; PMID:3419531
A;Accession: S06434
A;Molecule type: DNA
A;Residues: 1-1429 <YOC>
R;Greenwald, I.
Cell 43, 583-590, 1985
A;Reference number: A24769; MUID:86079540; PMID:3000611
A;Accession: A24769
A;Molecule type: DNA
A;Residues: 173-712 <GRE>
C;Genetics:
A;Introns: 50/2; 90/1; 109/1; 172/3; 545/1; 589/2; 632/2; 1273/3; 1389/3
C;Superfamily: ankyrin repeat homology; EGF homology
C;Keywords: Glycoprotein; transmembrane protein
F;254-284/Domain: EGF homology <EGF1>
F;507-540/Domain: EGF homology <EGF>
F;547-578/Domain: EGF homology <EGF2>
F;909-931/Domain: transmembrane #status predicted <TMM>
F;1093-1125/Domain: ankyrin repeat homology <AN1>
F;1206-1238/Domain: ankyrin repeat homology <AN2>
F;1240-1272/Domain: ankyrin repeat homology <AN3>

Query Match 29.8%; Score 48; DB 2; Length 1429;
Best Local Similarity 35.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKCV 27
DB 284 CQEGKNCVNNKCEAGSKCI 303

RESULT 86

S78549
 notch3 protein - human
 C:Species: Homo sapiens (man)
 C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S78549; S71825
 R:Joutel, A.; Tournier-Lasserre, E.
 submitted to the EMBL Data Library, April 1997
 A:Reference number: S78549
 A:Accession: S78549
 A:Molecule type: mRNA
 A:Residues: 1-2321 <JOU1>
 A:Cross-references: UNIPROT:Q9UM47; EMBL:U97669; NID:92668591; PIDN:AA91371.1; PID:92668591
 R:Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabriat, H.; Mouton, P.; Alamowitch, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserre, E.
 Nature 383, 707-710, 1996
 A:Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke
 A:Reference number: S71825; MUID:97032728; PMID:8878478
 A:Accession: S71825
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 67-113;138-194;268-333, 'G', 335-346;536-613;716-765;1240-1279;1815-1888 <JOU2>
 A:Cross-references: EMBL:U97669
 C:Genetics:
 A:Gene: notch3
 A:Map position: 19p13.1
 C:Function:
 A:Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C:Keywords: tandem repeat; transmembrane protein
 F:123-155/Domain: EGF homology <EGX1>
 F:162-194/Domain: EGF homology <EGF1>
 F:240-271/Domain: EGF homology <EGX2>
 F:318-349/Domain: EGF homology <EGF>
 F:473-504/Domain: EGF homology <EGX3>
 F:853-884/Domain: EGF homology <EGX4>
 F:928-959/Domain: EGF homology <EGX5>
 F:1838-1870/Domain: ankyrin repeat homology <AN1>
 F:1871-1903/Domain: ankyrin repeat homology <AN2>
 F:1905-1937/Domain: ankyrin repeat homology <AN3>
 F:1938-1970/Domain: ankyrin repeat homology <AN4>
 F:1971-2003/Domain: ankyrin repeat homology <AN5>

Query Match 29.8%; Score 48; DB 2; Length 2321;
 Best Local Similarity 33.3%; Pred. No. 5.7e+02;
 Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 7 KCFQHLDDCCSRKCNRFNKC 27

DB 578 RCESQVDCRSQPCRHGKCL 598

RESULT 87

T28625
 variant-specific surface protein 3 - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T28625
 R:Su, X.Z.; Heattwale, V.M.; Wertheimer, S.F.; Guinet, F.; Herrfeldt, J.A.; Peterson, D.S.
 Cell 82, 89-100, 1995
 A:Title: The large diverse gene family var encodes proteins involved in cytoadherence and C:Superfamily: alpha-2-macroglobulin receptor complex consists of noncovalently-associated C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-3943/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>
 F:27-64/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:72-108/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:115-148/Domain: EGF homology <EG1>
 F:154-188/Domain: EGF homology <EG2>
 F:198-239/Domain: LDL receptor YWTD-containing repeat homology <YW01>
 F:240-281/Domain: LDL receptor YWTD-containing repeat homology <YW02>
 F:292-334/Domain: LDL receptor YWTD-containing repeat homology <YW03>
 F:335-378/Domain: LDL receptor YWTD-containing repeat homology <YW04>
 F:379-420/Domain: LDL receptor YWTD-containing repeat homology <YW05>

Query Match 29.8%; Score 48; DB 2; Length 3006;
 Best Local Similarity 33.3%; Pred. No. 6.8e+02;
 Matches 9; Conservative 5; Mismatches 11; Indels 2; Gaps 1;

QY 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 25

DB 1052 CRGAKSCTQKGDCTCKRAACDYNK 1078

RESULT 88

S02392
 alpha-2-macroglobulin receptor precursor - human
 N:Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor C:Species: Homo sapiens (man)
 C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
 C:Accession: S02392; S30027; I37998; A39210; S12538
 R:Herz, J.; Hamann, U.; Rogne, S.; Mykleboost, O.; Gausepohl, H.; Stanley, K.K.
 EMBO J. 7, 4119-4127, 1988
 A:Title: Surface location and high affinity for calcium of a 500-kD liver membrane protein; A:Reference number: S02392; MUID:89210795; PMID:3266596
 A:Accession: S02392
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-4544 <HER>
 A:Cross-references: UNIPROT:Q07954; EMBL:X13916; NID:934338; PIDN:CAA32112.1; PID:934339
 R:Kristensen, T.
 submitted to the EMBL Data Library, October 1990
 A:Reference number: S30027
 A:Accession: S30027
 A:Molecule type: mRNA
 A:Residues: 3275-3864 <KRI>
 R:Herz, J.; Kowal, R.C.; Goldstein, J.L.; Brown, M.S.
 EMBO J. 9, 1769-1776, 1990
 A:Cross-references: EMBL:X55077
 A:Title: Proteolytic processing of the 600 kD low density lipoprotein receptor-related pr A:Reference number: S12538; MUID:90269210; PMID:2112085
 A:Contents: annotation: site of proteolytic cleavage
 R:Kutt, H.; Herz, J.; Stanley, K.K.
 Biochim. Biophys. Acta 1009, 229-236, 1989
 A:Title: Structure of the low-density lipoprotein receptor-related protein (LRP) promote A:Reference number: I37998; MUID:90089395; PMID:2597675
 A:Accession: I37998
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-11 <RES>
 A:Cross-references: EMBL:X15424; NID:934408; PIDN:CAA33464.1; PID:934409
 R:Strickland, D.K.; Ashcom, J.D.; Williams, S.; Burgess, W.H.; Migliorini, M.; Argraves, J. Biol. Chem. 265, 17401-17404, 1990
 A:Title: Sequence identity between the alpha2-macroglobulin receptor and low density lip A:Reference number: A39210; MUID:91009181; PMID:1698775
 A:Accession: A39210
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 150-166;234-238, 'X', 240-245, 'X', 247-252, 'G', 686-695;902-916;1096-1109, 'S', 174 C:Genetics:
 A:Gene: GDB:LRP1; APR; LRP; A2MR
 A:Cross-references: GDB:119694; OMIM:107770
 A:Map position: 12q13.1-12q13.3
 C:Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated C:Superfamily: alpha-2-macroglobulin receptor
 C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycoprotein F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-3943/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>
 F:27-64/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:72-108/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:115-148/Domain: EGF homology <EG1>
 F:154-188/Domain: EGF homology <EG2>
 F:198-239/Domain: LDL receptor YWTD-containing repeat homology <YW01>
 F:240-281/Domain: LDL receptor YWTD-containing repeat homology <YW02>
 F:292-334/Domain: LDL receptor YWTD-containing repeat homology <YW03>
 F:335-378/Domain: LDL receptor YWTD-containing repeat homology <YW04>
 F:379-420/Domain: LDL receptor YWTD-containing repeat homology <YW05>

F;479-520/Domain: EGF homology <EG3>
 F;572-614/Domain: LDL receptor WYTD-containing repeat homology <YW07>
 F;615-660/Domain: LDL receptor WYTD-containing repeat homology <YW08>
 F;661-711/Domain: LDL receptor WYTD-containing repeat homology <YW09>
 F;712-753/Domain: LDL receptor WYTD-containing repeat homology <YW10>
 F;754-800/Domain: LDL receptor WYTD-containing repeat homology <YW11>
 F;808-843/Domain: EGF homology <EG4>
 F;855-891/Domain: LDL receptor ligand-binding repeat homology <LDL3>
 F;896-932/Domain: LDL receptor ligand-binding repeat homology <LDL4>
 F;937-972/Domain: LDL receptor ligand-binding repeat homology <LDL5>
 F;977-1012/Domain: LDL receptor ligand-binding repeat homology <LDL6>
 F;1016-1052/Domain: LDL receptor ligand-binding repeat homology <LDL7>
 F;1063-1098/Domain: LDL receptor ligand-binding repeat homology <LDL8>
 F;1105-1141/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;1146-1183/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;1186-1222/Domain: EGF homology <EG5>
 F;1228-1262/Domain: EGF homology <EG6>
 F;1270-1309/Domain: LDL receptor WYTD-containing repeat homology <YW12>
 F;1310-1356/Domain: LDL receptor WYTD-containing repeat homology <YW13>
 F;1357-1399/Domain: LDL receptor WYTD-containing repeat homology <YW14>
 F;1400-1446/Domain: LDL receptor WYTD-containing repeat homology <YW15>
 F;1447-1489/Domain: LDL receptor WYTD-containing repeat homology <YW16>
 F;1490-1532/Domain: LDL receptor WYTD-containing repeat homology <YW17>
 F;1541-1579/Domain: EGF homology <EG7>
 F;1584-1627/Domain: LDL receptor WYTD-containing repeat homology <YW18>
 F;1628-1670/Domain: LDL receptor WYTD-containing repeat homology <YW19>
 F;1671-1714/Domain: LDL receptor WYTD-containing repeat homology <YW20>
 F;1715-1754/Domain: LDL receptor WYTD-containing repeat homology <YW21>
 F;1755-1797/Domain: LDL receptor WYTD-containing repeat homology <YW22>
 F;1798-1847/Domain: LDL receptor WYTD-containing repeat homology <YW23>
 F;1851-1887/Domain: EGF homology <EG8>
 F;1935-1977/Domain: LDL receptor WYTD-containing repeat homology <YW24>
 F;1978-2020/Domain: LDL receptor WYTD-containing repeat homology <YW25>
 F;2021-2064/Domain: LDL receptor WYTD-containing repeat homology <YW26>
 F;2065-2106/Domain: LDL receptor WYTD-containing repeat homology <YW27>
 F;2107-2152/Domain: LDL receptor WYTD-containing repeat homology <YW28>
 F;2160-2195/Domain: EGF homology <EG9>
 F;2200-2242/Domain: LDL receptor WYTD-containing repeat homology <YW29>
 F;2254-2295/Domain: LDL receptor WYTD-containing repeat homology <YW30>
 F;2345-2389/Domain: LDL receptor WYTD-containing repeat homology <YW31>
 F;2390-2430/Domain: LDL receptor WYTD-containing repeat homology <YW32>
 F;2431-2474/Domain: LDL receptor WYTD-containing repeat homology <YW33>
 F;2483-2518/Domain: EGF homology <EG10>
 F;2525-2562/Domain: LDL receptor ligand-binding repeat homology <LDL8>
 F;2567-2601/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;2606-2640/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;2653-2689/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;2697-2731/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;2735-2770/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;2775-2813/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;2819-2854/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;2859-2898/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;2905-2940/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F;2945-2981/Domain: EGF homology <EG11>
 F;2987-3022/Domain: EGF homology <EG12>
 F;3030-3069/Domain: LDL receptor WYTD-containing repeat homology <YW34>
 F;3070-3114/Domain: LDL receptor WYTD-containing repeat homology <YW35>
 F;3115-3157/Domain: LDL receptor WYTD-containing repeat homology <YW36>
 F;3158-3201/Domain: LDL receptor WYTD-containing repeat homology <YW37>
 F;3202-3242/Domain: LDL receptor WYTD-containing repeat homology <YW38>
 F;3243-3285/Domain: LDL receptor WYTD-containing repeat homology <YW39>
 F;3295-3331/Domain: EGF homology <EG13>
 F;3335-3370/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F;3375-3409/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F;3414-3449/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F;3454-3490/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F;3495-3532/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F;3537-3571/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F;3576-3610/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F;3614-3648/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F;3655-3691/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F;3696-3732/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F;3742-3777/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F;3786-3823/Domain: EGF homology <EG14>
 F;3829-3861/Domain: EGF homology <EG15>
 F;3869-3912/Domain: LDL receptor WYTD-containing repeat homology <YW40>
 F;3913-3970/Domain: LDL receptor WYTD-containing repeat homology <YW41>
 F;3945-4545/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
 F;3945-4421/Domain: 85K chain extracellular #status predicted <EXT>
 F;3971-4013/Domain: LDL receptor WYTD-containing repeat homology <YW42>
 F;4014-4057/Domain: LDL receptor WYTD-containing repeat homology <YW43>
 F;4058-4100/Domain: LDL receptor WYTD-containing repeat homology <YW44>
 F;4101-4143/Domain: LDL receptor WYTD-containing repeat homology <YW45>
 F;4152-4183/Domain: EGF homology <EG16>
 F;4201-4232/Domain: EGF homology <EG17>
 F;4237-4268/Domain: EGF homology <EG18>
 F;4273-4304/Domain: EGF homology <EG19>
 F;4309-4340/Domain: EGF homology <EG20>
 F;4345-4375/Domain: EGF homology <EG21>
 F;4378-4409/Domain: EGF homology <EG22>
 F;4422-4445/Domain: transmembrane #status predicted <TM>
 F;4446-4545/Domain: intracellular #status predicted <INT>
 F;167,2999/Modified site: erythro-beta-hydroxyaspartic acid (Asn) #status predicted
 F;2959/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F;4076,4126,4279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.5%; Score 48; DB 1; Length 4545;

Best Local Similarity 44.8%; Pred. No. 9e+02; Mismatches 13; Conservative 7; Mismatches 3; Indels 6; Gaps 4;

QY 1 CRXNKKCFQHLDDCCSRKC--NRFN-KC 26

DB 1222 CQIQSY-CAKHLK--CSQCDQNKFSVKC 1247

RESULT 90

NRDN

pancreatic ribonuclease [EC 3.1.27.5] - reindeer (tentative sequence)

N/Alternate names: RNase 1; RNase A

C/Species: Rangifer tarandus (reindeer)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C/Accession: B91418; A00812

R/Leijenaar-van den Berg, G.; Beintema, J.J.

FEBS Lett. 56, 101-107, 1975

A/Title: The amino acid sequences of reindeer, moose and fallow deer pancreatic ribonuclease

A/Reference number: A91418; MUID:76003215; PMID:1157925

A/Accession: B91418

A/Molecule type: protein

A/Residues: 1-124 <LEI>

A/Cross-references: UNIPROT:P00666

C/Superfamily: pancreatic ribonuclease

C/Keywords: hydrolase; nucleic acid digestion; pancreas

F;12,41,119/Active site: His, Lys, His #status predicted

F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 29.5%; Score 47.5; DB 1; Length 124;

Best Local Similarity 25.0%; Pred. No. 94;

Matches 8; Conservative 7; Mismatches 12; Indels 5; Gaps 1;

QY 1 CRXNKKCFQ----HLLDDCCSRKCNRFNKC 27

DB 65 CKNGSQNCYQNSANMHITDRETGSSKYPNCV 96

RESULT 91

A39384

finger protein HPF4 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 08-Dec-2000

C/Accession: A39384

R/Bellefroid, E.J.; Poncellet, D.A.; Lecocq, P.J.; Revelant, O.; Martial, J.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 3608-3612, 1991

A/Title: The evolutionarily conserved Krueppel-associated box domain defines a subfamily

A/Reference number: A39384; MUID:91219421; PMID:2023909

A/Accession: A39384

A/Status: preliminary

RESULT 92
H72858
apoptosis inhibitor - Autographa californica nuclear polyhedrosis virus
C/Spectes: Autographa californica nuclear polyhedrosis virus, ACMPNV
A/Note: dsDNA virus
C/Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C/Accession: H72858
R/Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A/Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A/Reference number: A72850; MUID:94303173; PMID:8030224
A/Accession: H72858
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <AYR>
A/Cross-references: UNIPROT:P41454; GS:L22858; NID:G510708; PIDN:AAA66701.1; PID:G559140
C/Genetics:
A/Gene: AC-IAP2

RESULT 93
T41814
IAP2 of71 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41814
R:Gomi, S.; Mejima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:10355780
A:Accession: T41814
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-249 <XAM>
A:Cross-references: UNIPROT:O92435; EMBL:L33180; PIDN:AAC63743.1
A:Experimental source: isolate T3
C:Genetics:
A:Note: iap2

A/Accession: 120306
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-285 <Wt>
A/Cross-references: UNIPROT:Q19120; EMBL:Z78411; PIDN:CAB01646.1; GSPDB:GN00023; CESP:F02D8
C/Genetics:
A/Experimental source: Clone F02D8
A/Map position: 5
A/Introns: 27/3; 57/3; 195/3; 235/3
Query Match 29.2% Score 47 DB 2 Length 285;


```

Best Local Similarity 39.1%; Pred. No. 1.9e+02;
Matches 9; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

QY 3 IXNQKCFQHLDDCCSRKCNRF 23
Db 147 IPPPKCFONTQGYKCCNRQLDQF 169

RESULT 97
AG3129
transcription regulator, AraC family agpT [imported] - Agrobacterium tumefaciens (strain
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AG3129
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavain, T.; Levy, R.; Li, M.; McClellan
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG3129
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-295 <KUR>
A:Cross-references: UNIPROT:Q8U6Z7; GB:AE008689; PIDN:AAU45453.1; PID:gl7743157; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: agpT
A:Map position: linear chromosome

Query Match 29.2%; Score 47; DB 2; Length 295;
Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 XNQKCFQHLDDCCSRKCN 21
Db 132 LQETVDHLAECCSRLVN 149

RESULT 98
B98158
agpt protein (AF235048) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B98158
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B98158
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-295 <KUR>
A:Cross-references: UNIPROT:Q8U6Z7; GB:AE007870; PIDN:AAK98788.1; PID:gi15158539; GSPDB:G
C:Genetics:
A:Gene: AGR_L_448
A:Map position: linear chromosome

Query Match 29.2%; Score 47; DB 2; Length 295;
Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 XNQKCFQHLDDCCSRKCN 21
Db 132 LQETVDHLAECCSRLVN 149

RESULT 99
B71604
rRNA methylase (SpoU family) (OO, TP) PFB0855c - malaria parasite (Plasmodium falciparum

```

```

C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: B71604
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Perte, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: B71604
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-351 <GAR>
A:Cross-references: UNIPROT:O96263; GB:AE001421; GB:AE001362; NID:g3845293; PIDN:AACT7196
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0855c

Query Match 29.2%; Score 47; DB 2; Length 351;
Best Local Similarity 37.5%; Pred. No. 2.1e+02;
Matches 9; Conservative 6; Mismatches 7; Indels 2; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFN 24
Db 33 CRXNQSCF--LNPCTHKVNDKRN 54

RESULT 100
T26564
hypothetical protein Y26D4A.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26564
R:White, S.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20234
A:Accession: T26564
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-365 <WIL>
A:Cross-references: UNIPROT:Q9U2Q2; EMBL:AL110478; NID:e1542139; PIDN:CAB54342.1; CESP:Y2
A:Experimental source: clone Y26D4A
C:Genetics:
A:Gene: CESP:Y26D4A.3
A:Introns: 30/1; 126/3; 174/2; 197/2; 223/1; 295/3; 335/2

Query Match 29.2%; Score 47; DB 2; Length 365;
Best Local Similarity 39.1%; Pred. No. 2.2e+02;
Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNQKCFQHLDDCCSRKCNRFNC 26
Db 284 SNQECQQRNQVVISRRARRINNC 306

Search completed: April 18, 2005, 20:38:46
Job time : 28.5 secs

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:00:51 ; Search time 117 Seconds
(without alignments)
118.172 Million cell updates/sec

Title: US-10-627-685A-26

Perfect score: 161
Sequence: 1 CRXNKCFOHLDCCSKCNRFNKC 27

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	161	100.0	67	2 Q71KT2	Q71KT2 conus purpu
2	161	100.0	72	1 CXX7 CONPU	P56633 conus purpu
3	78.5	48.8	67	2 Q6XE29	Q6XE29 conus ermin
4	73	45.3	67	2 Q71KT1	Q71KT1 conus purpu
5	71	44.1	67	2 Q71KS9	Q71KS9 conus purpu
6	71	44.1	67	2 Q71KT0	Q71KT0 conus purpu
7	71	44.1	72	1 CXOB CONST	P28881 conus stria
8	68	42.2	38	1 POI MUSDO	P81765 musca domes
9	66.5	41.3	1125	2 P92135	P92135 entamoeba d
10	66	41.0	26	1 CXOC CONCT	P58919 conus catus
11	63	39.1	2050	2 Q8IK03	Q8IK03 plasmodium
12	62	38.5	46	1 HSP1_MYODA	Q8WY8 myotis daub
13	61	37.9	29	1 CXOC CONMA	P17300 conus magus
14	61	37.9	207	2 Q7PQD5	Q7PQD5 anopheles g
15	60	37.3	1685	2 Q9U4A2	Q9U4A2 plasmodium
16	59	36.6	638	2 Q7PM27	Q7PM27 anopheles g
17	59	36.6	1410	2 Q20204	Q20204 caenorhabdi
18	58	36.0	382	1 EFL9 MOUSE	Q8K1E3 homo sapien
19	58	36.0	383	1 EFL9 HUMAN	Q6UY11 homo sapien
20	57	35.4	66	1 SCX1 OPICA	P60252 opistophtha
21	57	35.4	66	1 SCX2 OPICA	P60253 opistophtha
22	57	35.4	650	2 Q7Q0M5	Q7Q0M5 anopheles g
23	57	35.4	752	2 Q42374	Q42374 brachydanio
24	57	35.4	1245	2 Q80252	Q80252 fugu rubrip
25	57	35.4	2524	1 NOTC XENLA	P21783 xenopus lae
26	56.5	35.1	153	2 Q891K4	Q891K4 clostridium
27	56.5	35.1	194	2 Q24821	Q24821 entamoeba h
28	56.5	35.1	372	2 Q8MU89	Q8MU89 entamoeba h
29	56.5	35.1	372	2 Q8MZT3	Q8MZT3 entamoeba h
30	56.5	35.1	1292	2 Q24835	Q24835 entamoeba h
31	56.5	35.1	3467	2 Q81218	Q81218 plasmodium

ALIGNMENTS

32	56	34.8	664	2	Q9IAT6	Q9IAT6 brachydanio
33	56	34.8	708	2	Q9LGM8	Q9LGM8 oryza sativ
34	56	34.8	2703	1	NOTC_DROME	P07207 drosophila
35	55.5	34.5	25	1	CXOB_CONMA	P05485 conus magus
36	55.5	34.5	194	2	Q24822	Q24822 entamoeba h
37	55.5	34.5	372	2	Q8MZT1	Q8MZT1 entamoeba h
38	55.5	34.5	372	2	Q8MZT2	Q8MZT2 entamoeba h
39	55.5	34.5	1276	1	GILI_ENTHI	P32022 entamoeba h
40	55	34.2	33	1	SCXC_SOMA	P60254 scorio mau
41	55	34.2	112	2	Q9PSU2	Q9PSU2 xenopus lae
42	55	34.2	380	2	Q7XKS9	Q7XKS9 oryza sativ
43	55	34.2	402	2	LHX5_XENLA	P37137 xenopus lae
44	55	34.2	402	2	Q63ZK3	Q63ZK3 xenopus lae
45	55	34.2	403	1	LHX1_XENLA	P29674 xenopus lae
46	55	34.2	404	1	LHX1_HUMAN	P48742 homo sapien
47	55	34.2	406	1	LHX1_CHICK	P53411 gallus gall
48	55	34.2	406	1	LHX1_MESAU	P63008 mesocricetu
49	55	34.2	406	1	LHX1_MOUSE	P63006 mus musculu
50	55	34.2	406	1	LHX1_RAT	P63007 rattus norv
51	55	34.2	448	2	Q26107	Q26107 plasmodium
52	55	34.2	577	2	Q8HAD6	Q8HAD6 salmonella
53	55	34.2	585	2	Q8W06	Q8W06 mus musculu
54	55	34.2	587	2	Q8NBS4	Q8NBS4 homo sapien
55	55	34.2	589	1	DLI3_RAT	Q88671 rattus norv
56	55	34.2	592	1	DLI3_MOUSE	Q88516 mus musculu
57	55	34.2	618	1	DLI3_HUMAN	Q9NY17 homo sapien
58	55	34.2	1620	2	Q812A6	Q812A6 plasmodium
59	55	34.2	5309	2	Q7RRT3	Q7RRT3 plasmodium
60	54.5	33.9	71	1	CXOA_CONMA	P05484 conus magus
61	54.5	33.9	74	2	Q646V4	Q646V4 phytophthor
62	54.5	33.9	74	2	Q646V5	Q646V5 phytophthor
63	54.5	33.9	74	2	Q646W1	Q646W1 phytophthor
64	54.5	33.9	247	2	O18052	O18052 caenorhabdi
65	54.5	33.9	252	2	Q97GL5	Q97GL5 clostridium
66	54.5	33.9	1382	2	O18720	O18720 entamoeba d
67	54	33.5	73	1	CXOD_CONCT	P58920 conus catus
68	54	33.5	247	2	Q80LT7	Q80LT7 adoxophyes
69	54	33.5	405	1	LHX1_BRARE	Q90476 brachydanio
70	54	33.5	552	2	O45117	O45117 chironomus
71	54	33.5	911	2	Q68KF8	Q68KF8 xenopus lae
72	54	33.5	1372	2	P91526	P91526 caenorhabdi
73	54	33.5	1515	2	Q9DE37	Q9DE37 brachydanio
74	53.5	33.2	84	1	HSPC_ELECI	P83183 eledone cir
75	53.5	33.2	476	2	Q693N8	Q693N8 taxus x med
76	53.5	33.2	572	1	NH35 CAEEL	Q19345 caenorhabdi
77	53	32.9	33	1	ITXA_PANIM	P59868 caudinus im
78	53	32.9	85	2	Q8XKX8	Q8XKX8 clostridium
79	53	32.9	191	2	Q6LZL1	Q6LZL1 methanococc
80	53	32.9	225	2	Q7XZ30	Q7XZ30 griffithsia
81	53	32.9	234	2	Q86152	Q86152 dictyosteli
82	53	32.9	277	2	O23297	O23297 arabidopsis
83	53	32.9	283	2	Q8L467	Q8L467 arabidopsis
84	53	32.9	421	2	O44635	O44635 caenorhabdi
85	53	32.9	1286	2	Q7QCT2	Q7QCT2 anopheles g
86	53	32.9	2531	2	O16004	O16004 lytechinus
87	53	32.9	2556	1	NTC1 HUMAN	P46531 homo sapien
88	52.5	32.6	47	1	HSP1_PLETO	Q8W20 plecotus to
89	52.5	32.6	74	2	Q646U5	Q646U5 phytophthor
90	52.5	32.6	74	2	Q646U7	Q646U7 phytophthor
91	52.5	32.6	92	2	Q6PYV0	Q6PYV0 schistosoma
92	52.5	32.6	474	2	P93773	P93773 pinus sylve
93	52.5	32.6	764	2	Q6K5W7	Q6K5W7 oryza sativ
94	52.5	32.6	1285	1	SL17_ENTHI	P23502 entamoeba h
95	52	32.3	354	2	Q8XV21	Q8XV21 caenorhabdi
96	52	32.3	487	2	Q8MSX5	Q8MSX5 drosophila
97	52	32.3	539	1	WNT4_DROME	P40389 drosophila
98	52	32.3	778	2	Q91BG4	Q91BG4 xenopus lae
99	52	32.3	1069	2	Q96VI2	Q96VI2 pneumocysti
100	52	32.3	2139	1	CRB_DROME	P10040 drosophila


```

RESULT 1
Q71KT2 ID Q71KT2 PRELIMINARY; PRT; 67 AA.
AC Q71KT2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
ON NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480312; AAQ95864.1; -.
DR HSSP; P56633; IAV3.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; I.
FT NON_TER 1
FT CHAIN 41 67 four-loop conotoxin.
SQ SEQUENCE 67 AA; 7712 MW; E7E77CC61873E1DB CRC64;

Query Match 100.0%; Score 161; DB 2; Length 67;
Best Local Similarity 96.3%; Pred. No. 1.4e-12;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNFNKCV 27
Db 41 CRIPNQKCFQHLDDCCSRKCNFNKCV 57

RESULT 2
CKX7_CNFU STANDARD; PRT; 72 AA.
ID CKX7_CNFU
AC P56633;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kappa-conotoxin PVIIA precursor (Fin-popping peptide).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
ON NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A., SYNTHESIS, AND MASS SPECTROMETRY.
RA Shon K.-J., Stocker M., Terlau H., Stuehmer W., Jacobsen R.B.,
RA Walker C.S., Grille M.M., Watkins M., Hillyard D.R., Gray W.R.,
RA Olivera B.M.;
RT "Kappa-conotoxin PVIIA is a peptide inhibiting the shaker K+
channel.";
RL J. Biol. Chem. 273:33-38(1998).
RN [2]
RP SEQUENCE OF 46-72, AND SYNTHESIS.
RA Terlau H., Shon K.-J., Grille M.M., Stocker M., Stuehmer W.,
RA Olivera B.M.;
RT "Strategy for rapid immobilization of prey by a fish-hunting marine
snail.";
RL Nature 381:148-151(1996).
RN [3]
RP STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=98104087; PubMed=9438859; DOI=10.1016/S0969-2126(97)00307-9;
RA Scanlon M.J., Naranjo D., Thomas L., Alewood P.F., Lewis R.J.,

Raik D.J.;
"Solution structure and proposed binding mechanism of a novel
potassium channel toxin kappa-conotoxin PVIIA.";
Structure 5:1585-1597(1997).
[4]
RP STRUCTURE BY NMR.
RX MEDLINE=98217295; PubMed=9548922; DOI=10.1021/bi9730341;
RA Savarin P., Guenuegues M., Gilquin B., Lamthanh H., Gasparini S.,
RA Zinn-Justin S., Menez A.;
RT "Three-dimensional structure of kappa-conotoxin PVIIA, a novel
potassium channel-blocking toxin from cone snails.";
Biochemistry 37:5407-5416(1998).
[5]
RP MUTAGENESIS OF ARG-47; ILE-48; PRO-49; ASN-50; GLN-51; LYS-52; PHE-54;
PHE-54; GLN-55; HIS-56; LEU-57; ASP-58; ASP-59; SER-62; ARG-63;
LYS-64; ARG-67; PHE-68; ASN-69 AND LYS-70.
RX MEDLINE=20387358; PubMed=10818087; DOI=10.1074/jbc.C900990199;
RA Jacobsen R.B., Koch E.D., Lange-Malecki B., Stocker M., Verhey J.,
RA Van Wagoner R.M., Vyzovkina A., Olivera B.M., Terlau H.;
RT "Single amino acid substitutions in kappa-conotoxin PVIIA disrupt
interaction with the shaker K+ channel.";
J. Biol. Chem. 275:24639-24644(2000).
[6]
RP BLOCKADE OF SHAKER CHANNEL BY PVIIA.
RX MEDLINE=99329121; PubMed=10398696;
RA Terlau H., Bocaccio A., Olivera B.M., Conti F.;
RT "The block of Shaker K+ channels by kappa-conotoxin PVIIA is state
dependent.";
J. Gen. Physiol. 114:125-140(1999).
[7]
RP MODEL OF THE SHAKER-PVIIA INTERACTION.
RX MEDLINE=21678121; PubMed=11820396;
RA Moran O.;
RT "Molecular simulation of the interaction of kappa-conotoxin-PVIIA with
the shaker potassium channel pore.";
Eur. Biophys. J. 30:528-536(2001).
[8]
RP BLOCKADE OF SHAKER CHANNEL BY PVIIA.
RX MEDLINE=22017751; PubMed=12023223;
RA Naranjo D.;
RT "Inhibition of single Shaker K channels by kappa-conotoxin-PVIIA.";
Biophys. J. 82:3003-3011(2002).
-!- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
potassium channels. The rat brain voltage-gated potassium channel
protein Kv1.1 is resistant to this toxin, but the voltage-gated
potassium channel protein Shaker (Drosophila) is sensitive. The
interaction site between the Shaker channel and this toxin is
within the S5-S6 loop of the Shaker channel. In fish, this toxin
induces hyperactivity, followed by continuous contraction and
extension of major fins, without immobilization or death.
Injection of this peptide together with the delta-conotoxin PVIA
causes the sudden tetanus of prey (STOP) syndrome, which is a
single, lethal "fin-pop" in envenomated fish. In mice, induces
hyperactivity.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- MASS SPECTROMETRY: MW=3268.4; METHOD=PAB; RANGE=46-72; NOTE=Ref.1.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
family.
-!- CAUTION: Because analogs resulting of mutagenesis of Hyp-49, Asn-
50, Leu-57 and Asp-59 gave very low yields upon folding, the
results of mutagenesis on these residues should be interpreted
with caution.
PIR; A58997; A58997.
PDB; 1AV3; NMR; @=1-27.
PDB; 1KCP; NMR; @=1-27.
InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Conotoxin; I.
KW 3D-structure; Direct protein sequencing; Hydroxylation;
KW Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;
KW Signal; Toxin.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 45

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FT PEPTIDE 46 72 Kappa-conotoxin PVIIA.
FT DISULFID 46 61
FT DISULFID 53 65
FT DISULFID 60 71
FT MOD_RES 49 49
FT MUTAGEN 47 47
FT MUTAGEN 48 48
FT MUTAGEN 49 49
FT MUTAGEN 50 50
FT MUTAGEN 51 51
FT MUTAGEN 52 52
FT MUTAGEN 54 54
FT MUTAGEN 54 54
FT MUTAGEN 55 55
FT MUTAGEN 56 56
FT MUTAGEN 57 57
FT MUTAGEN 58 58
FT MUTAGEN 59 59
FT MUTAGEN 62 62
FT MUTAGEN 63 63
FT MUTAGEN 64 64
FT MUTAGEN 67 67
FT MUTAGEN 68 68
FT MUTAGEN 69 69
FT MUTAGEN 70 70
FT STRAND 47 47
FT TURN 49 50
FT TURN 52 52
FT HELIX 55 57
FT STRAND 60 60
FT STRAND 65 65
FT TURN 67 68
FT STRAND 70 72
SQ SEQUENCE 72 AA; 8317 MW; 53BFAF79BE751C16 CRC64;

Query Match 100.0%; Score 161; DB 1; Length 72;
Best Local Similarity 96.3%; Pred. No. 1.5e-12;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 27
Db 46 CRIPNKKCFQHLDDCCSRKCNRFNKC 72
|||||
|||||

RESULT 3
Q6XE29 PRELIMINARY; PRT; 67 AA.
AC Q6XE29;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus emineus (Atlantic fish-hunting cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=55423;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY236862; AAQ75888.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
FT CHAIN 1
SQ SEQUENCE 67 AA; 7575 MW; EBD557FB2EE9134 CRC64;

Query Match 48.8%; Score 78.5; DB 2; Length 67;
Best Local Similarity 46.2%; Pred. No. 0.019;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

FT PEPTIDE 46 72 Kappa-conotoxin PVIIA.
FT DISULFID 46 61
FT DISULFID 53 65
FT DISULFID 60 71
FT MOD_RES 49 49
FT MUTAGEN 47 47
FT MUTAGEN 48 48
FT MUTAGEN 49 49
FT MUTAGEN 50 50
FT MUTAGEN 51 51
FT MUTAGEN 52 52
FT MUTAGEN 54 54
FT MUTAGEN 54 54
FT MUTAGEN 55 55
FT MUTAGEN 56 56
FT MUTAGEN 57 57
FT MUTAGEN 58 58
FT MUTAGEN 59 59
FT MUTAGEN 62 62
FT MUTAGEN 63 63
FT MUTAGEN 64 64
FT MUTAGEN 67 67
FT MUTAGEN 68 68
FT MUTAGEN 69 69
FT MUTAGEN 70 70
FT STRAND 47 47
FT TURN 49 50
FT TURN 52 52
FT HELIX 55 57
FT STRAND 60 60
FT STRAND 65 65
FT TURN 67 68
FT STRAND 70 72
SQ SEQUENCE 72 AA; 8317 MW; 53BFAF79BE751C16 CRC64;

4-hydroxyproline.
R->A, K, Q: 100% reduction of toxicity.
I->A: 3-fold decrease of toxicity.
P->A: 100% reduction of toxicity.
N->A: 100% reduction of toxicity.
Q->A: 13-fold decrease of toxicity.
K->A, R: 100% reduction of toxicity.
F->A, M: 100% reduction of toxicity.
F->Y: 11-fold decrease of toxicity.
Q->A: 3-fold decrease of toxicity.
H->A: 3-fold decrease of toxicity.
L->A: 100% reduction of toxicity.
D->A: 1.5-fold decrease of toxicity.
S->A: 100% reduction of toxicity.
R->A: 3.5-fold decrease of toxicity.
K->A: 1.2-fold decrease of toxicity.
F->A: 5-fold decrease of toxicity.
N->A: 17-fold decrease of toxicity.
K->A: 19-fold decrease of toxicity.
K->A: 117-fold decrease of toxicity.
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QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
Db 42 CKPKGRKCFPHQKCCNKCTCR-SKC 66
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|||||

RESULT 4
Q71KTL PRELIMINARY; PRT; 67 AA.
AC Q71KTL;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480313; AAQ05865.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
FT CHAIN 41
FT CHAIN 67
SQ SEQUENCE 67 AA; 7358 MW; E311E06BB6AF702E CRC64;

Query Match 45.3%; Score 73; DB 2; Length 67;
Best Local Similarity 50.0%; Pred. No. 0.088;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKC 20
Db 42 CKTPGRKCFPHQKCCGRAC 61
|||||
|||||

RESULT 5
Q71KS9 PRELIMINARY; PRT; 67 AA.
AC Q71KS9;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480315; AAQ05867.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
FT CHAIN 41
FT CHAIN 67
SQ SEQUENCE 67 AA; 7488 MW; 1B483B1BB6AF7755 CRC64;

Query Match 44.1%; Score 71; DB 2; Length 67;
Best Local Similarity 50.0%; Pred. No. 0.15;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
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OY 1 CRXNQKCFQHLDDCCSRKC 20
Db 42 CKTKGKCFPHQKDCGGRAC 61

RESULT 6
Q71KTO PRELIMINARY; PRT; 67 AA.
AC Q71KTO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF480314; AAQ05866.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
FT CHAIN 41 67 four-loop conotoxin.
SQ SEQUENCE 67 AA; 7529 MW; 33E83B1EB6AF7435 CRC64;

Query Match 44.1%; Score 71; DB 2; Length 67;
Best Local Similarity 50.0%; Pred. No. 0.15;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRXNQKCFQHLDDCCSRKC 20
Db 42 CKTKGKCFPHQKDCGGRAC 61

RESULT 7
CXOB CONST STANDARD; PRT; 72 AA.
AC P28881; Q9UB25;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Omega-conotoxin SVIB precursor (SNX-183).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE FROM N.A.
RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
RL "Conopeptides from Conus striatus and Conus textile by cDNA cloning.";
RN Peptides 20:1139-1144 (1999).
[2]
RP SEQUENCE OF 46-71, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=93003172; PubMed=1390774;
RA Ramilo C., Zafaralla G.C., Nadaesi L., Hammerland L.G., Yoshikami D.,
RA Gray W.R., Kristipati R., Ramachandran J., Miljanich G., Olivera B.M.,
RA Cruz L.J.;
RT "Novel alpha" and omega-conotoxins from Conus striatus venom.";
RL Biochemistry 31:9919-9926 (1992).
[3]
RP STRUCTURE BY NMR.
RX MEDLINE=97070382; PubMed=8913308; DOI=10.1006/jmbi.1996.0576;

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RA Nielsen K.J., Thomas L., Lewis R.J., Alewood P.F., Craik D.J.;
RT "A consensus structure for omega-conotoxins with different
RT selectivities for voltage-sensitive calcium channel subtypes:
RT comparison of WVIIA, SVIB and SNX-202.";
RL J. Mol. Biol. 263:297-310 (1996).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
CC and block voltage-sensitive calcium channels (VSCC). This toxin
CC blocks N-, P-, and Q-type calcium channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF146346; AAD31906.1; -
CC FIR; C44379; C44379.
CC PDB; 1MWJ; NMR; @=46-72.
CC InterPro; IPR004214; Conotoxin.
CC Pfam; PF02950; Conotoxin; 1.
CC 3D-structure; Amidation; Calcium channel inhibitor;
CC Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
CC Presynaptic neurotoxin; Signal; Toxin.
CC FT SIGNAL 1 22 Potential.
CC FT PROPEP 23 45
CC FT PEPTIDE 46 71 Omega-conotoxin SVIB.
CC FT DISULFID 46 61
CC FT DISULFID 53 65
CC FT DISULFID 60 71
CC FT MOD_RES 71 71
CC FT SEQUENCE 72 AA; 7741 MW; 1F753546AAD39908 CRC64;
CC
CC Query Match 44.1%; Score 71; DB 1; Length 72;
CC Best Local Similarity 42.3%; Pred. No. 0.16;
CC Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

OY 1 CRXNQKCFQHLDDCCSRKCNFNKC 26
Db 46 CKTKGQSCRKTSYDCCSGSGRSGKC 71

RESULT 8
POI_MUSDO STANDARD; PRT; 38 AA.
AC P81765;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tyrosinase inhibitor (Phenol oxidase inhibitor) (Phenoloxidase
DE inhibitor) (POI).
OS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
OC Muscidae; Musca.
OX NCBI_TaxID=7370;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC TISSUE=Hemolymph; PubMed=7708756;
RX MEDLINE=9524060;
RA Daquing A.C., Nakamura S., Takao T., Shimonishi Y., Tsukamoto T.;
RT "Primary structure of a potent endogenous dopa-containing inhibitor of
RT phenol oxidase from Musca domestica.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:2964-2968 (1995).
[2]
RP SEQUENCE OF 6-9, CHARACTERIZATION, AND DEVELOPMENTAL STAGE.
RC TISSUE=Hemolymph;

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RX MEDLINE=92231987; PubMed=1567460;
RA Tsukamoto T., Ichimaru Y., Kanegae N., Watanabe K., Yamaura I.,
RA Katsura Y., Funatsu M.,
RT "Identification and isolation of endogenous insect phenoloxidase
inhibitors."
RL Biochem. Biophys. Res. Commun. 184:86-92(1992).
[3]
RP SYNTHESIS, AND DISULFIDE BONDS.
RX MEDLINE=99152007; PubMed=10026302; DOI=10.1021/bi9819834;
RA Daquinag A.C., Sato T., Koda H., Takao T., Fukuda M., Shimomishi Y.,
RA Tsukamoto T.,
RT "A novel endogenous inhibitor of phenoloxidase from Musca domestica
has a cysteine motif commonly found in snail and spider toxins."
RL Biochemistry 38:2179-2188(1999).
CC -I- FUNCTION: Potent reversible, competitive inhibitor of tyrosinase
(phenol oxidase) in the nanomolar range.
CC -I- SUBUNIT: Monomer.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- DEVELOPMENTAL STAGE: POI activity increases throughout
pupariation, and is highest in final instar pupae. No activity in
newly emerged adults.
CC -I- MASS SPECTROMETRY: MW=4213.1; MW_ERR=0.2; METHOD=Electrospray;
RANGE=1-38; NOTE=Ref.1.
KW Direct protein sequencing; Hydroxylation.
FT DISULFID 11 25
FT DISULFID 18 29
FT DISULFID 24 36
FT MOD RES 32 32 3',4'-dihydroxyphenylalanine.
SQ SEQUENCE 38 AA; 4204 MW; E597BE0BF286792 CRC64;

Query Match 42.2%; Score 68; DB 1; Length 38;
Best Local Similarity 39.3%; Pred. No. 0.22;
Matches 11; Conservative 7; Mismatches 8; Indels 2; Gaps 2;

QY 1 CRUXNOKCFQHLDDCCSRKCNRF-NKCV 27
DB 11 CLANGSKCYSH-DVCCTRCHNYAKCV 37

RESULT 9
P92135 PRELIMINARY; PRT; 1125 AA.
ID P92135
AC P92135;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gal/GalNAc lectin heavy subunit (Fragment).
GN Name=hg12;
OS Entamoeba dispar.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=46681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAW 760;
RA Dodson J.M., Clark C.G., Lockhart L.A., Leo B.M., Schroeder J.W.,
RA Mann B.J.,
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U95822; AAB50229.1; -
DR HSSP; P60045; IMF4.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF_like.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
KW Lectin.
FT NON_TER 1 1
FT NON_TER 1125 1125
SQ SEQUENCE 1125 AA; 126050 MW; 8DA832DE48A717C4 CRC64;

Query Match 41.3%; Score 66.5; DB 2; Length 1125;
Best Local Similarity 44.8%; Pred. No. 6.7;
Matches 13; Conservative 4; Mismatches 9; Indels 3; Gaps 2;

QY 1 CRUXNOKCFQHLDDCCSRK--CNRFN-KC 26
| : : : ||||| | |||

Db 688 CSMTDNVIRYHDDCCSRKSCQGNFNGKC 716
RESULT 10
CXOC_CONCT STANDARD; PRT; 26 AA.
AC P58919;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Omega-conotoxin CVIC.
OS Conus catus (Cat cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002252200;
RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.,
RT "Novel omega-conotoxins from Conus catus discriminate among neuronal
calcium channel subtypes."
RL J. Biol. Chem. 275:35335-35344(2000).
CC -I- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
and block voltage-sensitive calcium channels (VSCC) (By
similarity). This toxin blocks N-, P-, and Q-type calcium
channels.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -I- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
family.
DR HSSP; P05484; LDW4.
KW Amidation; Calcium channel inhibitor; Direct protein sequencing;
KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
FT DISULFID 1 16 By similarity.
FT DISULFID 8 20 By similarity.
FT DISULFID 15 26 By similarity.
FT MOD RES 26 26 Cysteine amide.
SQ SEQUENCE 26 AA; 2790 MW; 56EFC382335C4A8B CRC64;

Query Match 41.0%; Score 66; DB 1; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.28;
Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRUXNOKCFQHLDDCCSRKCNRFNKC 26
| : : : ||||| | |||
DB 1 CRGQSCSKLMYDCCCTGSCSRGKC 26

RESULT 11
Q81K03 PRELIMINARY; PRT; 2050 AA.
ID Q81K03
AC Q81K03;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF10_0037;
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.,
 RT "Genome sequence of the human malaria parasite Plasmodium
 RT falciparum.",
 RL Nature 419:498-511(2002).
 DR EMBL; AE014829; AAN35235.1; -.
 DR HSSP; Q93IC2; 1MWX.
 SQ Hypothetical protein.
 SQ SEQUENCE 2050 AA; 241382 MW; 0A0586A5B42A3B8C CRC64;
 Query Match 39.1%; Score 63; DB 2; Length 2050;
 Best Local Similarity 40.0%; Pred. No. 30;
 Matches 12; Conservative 8; Mismatches 6; Indels 4; Gaps 2;

QY 1 CRXNKQCFQH--LDDCCSRKCNFN-KC 26
 DB 574 CNKLNKCTQECNKLNKCTQECNKLNK 603

RESULT 12
 HSP1 MYODA
 ID HSP1 MYODA STANDARD; PRT; 46 AA.
 AC Q8WNY8;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Sperm protamine P1.
 GN Name=PRM1;
 OS Myotis daubentonii (Daubenton's bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Vespertilionidae;
 OC Myotis.
 OX NCBI_TaxID=98922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21881971; PubMed=11884159; DOI=10.1006/jmbi.1999.2817;
 RA Van Den Bussche R.A., Hofer S.R., Hansen E.W.;
 RT "Characterization and phylogenetic utility of the mammalian protamine
 RT P1 gene.",
 RL Mol. Phylogenet. Evol. 22:333-341(2002).
 CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
 CC sperm during the haploid phase of spermatogenesis. They compact
 CC sperm DNA into a highly condensed, stable and inactive complex (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: Testis.
 CC -1- SIMILARITY: Belongs to the protamine P1 family.

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 or send an email to license@isb-sib.ch).

 DR EMBL; AF435946; AAL3580.1; -.
 DR InterPro; IPR000221; Protamine_P1.
 DR Pfam; PF00260; Protamine_P1; 1.
 DR PROSITE; PS00048; PROTAMINE_P1; FALSE_NEG.
 KW Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
 KW Nucleosome core; Spermatogenesis; Testis.
 FT INIT MET 0 0 By similarity.
 SQ SEQUENCE 46 AA; 6397 MW; CDBDD686E6A7BED CRC64;

Query Match 38.5%; Score 62; DB 1; Length 46;
 Best Local Similarity 28.1%; Pred. No. 1.4;
 Matches 9; Conservative 9; Mismatches 8; Indels 6; Gaps 1;

QY 1 CRXNKQCFQHLDDCCSRK-----CNRFNK 26
 DB 12 CRRRRRCVRRRRRCRRRRRCRRRRRCRR 43

RESULT 13
 CXOC CONMA STANDARD; PRT; 29 AA.
 ID CXOC CONMA
 AC P37300;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Omega-conotoxin MVIIc precursor (SNX-230) (Fragment).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6492;
 RN [1]
 RP SEQUENCE FROM N.A., AND SYNTHESIS.
 RX MEDLINE=92337922; PubMed=1352986; DOI=10.1016/0896-6273(92)90221-X;
 RA Hillyard D.R., Monje V.D., Mintz I.M., Bean B.P., Nadasdi L.,
 RA Ramachandran J., Miljanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
 RA Cruz L.J., Imperial J.S., Olivera B.M.;
 RT "A new Conus peptide ligand for mammalian presynaptic Ca2+ channels.",
 RL Neuron 9:69-77(1992).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95248539; PubMed=7731037;
 RA Farr-Jones S., Miljanich G.P., Nadasdi L., Ramachandran J.,
 RA Basus V.J.;
 RT "Solution structure of omega-conotoxin MVIIc, a high affinity ligand
 RT of P-type calcium channels, using 1H NMR spectroscopy and complete
 RT relaxation matrix analysis.",
 RL J. Mol. Biol. 248:106-124(1995).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99303703; PubMed=10373375; DOI=10.1006/jmbi.1999.2817;
 RA Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
 RA Lewis R.J.;
 RT "Structure-activity relationships of omega-conotoxins MVIIA, MVIIc and
 RT 14 loop splice hybrids at N and P/Q-type calcium channels.",
 RL J. Mol. Biol. 289:1405-1421(1999).
 RN [4]
 RP MUTAGENESIS OF TYR-15.
 RX MEDLINE=95408251; PubMed=7677735;
 RA Kim J.I., Takahashi M., Martin-Moutot N., Seagar M.J., Ohtake A.,
 RA Sato K.;
 RT "Tyrl3 is essential for the binding of omega-conotoxin MVIIc to the
 RT P/Q-type calcium channel.",
 RL Biochem. Biophys. Res. Commun. 214:305-309(1995).
 CC -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC). This toxin
 CC blocks N-type calcium channels as well as types of high-threshold
 CC voltage-gated calcium channels resistant to both dihydropyridines
 CC and omega-conotoxin GVIA.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
 CC family.

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 or send an email to license@isb-sib.ch).

 DR EMBL; S40826; AAB22674.1; -.
 DR PIR; JH0699; JH0699.
 DR PDB; 1CNN; NMR; A=3-29.
 DR PDB; 1OMN; NMR; @=3-29.
 KW 3D-structure; Amidation; Calcium channel inhibitor; Hydroxylation;
 KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
 FT NON_TER 1


```
FT PROPEP      <1      2      Omega-conotoxin MVIIc.
FT PEPTIDE     3      28      Essential for calcium channel binding.
FT BINDING     15      15
FT DISULFID    3      18
FT DISULFID    10     22
FT DISULFID    17     28
FT MOD_RES     9      9      Hydroxyproline (Probable).
FT MOD_RES     28     28      Cysteine amide (G-29 provides amide
FT MUTAGEN     15     15      group).
FT TURN        6      7      Y->A: High decrease in binding.
FT STRAND      12     14
FT HELIX       24     25
FT STRAND      27     27
SQ SEQUENCE    29 AA; 3071 MW; AC7A68948474728A CRC64;

Query Match      37.9%; Score 61; DB 1; Length 29;
Best Local Similarity 38.5%; Pred. No. 1.2;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKCNRFNK 26
   | : : : : | | | | |
Db 3 CRKGAPCRKTYDCCSGSGRGKC 28

RESULT 14
ID Q7PD5 PRELIMINARY; PRT; 207 AA.
AC Q7PD5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000015215 (Fragment).
GN Name=ENSANGG0000012726;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAB0100897; EAA08999.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; P:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 2.
FT NON_TER 207 207
SQ SEQUENCE 207 AA; 22432 MW; 2F4552091F91FBE8 CRC64;

Query Match      37.9%; Score 61; DB 2; Length 207;
Best Local Similarity 46.4%; Pred. No. 7.1;
Matches 13; Conservative 3; Mismatches 10; Indels 2; Gaps 2;

QY 1 CRXNOKCFQHLDDCCSRKCNRFN-KCV 27
   | : : : : | | | | |
Db 28 CARNNEYCLTH-RDCCSGSCLSPSKCV 54

RESULT 15
Q9U4A2 PRELIMINARY; PRT; 1685 AA.
AC Q9U4A2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Variant surface protein PfEMP1 (Fragment).
```

```
GN Name=var;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20144115; PubMed=10677532; DOI=10.1073/pnas.040545897;
RA Smith J.D., Graig A.G., Kriek N., Hudson-Taylor D., Kyes S., Fagen T.,
RA Pinches R., Baruch D.I., Newbold C.I., Miller L.H.;
RT Identification of a Plasmodium falciparum intercellular adhesion
RT molecule-1 binding domain: a parasite adhesion trait implicated in
RT cerebral malaria.
RL Proc. Natl. Acad. Sci. U.S.A. 97:1766-1771 (2000).
DR EMBL; AF193424; AAF18980.1; -.
DR GO; GO:0005539; F:glycosaminoglycan binding; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR000454; Eub ATPase_Caub.
DR InterPro; IPR004258; PFEMP.
DR Pfam; PF03011; PFEMP; 1.
DR PROSITE; PS00605; ATPASE_C; UNKNOWN_1.
FT NON_TER 1685 1685
SQ SEQUENCE 1685 AA; 193671 MW; D1FD426666B0551E CRC64;

Query Match      37.3%; Score 60; DB 2; Length 1685;
Best Local Similarity 33.3%; Pred. No. 60;
Matches 9; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 1 CRXNOKCFQHLDDC--CSRKCNRFNK 25
   | : : : : | | | | |
Db 1048 CKTKKKCTNKSDDCNTCTEACTAYNR 1074

RESULT 16
Q7PM27 PRELIMINARY; PRT; 638 AA.
AC Q7PM27;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000014402 (Fragment).
GN Name=ENSANGG0000011913;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008980; EAA14483.2; -.
DR HSSP; PI9438; IEXT.
DR InterPro; IPR003341; DUF139.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF02363; C triplex; 15.
DR Pfam; PF00008; EGF; 1.
DR PROSITE; PS01186; EGF_2; 4.
FT NON_TER 638 638
SQ SEQUENCE 638 AA; 69390 MW; 026DB44846AB483F CRC64;

Query Match      36.6%; Score 59; DB 2; Length 638;
Best Local Similarity 36.0%; Pred. No. 34;
Matches 9; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 RIXNOKCFQHLDDCCSRKCNRFNK 26
   | : : : : | | | | |
Db 30 RLSNRHCIPHCDDCDGNGICTKPGYC 54
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DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00008; EGF; 5.
DR PRINTS: PR00010; EGFBL00D.
DR SMART: SM00181; EGF; 6.
DR SMART: SM00179; EGF_CA; 4.
DR PROSITE: PS00010; ASX HYDROXYL; 2.
DR PROSITE: PS00022; EGF_1; 6.
DR PROSITE: PS01186; EGF_2; 6.
DR PROSITE: PS00026; EGF_3; 6.
DR PROSITE: PS01187; EGF_CA; 2.
KW Alternative splicing; Calcium; Calcium-binding; EGF-like domain;
Repeat; Signal; Transmembrane.
FT SIGNAL 1 26
FT CHAIN 27 383
FT DOMAIN 27 306
FT TRANSMEM 307 327
FT DOMAIN 328 383
FT DOMAIN 27 58
FT DOMAIN 62 89
FT DOMAIN 91 129
FT DOMAIN 131 172
FT DOMAIN 174 210
FT DOMAIN 212 248
FT DISULFID 29 40
FT DISULFID 33 46
FT DISULFID 48 57
FT DISULFID 66 71
FT DISULFID 79 88
FT DISULFID 95 107
FT DISULFID 101 117
FT DISULFID 119 128
FT DISULFID 135 148
FT DISULFID 142 160
FT DISULFID 162 171
FT DISULFID 178 189
FT DISULFID 183 198
FT DISULFID 200 209
FT DISULFID 216 227
FT DISULFID 221 236
FT DISULFID 238 247
FT CARBOHYD 157 157
FT VARSPIC 1 179
SQ SEQUENCE 383 AA; 40547 MW; 701AC68043863EA7 CRC64;

Query Match 36.0%; Score 58; DB 1; Length 383;
Best Local Similarity 52.6%; Pred. No. 28;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFOHLDCCSRKCNRFNC 26
DB 209 CTINLDDCASRPCORGAR 227

RESULT 20
SCX1 OPICA
ID SCX1 OPICA STANDARD; PRT; 66 AA.
AC P60252;
DT 29-MAR-2004 (Rel. 43, Created)
DT 25-OCT-2004 (Rel. 43, Last sequence update)
DE Opicalcine 1 precursor.
OS Opisthophthalmus carinatus (African yellow leg scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Tardigrada; Scorpioneoidea; Scorpionidae; Scorpioninae; Opisthophthalmus.
OX NCBI_TaxID=190115;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22838230; PubMed=12958203; DOI=10.1096/fj.02-1044fje;
RA Zhu S.-Y., Darbon H., Dyason K., Verdonck F., Tytgat J.;
RT "Evolutionary origin of inhibitor cysteine knot peptides.";

FASEB J. 17:1765-1767(2003).
-!- FUNCTION: Potently and reversibly modifies channel gating behavior
of the type 1 ryanodine receptor (RyR1) by inducing prominent
subconductance behavior. Binds a different site as ryanodine (By
similarity).
CC
CC -!- SUBCELLULAR LOCATION: Secreted.
CC
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC
CC -!- SIMILARITY: Belongs to the scorpion calcine family.
CC
-----
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-----
CC
CC EMBL: AY25784; AAP73822.1;
KW Calcium channel inhibitor; Cleavage on pair of basic residues;
KW Ionic channel inhibitor; Neurotoxin; Signal; Toxin.
FT SIGNAL 1 22
FT PROPEP 23 33
FT CHAIN 34 66
FT DISULFID 36 50
FT DISULFID 43 54
FT DISULFID 49 65
FT SEQUENCE 66 AA; 7644 MW; 2CC7799E9F3AEF41 CRC64;

Query Match 35.4%; Score 57; DB 1; Length 66;
Best Local Similarity 47.6%; Pred. No. 8;
Matches 10; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 8 CFOHLDCCSRKCNRFNC 22
DB 36 CLPHLRCKENNDCCSKCKR 56

RESULT 21
SCX2 OPICA
ID SCX2 OPICA STANDARD; PRT; 66 AA.
AC P60253;
DT 29-MAR-2004 (Rel. 43, Created)
DT 25-OCT-2004 (Rel. 43, Last sequence update)
DE Opicalcine 2 precursor.
OS Opisthophthalmus carinatus (African yellow leg scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Tardigrada; Scorpioneoidea; Scorpionidae; Scorpioninae; Opisthophthalmus.
OX NCBI_TaxID=190115;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22838230; PubMed=12958203; DOI=10.1096/fj.02-1044fje;
RA Zhu S.-Y., Darbon H., Dyason K., Verdonck F., Tytgat J.;
RT "Evolutionary origin of inhibitor cysteine knot peptides.";

FASEB J. 17:1765-1767(2003).
-!- FUNCTION: Potently and reversibly modifies channel gating behavior
of the type 1 ryanodine receptor (RyR1) by inducing prominent
subconductance behavior. Binds a different site as ryanodine (By
similarity).
CC
CC -!- SUBCELLULAR LOCATION: Secreted.
CC
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC
CC -!- SIMILARITY: Belongs to the scorpion calcine family.
CC
KW Calcium channel inhibitor; Cleavage on pair of basic residues;
KW Ionic channel inhibitor; Neurotoxin; Signal; Toxin.
FT SIGNAL 1 22
FT PROPEP 23 33
FT CHAIN 34 66
FT DISULFID 36 50
FT DISULFID 43 54
FT DISULFID 49 65
FT SEQUENCE 66 AA; 7644 MW; 6DC7632E9F205F5D CRC64;

```



```
Query Match " 35.4%; Score 57; DB 1; Length 66;
Best Local Similarity 47.6%; Pred. No. 8;
Matches 10; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 8 CQOHL-----DCCSRKNCV 22
DB 36 CLPHLAKRCENNDCCSKKCR 56

RESULT 22
Q7Q0M5 PRELIMINARY; PRT; 650 AA.
AC Q7Q0M5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE BbIP2886 (Fragment)
GN Name=ebIG2886; ORFNames=ENSANGG00000002379;
OS Anopheles gambiae str. PBST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008980; EAA14361.1; -.
DR HSSP; P00740; IEDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; ASX_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 7.
DR Pfam; PF07645; EGF_Ca; 1.
DR PRINTS; PR00010; EGFBLD.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
FT NON_TER 1
FT NON_TER 650
SQ SEQUENCE 650 AA; 71172 MW; 19C43512C5B5FCC8 CRC64;

Query Match 35.4%; Score 57; DB 2; Length 650;
Best Local Similarity 33.3%; Pred. No. 60;
Matches 8; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 4 XNQCFOHLDDCCSRKNCV 27
DB 15 QNEKSIDHNEKCCSEKADAGRCI 38

RESULT 23
O42374 PRELIMINARY; PRT; 752 AA.
AC O42374;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Notch receptor protein (fragment).
GN Name=notch2; Synonyms=Notch6;
```

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OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Westin J., Lardelli M.;
RT "Three novel Notch genes in zebrafish: implications for vertebrate
RT Notch gene evolution and function.";
RL Dev. Genes Evol. 207:51-63(1997).
DR EMBL; Y10354; CAA71380.1; -.
DR HSSP; P00740; IEDM.
DR ZFIN; ZDB-GENE-000329-4; notch2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR000152; ASX_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00008; EGF; 15.
DR Pfam; PF07645; EGF_Ca; 1.
DR Pfam; PF00066; Notch; 2.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00179; EGF_CA; 10.
DR SMART; SM00004; NL; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 9.
DR PROSITE; PS00022; EGF_1; 17.
DR PROSITE; PS01186; EGF_2; 15.
DR PROSITE; PS00026; EGF_3; 17.
DR PROSITE; PS01187; EGF_CA; 7.
KW EGF-like domain; Receptor.
FT NON_TER 1
FT NON_TER 752
SQ SEQUENCE 752 AA; 82103 MW; 30939E16E0327F8A CRC64;

Query Match 35.4%; Score 57; DB 2; Length 752;
Best Local Similarity 37.5%; Pred. No. 68;
Matches 9; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 4 XNQCFOHLDDCCSRKNCV 27
DB 132 SGDNQCQTHIDCCSNPCRNCGTCV 155

RESULT 24
Q802S2 PRELIMINARY; PRT; 1245 AA.
AC Q802S2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SMC1 beta protein.
GN Name=smc1b;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Cobbe N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ534332; CAD58847.2; -.
DR HSSP; Q9XOR4; 1E69.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
```


DR GO; GO:0005524; F-ATP binding; IEA.
 DR GO; GO:0042626; F-ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0007059; P:chromosome segregation; IEA.
 DR GO; GO:0008610; P:transport; IEA.
 DR InterPro; IPR003439; ABC transporter.
 DR InterPro; IPR003405; SMC C.
 DR InterPro; IPR010935; SMC hinge.
 DR InterPro; IPR003395; SMC N.
 DR Pfam; PF02483; SMC C; 1.
 DR Pfam; PF06470; SMC hinge; 1.
 DR Pfam; PF02463; SMC N; 1.
 SQ SEQUENCE 1245 AA; 142930 MW; C93C54289FEA2500 CRC64;
 Query Match 35.4%; Score 57; DB 2; Length 1245;
 Best Local Similarity 42.9%; Pred. No. 1.1e-02;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 6 KQCFQHLDDCCSKCNKFNKC 26
 DB 1056 KRCQEFQVKFQRCQFNKC 1076
 RESULT 25
 NCBI_XENLA STANDARD; PRT; 2524 AA.
 ID NOTC_XENLA
 AC P21783;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Neurogenic locus notch protein homolog precursor (NOTCH protein).
 GN Name=NOTCH;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90385285; PubMed=2402639;
 RA Coffman C., Harris W., Kintner C.;
 RT "Notch, the Xenopus homolog of Drosophila notch."; Science 249:1438-1441(1990).
 RL [2]
 RP REVISIONS TO 1759-1782.
 RA Kintner C.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DEVELOPMENTAL STAGE: Expressed almost uniformly in early embryos.
 CC -1- SIMILARITY: Belongs to the NOTCH family.
 CC -1- SIMILARITY: Contains 6 ANK repeats.
 CC -1- SIMILARITY: Contains 36 EGF-like domains.
 CC -1- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M33874; AAB02039.1; --
 DR HSSP; P46531; 1PB5
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx hydroxyl_s.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR001438; EGF II.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR010660; NOD.
 DR InterPro; IPR008297; Notch.
 DR InterPro; IPR000800; Notch_region.
 DR Pfam; PF00023; Ank; 6.

DR Pfam; PF00008; EGF; 36.
 DR Pfam; PF06816; NOD; 1.
 DR Pfam; PF00066; Notch; 3.
 DR PIRSF; PIRSF002279; Notch; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00010; EGF-BLOOD.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF CA; 24.
 DR SMART; SM00004; NL_3.
 DR PROSITE; PS02027; ANK_REPEAT; 1.
 DR PROSITE; PS00088; ANK_REPEAT; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 23.
 DR PROSITE; PS00022; EGF_1; 34.
 DR PROSITE; PS01186; EGF_2; 29.
 DR PROSITE; PS00026; EGF_3; 36.
 DR PROSITE; PS01187; EGF CA; 21.
 KW ANK repeat; Differentiation; EGF-like domain; Glycoprotein;
 KW Neurogenesis; Notch signaling; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 19
 FT CHAIN 20 2524
 FT DOMAIN 20 1728
 FT TRANSMEM 1729 1750
 FT DOMAIN 1751 2524
 FT DOMAIN 20 57
 FT DOMAIN 58 99
 FT DOMAIN 102 140
 FT DOMAIN 141 177
 FT DOMAIN 179 215
 FT DOMAIN 217 254
 FT DOMAIN 256 292
 FT DOMAIN 294 332
 FT DOMAIN 334 370
 FT DOMAIN 371 409
 FT DOMAIN 411 449
 FT DOMAIN 451 487
 FT DOMAIN 489 525
 FT DOMAIN 527 563
 FT DOMAIN 565 600
 FT DOMAIN 602 638
 FT DOMAIN 640 675
 FT DOMAIN 677 713
 FT DOMAIN 715 750
 FT DOMAIN 752 788
 FT DOMAIN 790 826
 FT DOMAIN 828 866
 FT DOMAIN 868 904
 FT DOMAIN 906 942
 FT DOMAIN 944 980
 FT DOMAIN 982 1018
 FT DOMAIN 1020 1056
 FT DOMAIN 1058 1094
 FT DOMAIN 1096 1142
 FT DOMAIN 1144 1180
 FT DOMAIN 1182 1218
 FT DOMAIN 1220 1264
 FT DOMAIN 1266 1304
 FT DOMAIN 1306 1346
 FT DOMAIN 1347 1383
 FT DOMAIN 1386 1424
 FT REPEAT 1441 1478
 FT REPEAT 1479 1520
 FT REPEAT 1521 1560
 FT REPEAT 1560 1599
 FT REPEAT 1599 1638
 FT REPEAT 1638 1677
 FT REPEAT 1677 1716
 FT REPEAT 1716 1755
 FT REPEAT 1755 1794
 FT REPEAT 1794 1833
 FT REPEAT 1833 1872
 FT REPEAT 1872 1911
 FT REPEAT 1911 1950
 FT REPEAT 1950 1989
 FT REPEAT 1989 2028
 FT REPEAT 2028 2067
 FT REPEAT 2067 2106
 FT DISULFID 22 35
 FT DISULFID 29 45
 FT DISULFID 47 56
 FT DISULFID 62 74

Potential.
 Neurogenic locus notch protein homolog.
 Extracellular (Potential).
 Potential.
 Cytoplasmic (Potential).
 EGF-like 1.
 EGF-like 2.
 EGF-like 3.
 EGF-like 4.
 EGF-like 5.
 EGF-like 6.
 EGF-like 7.
 EGF-like 8.
 EGF-like 9.
 EGF-like 10.
 EGF-like 11.
 EGF-like 12.
 EGF-like 13.
 EGF-like 14.
 EGF-like 15.
 EGF-like 16.
 EGF-like 17.
 EGF-like 18.
 EGF-like 19.
 EGF-like 20.
 EGF-like 21.
 EGF-like 22.
 EGF-like 23.
 EGF-like 24.
 EGF-like 25.
 EGF-like 26.
 EGF-like 27.
 EGF-like 28.
 EGF-like 29.
 EGF-like 30.
 EGF-like 31.
 EGF-like 32.
 EGF-like 33.
 EGF-like 34.
 EGF-like 35.
 EGF-like 36.
 Lin/Notch 1.
 Lin/Notch 2.
 Lin/Notch 3.
 ANK 1.
 ANK 2.
 ANK 3.
 ANK 4.
 ANK 5.
 ANK 6.
 By similarity.
 By similarity.
 By similarity.
 By similarity.


```
OS Plasmodium.falciparum (isolate 3D7).
OC Sukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255708; PubMedId=12368667; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F.J., Doggett J.,
RA Felwell T., Goble A., Goodhead I., Guillemin R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holtroyd S., Horrocks P.,
RA Humphray S., Jegels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Kontofortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitz E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA "Sequencing of Plasmodium falciparum chromosomes 1, 3-9 and 13."
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002)
DR EMBL: AL034557; CAD9096.1; -.
DR GO: GO:0005339; F-glycosaminoglycan binding; IEA.
DR GO: GO:0009405; Pathogenesis; IEA.
DR InterPro: IPRO00345; Cytochrome_B5.
DR Pfam: PF03011; PFEMP.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN 1.
SQ SEQUENCE 3467 AA; 398216 MW; 89FCBA37025989D2 CRC64;

Query Match          35.1%; Score 56.5; DB 2; Length 3467;
Best Local Similarity 13.9%; Pred. No. 3e+02;
Matches 15; Conservative

Oy   1 CRTXNOK-----CFQHLDDCCSR-----KCNRFNKC 26
      |||||              | : | | | | |
Db    318 CRIRNHKRKKDKACRNDKERLYCSQGYDYCTRIEKGSCSRKNKC 364
           |||||              | : | | | | |

RESULT 32
QIAT6 PRELIMINARY;             PRG;       664 AA.
AC QIAT6;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE DeltaC.
GN Names:dltc; Synonyms=deltC;
GC Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20054100; PubMed=10585570; DOI=10.1016/S0925-4773(99)00231-2;
RA Smithers L.E., Haddon C., Jiang Y.-J., Lewis J.;
RT "Sequence and embryonic expression of deltaC in the zebrafish.";
RL Mech. Dev. 90:119-123(2000).
DR EMBL: AF146429; AAF27299.1; -.
DR HSSP: P00740; 1EDM.
DR ZFIN: ZDB-GENE-000125-4; dlc.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007154; P:cell communication; IEA.
DR InterPro: IPRO00152; Asx hydroxyl_S.
DR InterPro: IPRO01774; DSL_
DR InterPro: IPRO00742; EGF_2.
DR InterPro: IPRO01981; EGF-Ca.
DR InterPro: IPRO01438; EGF II.
DR InterPro: IPRO06209; EGF like.
```


RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Warkulow G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X., Zhong F., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of *Drosophila melanogaster*,"
RL Science 287:2185-2195(2000).
RN [4]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bertencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RA "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review,"
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-Oregon-R;
RX MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell L.B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA Dreaño S., Gloux S., Lelaure V., Mottier S., Galibert F., Borokova D.,
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Fabios B.,
RA Modell J., Peter A., Schottelr P., Werner M., Mourikioti F.,
RA Beinert N., Dowe G., Schaefer U., Jacek H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McWilliam P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of *D.*
RT *melanogaster*,"
RL Science 287:2220-2222(2000).
RN [6]
RP SEQUENCE OF 2505-2611 FROM N.A.
RX MEDLINE=85099329; PubMed=2981631; DOI=10.1016/0092-8674(85)90308-3;
RA Wharton K.A., Vedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;
RT "opa: a novel family of transcribed repeats shared by the Notch locus
RN and other developmentally regulated loci in *D. melanogaster*,"
RL Cell 40:55-62(1985).
RN [7]
RP SEQUENCE OF 1-8 FROM N.A.
RX MEDLINE=87257846; PubMed=3037327;
RA Kelley M.R., Kidd S., Berg R.L., Young M.W.;
RT "Restriction of P-element insertions at the Notch locus of *Drosophila*
RN *melanogaster*,"
RL Mol. Cell. Biol. 7:1545-1548(1987).
RN [8]
RP INTERACTION WITH DX, AND MUTANT SU42C.
RX MEDLINE=94215489; PubMed=8162848;
RA Diederich R.J., Matsuno K., Hing H., Artavanis-Tsakonas S.;
RT "Cytosolic interaction between *delta*tex and Notch ankyrin repeats
RN implicates *delta*tex in the Notch signaling pathway,"
RL Development 120:473-481(1994).
RN [9]
RP INTERACTION WITH DX
RX MEDLINE=95401878; PubMed=7671825;
RA Matsuno K., Diederich R.J., Go M.J., Blaumueller C.M.,
RA Artavanis-Tsakonas S.;
RT "Delta ϵ acts as a positive regulator of Notch signaling through

interactions' with the Notch ankyrin repeats."; [10]
S3 CLEAVAGE BY PSN.
Struhl G., Greenwald I.,
"Presenilin is required for activity and nuclear access of Notch in Drosophila."; [11]
Nature 398:522-525 (1999).
S3 CLEAVAGE BY PSN.
MEDLINE=9221488; PubMed=10206647; DOI=10.1038/19096;
Ye Y., Lukinova N., Fortini M.E.;
"Neurogenic phenotypes and altered Notch processing in Drosophila Presenilin mutants."; [12]
Nature 398:525-529 (1999).
S2 CLEAVAGE BY KUZ.
MEDLINE=21657146; PubMed=11799064; DOI=10.1101/gad.942302;
Lieber T., Kidd S., Young M.W.;
"kuzbanian-mediated cleavage of Drosophila Notch."; [13]
Genes Dev. 16:209-221 (2002).
MUTANT MCD5.
MEDLINE=21575956; PubMed=11719214; DOI=10.1016/S0960-9822(01)00562-0;
Raman P., Khechumian K., Seugnet L., Arbogast N., Ackermann C., Heitzler P.;
"Novel Notch alleles reveal a Deltex-dependent pathway repressing neural fate."; [14]
Curr. Biol. 11:1729-1738 (2001).
MEDLINE=22256570; PubMed=12369105;
Portin P.;
"General outlines of the molecular genetics of the Notch signalling pathway in Drosophila melanogaster: a review."; [15]
Hereditas 136:89-96 (2002).
-!- FUNCTION: Signaling protein, which regulates, with both positive and negative signals, the differentiation of at least central and peripheral nervous system and eye, wing disk, oogenesis, segmental appendages such as antennae and legs, and muscles, through lateral inhibition or induction. Functions as a receptor for membrane-bound ligands Delta and Serrate to regulate cell-fate determination. Upon ligand activation, and releasing from the cell membrane, the Notch intracellular domain (NICD) forms a transcriptional activator complex with Su(H) (Suppressor of hairless) and activates genes of the E(spl) complex. Essential for proper differentiation of ectoderm.
-!- SUBUNIT: Interacts with Su(H) when activated. Interacts with Dx via its ANK repeats.
-!- SUBCELLULAR LOCATION: Type I membrane protein. Upon activation and S3 cleavage, it is released from the cell membrane and enters into the nucleus in conjunction with Su(H).
-!- PTM: Upon binding its ligands such as Delta or Serrate, it is cleaved (S2 cleavage) in its extracellular domain, close to the transmembrane domain. S2 cleavage is probably mediated by Kuz. It is then cleaved (S3 cleavage) downstream of its transmembrane domain, releasing it from the cell membrane. S3 cleavage requires Pen.
-!- SIMILARITY: Belongs to the NOTCH family.
-!- SIMILARITY: Contains 6 ANK repeats.
-!- SIMILARITY: Contains 36 EGF-like domains.
-!- SIMILARITY: Contains 13 Notch repeats.
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Query Match 34.8%; Score 56; DB 1; Length 2703;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 4 XNOKCFQHLDDCCSRKCNRFNKC 27
DB 822 TGQCTNIDDCVTNPGNGGTCT 845
RESULT 35
CXOB CONMA STANDARD; PRT; 25 AA.
AC P05485;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Omega-conotoxin MVIIB (SNX-159).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE.
RX MEDLINE=87299637; PubMed=2441741;
RA Olivera B.M., Cruz L.J., de Santos V., Lechmanant G.W., Griffin D., Zeikus R.D., McIntosh J.M., Galyean R., Varga J., Gray W.R., Rivier J.E.;
RT "Neuronal calcium channel antagonists. Discrimination between calcium channel subtypes using omega-conotoxin from Conus magus venom."; [1]
Biochemistry 26:2086-2090 (1987).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type family.
CC PIR; JH0701; JH0701.
DR HSSP; P05484; 1DM4.
KW Amidation; Calcium channel inhibitor; Direct protein sequencing; Tonic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
FT DISULFID 1 16
FT DISULFID 8 20
FT DISULFID 15 25
FT MOD RES 25 25 Cysteine amide.
SQ SEQUENCE 25 AA; 2626 MW; E4B9CE5EPAA3734D CRC64;
Query Match 34.5%; Score 55.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 5.2;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
QY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
DB 1 CKGKGASCHRTSYDCTGSCNR-GKC 25
RESULT 36
Q24822 PRELIMINARY; PRT; 194 AA.
AC Q24822;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE GalNAC lectin heavy subunit (Fragment).
GN Namehgl5;
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HM1:IMS;
RA Ramakrishnan G., Ragland B.D., Purdy J.E., Mann B.J.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.


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DR EMBL; U33444; AAA75552.1; --
DR PIR; S70664; S70664.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF-like.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
KW Lectin.
FT NON TER 1
FT NON TER 194 194
SQ SEQUENCE 194 AA; 21438 MW; 8A9DFEFC481C671D CRC64;

Query Match 34.5%; Score 55.5; DB 2; Length 194;
Best Local Similarity 40.0%; Pred. No. 32;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
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DB 119 CSMGTDNVTIYHDDCNRSKSCQGNFGKCI 148

RESULT 37
QBMZT1
ID QBMZT1 PRELIMINARY; PRT; 372 AA.
AC QBMZT1;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Gal/GalNAc lectin heavy subunit region D (Fragment).
GN Name=hgl;
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3;
RA Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Traipaidze N.,
RA Pearson W.R., Loftus B., Petri W.A. Jr.;
RT "Entamoeba histolytica; sequence conservation of the Gal/GalNAc lectin
RT from clinical isolates.";
RL Exp. Parasitol. 101:157-163(2002).
DR EMBL; AF501278; AAM22199.1; --
DR GO; GO:0005529; F:sugar binding; IEA.
KW Lectin.
FT NON TER 1
FT NON TER 372 372
SQ SEQUENCE 372 AA; 41994 MW; 49AA800C6ECE259F CRC64;

Query Match 34.5%; Score 55.5; DB 2; Length 372;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
   : : : : : : : : : : : : : : : :
DB 80 CSMGTDNVTIYHDDCNRSKSCQGNFGKCI 109

RESULT 38
QBMZT2
ID QBMZT2 PRELIMINARY; PRT; 372 AA.
AC QBMZT2;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Gal/GalNAc lectin heavy subunit region D (Fragment).
GN Name=hgl;
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3;
RA Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Traipaidze N.,
RA Pearson W.R., Loftus B., Petri W.A. Jr.;
RT "Entamoeba histolytica; sequence conservation of the Gal/GalNAc lectin
RT from clinical isolates.";
RL Exp. Parasitol. 101:157-163(2002).
DR EMBL; AF501278; AAM22199.1; --
DR GO; GO:0005529; F:sugar binding; IEA.
KW Lectin.
FT NON TER 1
FT NON TER 372 372
SQ SEQUENCE 372 AA; 41994 MW; 49AA800C6ECE259F CRC64;

Query Match 34.5%; Score 55.5; DB 2; Length 372;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
   : : : : : : : : : : : : : : : :
DB 80 CSMGTDNVTIYHDDCNRSKSCQGNFGKCI 109

from clinical isolates.";
RL Exp. Parasitol. 101:157-163(2002).
DR EMBL; AF501277; AAM22198.1; --
DR GO; GO:0005529; F:sugar binding; IEA.
KW Lectin.
FT NON TER 1
FT NON TER 372 372
SQ SEQUENCE 372 AA; 41961 MW; 1FF00CE22BFB5100 CRC64;

Query Match 34.5%; Score 55.5; DB 2; Length 372;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
   : : : : : : : : : : : : : : : :
DB 80 CSMGTDNVTIYHDDCNRSKSCQGNFGKCI 109

RESULT 39
GILI_ENTHI
ID GILI_ENTHI STANDARD; PRT; 1276 AA.
AC F32022;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Galactose-inhibitable lectin 170 kDa subunit.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=91195330; PubMed=2014248;
RA Mann B.J., Torian B.E., Vedvick T.S., Petri W.A. Jr.;
RT "Sequence of a cysteine-rich galactose-specific lectin of Entamoeba
RT histolytica.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3248-3251(1991).
CC -!- FUNCTION: Lectin that binds galactose.
CC -!- SURUNIT: Heterodimer of a heavy (170 kDa) and a light subunit (35
CC -!- PTM: N-glycosylated.
CC -!- PTM: N-glycosylated.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M59850; -; NOT ANNOTATED CDS.
KW Direct protein sequencing; Glycoprotein; Lectin; Transmembrane.
FT TRANSMEM 1210 1235 Potential.
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 321 321 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 361 361 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 452 452 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 471 471 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 627 627 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 643 643 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 874 874 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 976 976 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1122 1122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1187 1187 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1197 1197 N-linked (GlcNAc...) (Potential).
FT VARIANT 441 441 R -> K.
SQ SEQUENCE 1276 AA; 143239 MW; A6B903F11DC2D5B4 CRC64;

Query Match 34.5%; Score 55.5; DB 1; Length 1276;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
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DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR TIGRFS; TIGR01557; myb_SHAQYP; 1.
DR PROSITE; PS00110; RESPONSE_REGULATORY; 1.
DR Phosphorylation; Sensory transduction.
KW SEQUENCE 380 AA; 42765 MW; 69DBD43F0CD200E1 CRC64;
SQ

Query Match      34.2%; Score 55; DB 2; Length 380;
Best Local Similarity 44.0%; Pred. No. 65;
Matches 11; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

QY 3 IXNQKCFQHLDDCCSRKCNRFNKC 27
DB 17 IDEDKC--HADSTCSMICTQLNFCV 39

RESULT 43
LHX5_XENLA
ID LHX5_XENLA STANDARD; PRT; 402 AA.
AC P37137;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE LIM/homeobox protein Lhx5 (Homeobox protein LIM-5) (XLIM-5) (XLIM-2A).
GN Name=LHX5; Synonyms=LIM-2A, LIM2A, LIM5;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95377545; PubMed=7649385; DOI=10.1006/dbio.1995.1238;
RA Toyama R., Curtiss P.E., Otani H., Kimura M., David I.B., Taira M.;
RT "The LIM class homeobox gene lim5: implied role in CNS patterning in
  xenopus and zebrafish.";
RL Dev. Biol. 170:583-593 (1995).
RN [2]
RP SEQUENCE OF 188-225 FROM N.A.
RX MEDLINE=92192449; PubMed=1347750;
RA Taira M., Janrich M., Good P.J., David I.B.;
RT "The LIM domain-containing homeo box gene Xlim-1 is expressed
  specifically in the organizer region of Xenopus gastrula embryos.";
RL Genes Dev. 6:356-366 (1992).
CC -1- FUNCTION: Probably involved in the patterning of the nervous
  system, in particular in the early specification of the
  diencephalon.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC -----
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CC -----
DR EMBL; L42546; AAA99464.1; -
DR EMBL; Z11587; CAA77672.1; -
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T04209; -
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeoboxdomain_like.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM homeo.
DR Pfam; PF00046; Homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.

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DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
DR PROSITE; PS00478; LIM_DOMAIN 1; 2.
DR PROSITE; PS00023; LIM_DOMAIN 2; 2.
KW Developmental protein; DNA-binding; Homeobox; LIM domain;
  Metal-binding; Nuclear protein; Repeat; Transcription regulation;
  Zinc.
FT DOMAIN 3 61 LIM 1.
FT DOMAIN 62 125 LIM 2.
FT DNA BIND 180 239 Homeobox.
SQ SEQUENCE 402 AA; 49959 MW; A5852B94747E09F9 CRC64;

Query Match      34.2%; Score 55; DB 1; Length 402;
Best Local Similarity 44.0%; Pred. No. 69;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
DB 23 RAHWKVCVQ----CCECKNLTEK 43

RESULT 44
Q63ZR3
ID Q63ZE3 .PRELIMINARY; PRT; 402 AA.
AC Q63ZR3;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
  Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
  Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
  PubMed=12477932; DOI=10.1073/pnas.242603899;
  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
  Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
  Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
  Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
  Jones S.J., Marra M.A.;
  "Generation and initial analysis of more than 15,000 full-length human
  and mouse cDNA sequences.";
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
  Klein S., Gerhard D.S.;
  Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC082847; AAH82847.1; -.
KW Hypothetical protein.
SQ SEQUENCE 402 AA; 44898 MW; 1928D588311BDASB CRC64;

Query Match      34.2%; Score 55; DB 2; Length 402;
Best Local Similarity 44.0%; Pred. No. 69;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
   |::|||  |||||
Db 23 RAWHVKCVQ-----CCECKCNLTCK 43

RESULT 45
LHX1_XENLA STANDARD; PRT; 403 AA.
ID LHX1_XENLA
AC P29674;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE LIM/homeobox protein Lhx1 (Homeobox protein LIM-1) (XLIM-1).
GN Names=LHX1; Synonyms=LIM-1, LIM1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92192449; PubMed=1347750;
RA Taira M., Jamrich M., Good P.J., David I.B.;
RT "The LIM domain-containing homeo box gene Xlim-1 is expressed
RL specifically in the organizer region of Xenopus gastrula embryos.";
RL Genes Dev. 6:356-366(1992).
CC -!- FUNCTION: Probably involved in the establishment of the body plan
CC during gastrulation in embryos.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: In the dorsal LIP and in the dorsal mesoderm
CC as it extend anteriorly (the Spemann's organizer).
CC -!- DEVELOPMENTAL STAGE: Major expression phase at the gastrula stage.
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC -----
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CC -----
DR EMBL; X63889; CAA45353.1; -.
DR PIR; S23802; S23802.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T01962; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM_homeo.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PD00024; HOMEBOX.
DR Pfam; PF00412; LIM; 2.
DR PRODOM; PD000010; Homeobox; 1.
DR PRODOM; PD000094; LIM; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS0023; LIM_DOMAIN_2; 2.
KW Developmental protein; DNA-binding; Homeobox; LIM domain;
KW Metal-binding; Nuclear protein; Repeat; Zinc.
FT DOMAIN 4 54 LIM 1.
FT DOMAIN 63 117 LIM 2.
FT DNA_BIND 179 238 Homeobox.
FT
```

```
SQ SEQUENCE 403 AA; 44934 MW; 4147EB3A2774C110 CRC64;

Query Match      34.2%; Score 55; DB 1; Length 403;
Best Local Similarity 44.0%; Pred. No. 69;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
   |::|||  |||||
Db 22 RAWHVKCVQ-----CCECKCNLTCK 42

RESULT 46
LHX1_HUMAN STANDARD; PRT; 404 AA.
ID LHX1_HUMAN
AC P48742;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE LIM/homeobox protein Lhx1 (Homeobox protein Lim-1).
GN Names=LHX1; Synonyms=LIM1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=97355680; PubMed=9212161;
RA Dong W.F., Heng H.H., Lowsky R., Xu Y., Decoteau J.F., Shi X.-M.,
RA Tsui L.-C., Minden M.D.;
RT "Cloning, expression, and chromosomal localization to 11p12-13 of a
RL human LIM/homeobox gene, hLim-1.";
RL DNA Cell Biol. 16:671-678(1997).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
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CC -----
DR EMBL; U14755; AAA21644.1; -.
DR PIR; G01507; G01507.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T01960; -.
DR Genew; HGNC:6593; LHX1.
DR MIM; 601999; -.
DR GO; GO:0003702; F:RNA polymerase II transcription factor acti. . .; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM_homeo.
DR Pfam; PF00046; Homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR PRINTS; PD00024; HOMEBOX.
DR PRODOM; PD000010; Homeobox; 1.
DR PRODOM; PD000094; LIM; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS0023; LIM_DOMAIN_2; 2.
KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
KW Repeat; Zinc.
FT DOMAIN 4 54 LIM 1.
FT DOMAIN 63 117 LIM 2.
FT DNA_BIND 180 239 Homeobox.
FT SEQUENCE 404 AA; 44482 MW; CAP2847A340B393F CRC64;
SQ
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Query Match 34.2%; Score 55; DB 1; Length 406;
Best Local Similarity 44.0%; Pred. No. 70;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps


```

KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
KW Repeat; Zinc. 4 54 LIM 1.
FT DOMAIN 63 117 LIM 2.
FT DOMAIN 180 239 Homeobox.
FT DNA BIND 180 239 Homeobox.
FT CONFLICT 12 12 L->LAROVRPVL (in Ref. 2).
FT CONFLICT 24 31 Missing (in Ref. 2).
FT CONFLICT 236 236 R -> A (in Ref. 2).
FT CONFLICT 335 335 H -> HH (in Ref. 2).
SQ SEQUENCE 406 AA; 44780 MW; CC8637984998ADAF CRC64;

Query Match 34.28; Score 55; DB 1; Length 406;
Best Local Similarity 44.08; Pred. No. 70;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNQKCFQHLDDCCSRKCNRFNKK 26
DQ 22 RAHWKVCVQ---CCECKCNLTEKC 42

RESULT 50
LHX1 RAT
ID LHX1 RAT STANDARD; PRT; 406 AA.
AC P63007; P36199;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE LIM/homeobox protein Lhx1 (Homeobox protein LIM-1) (Rlim).
GN Name:Lhx1; Synonyms=Lim-1, Lim1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94336075; PubMed=7914684; DOI=10.1016/0304-3940(94)90334-4;
RA Fuyuyama T., Inagaki S., Iwahashi Y., Takagi H.;
RL "Distribution of Rlim, an LIM homeodomain gene, in the rat brain.";
RT Neurosci. Lett. 170:266-268(1994).
CC CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC CC -1- SIMILARITY: Contains 1 homeobox domain.
CC CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
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CC -----
DR EMBL; S71523; AAC50696.1; --
DR HSPSP; P06601; 1FJL.
DR RGD; 71074; Lhx1.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM homeo.
DR Pfam; PF00046; Homeobox_1.
DR Pfam; PF00412; LIM; 2.
DR PRINTS; PR00024; HOMEBOX.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00478; LIM DOMAIN 1; 2.
DR PROSITE; PS00023; LIM DOMAIN 2; 2.
KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
KW Repeat; Zinc. 4 54 LIM 1.
FT DOMAIN 63 117 LIM 2.
FT DOMAIN 180 239 Homeobox.
SQ SEQUENCE 406 AA; 44780 MW; CC8637984998ADAF CRC64;

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Query Match 34.2%; Score 55; DB 1; Length 406;
Best Local Similarity 44.0%; Pred. No. 70;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNOKCFQHLDDCCSRKCNRF 26
DB 22 RAWHKVCQ-----CEECKNLTEKC 42

RESULT 51
Q26107 PRELIMINARY; PRT; 448 AA.
AC Q26107;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Surface antigen.
GN Name=Prs48/45;
OS Plasmodium reichenowi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5854;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97467681; PubMed=9326890; DOI=10.1006/expr.1997.4204;
RA Milek R.L., Kocken C.H., Kaan A.M., Jansen J., Meijers H.,
RA Konings R.N.;
RT "Plasmodium reichenowi: deduced amino acid sequence of sexual stage-specific surface antigen Prs48/45 and comparison with its homologue in Plasmodium falciparum";
RL Exp. Parasitol. 87:150-152(1997).
DR EMBL; L33882; AAA91881.1; -;
DR InterPro; IPR010884; S48.45.
DR Pfam; PF07422; S48.45; 1-;
SQ SEQUENCE 448 AA; 51563 MW; D2E630F439D3757 CRC64;

Query Match 34.2%; Score 55; DB 2; Length 448;
Best Local Similarity 40.9%; Pred. No. 76;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKCNRF 22
DB 227 CELINKKCFQFTNDKALYSNK 248

RESULT 52
Q8HAD6 PRELIMINARY; PRT; 577 AA.
AC Q8HAD6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sb2.
GN Names=sb2;
OS Salmonella typhimurium phage Sf64B.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=175950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2925870; PubMed=14563886;
RX DOI=10.1128/JB.185.21.6481-6485.2003;
RA Mnoilawa P.T., Schmeigler H., Heuzenroeder M.W.;
RT "Bacteriophage Sf64B, a genetic mosaic of genes from diverse sources isolated from Salmonella enterica serovar typhimurium DT 64.";
RL J. Bacteriol. 185:6481-6485(2003).
DR EMBL; AY055382; AAL25881.1; -;
DR InterPro; IPR005021; Phage_term.
DR Pfam; PF03354; Terminase_1; 1-;
SQ SEQUENCE 577 AA; 65361 MW; 808B047EC2D6F024 CRC64;

Query Match 34.2%; Score 55; DB 2; Length 577;
Best Local Similarity 39.1%; Pred. No. 95;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKCNRF 23
DB 27 CQVIQACQQRHDDMAAEKSKRF 49

RESULT 53
Q8W06 PRELIMINARY; PRT; 585 AA.
AC Q8W06;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-like 3, isoform 1.
GN Name=Dll3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 6 EGF-like domains.
DR EMBL; BC052002; AAHS2002.1; -;
DR HSP; P00740; 1EDM.
DR MGD; MGI:1096877; Dll3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0007386; P:compartment specification; IMP.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00008; EGF; 5.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00181; EGF; 6.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 5.
DR PROSITE; PS00334; MYB_2; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 585 AA; 61125 MW; EB276F608998D4E9 CRC64;

Query Match 34.2%; Score 55; DB 2; Length 585;
Best Local Similarity 37.9%; Pred. No. 97;
Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;


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Qy 1 CR--IXNQKCFQHLDDCCSKCNRFNKCVCV 27
  || : : ||| ||| ||| |||
Db 377 CRAGFAGPRCEHDLDDCAGACACAGGTCVCV 405

RESULT 54
Q8NBS4 Q8NBS4 PRELIMINARY; PRT; 587 AA.
AC Q8NBS4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ90821.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nimomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
DR EMBL; AK075302; BAC11535.1; -.
DR HSSP; P00740; LEDM.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006209; EGF_5.
DR PRINTS; PR00010; EGFBLD.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 5.
DR InterPro; IPR001005; MYB_DNA_binding.
DR Pfam; PF00008; EGF_5.
DR SMART; SM00181; EGF; 6.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS00334; MYB_2; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 587 AA; 61144 MW; 2FF5E3EA66789B1B CRC64;

Query Match 34.2%; Score 55; DB 2; Length 587;
Best Local Similarity 37.9%; Pred. No. 97;
Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

Qy 1 CR--IXNQKCFQHLDDCCSKCNRFNKCVCV 27
  || : : ||| ||| ||| |||
Db 379 CRAGFAGPRCEHDLDDCAGACACAGGTCVCV 407

RESULT 55
DL3_RAT DL3_RAT STANDARD; PRT; 589 AA.
AC O88671;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Delta-like protein 3 precursor (Drosophila Delta homolog 3).
GN Names=Dll3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RA Boulter J., Greenfield A., Weinmaster G.;
RT "Rattus norvegicus mRNA for Delta 3: a putative ligand for Notch.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Inhibits primary neurogenesis. May be required to divert
neurons along a specific differentiation pathway. Play a role in

```

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CC the formation of somite boundaries during segmentation of the
CC paraxial mesoderm. (By similarity).
CC -1- SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The DSL domain is required for binding to the Notch
CC receptor.
CC -1- SIMILARITY: Contains 1 DSL domain.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF084576; AAC33303.1; -.
DR HSSP; P00740; LEDM.
DR RGD; 70953; D113.
DR GO; GO:0005112; P:Notch binding; ISS.
DR GO; GO:0001709; P:cell fate determination; ISS.
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
DR GO; GO:0007399; P:neurogenesis; ISS.
DR GO; GO:0007219; P:Notch signaling pathway; ISS.
DR GO; GO:0001501; P:skeletal development; ISS.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 5.
DR PRINTS; PR00010; EGFBLD.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS50026; EGF_3; 6.
KW Developmental protein; Differentiation; EGF-like domain;
KW Notch signaling pathway; Repeat; Signal; Transmembrane.
FT SIGNAL 1 32 By similarity.
FT CHAIN 33 589 Delta-like protein 3.
FT DOMAIN 33 494 Extracellular (Potential).
FT TRANSMEM 495 515 Potential.
FT DOMAIN 516 589 Cytoplasmic (Potential).
FT DOMAIN 174 213 DSL.
FT DOMAIN 218 251 EGF-like 1.
FT DOMAIN 276 312 EGF-like 2.
FT DOMAIN 314 353 EGF-like 3.
FT DOMAIN 355 391 EGF-like 4.
FT DOMAIN 393 429 EGF-like 5.
FT DOMAIN 431 467 EGF-like 6.
FT DOMAIN 503 511 Poly-Ala.
FT DISULFID 222 233 By similarity.
FT DISULFID 226 239 By similarity.
FT DISULFID 241 250 By similarity.
FT DISULFID 280 291 By similarity.
FT DISULFID 285 300 By similarity.
FT DISULFID 302 311 By similarity.
FT DISULFID 318 329 By similarity.
FT DISULFID 323 341 By similarity.
FT DISULFID 343 352 By similarity.
FT DISULFID 359 370 By similarity.
FT DISULFID 364 379 By similarity.
FT DISULFID 381 390 By similarity.
FT DISULFID 397 408 By similarity.
FT DISULFID 402 417 By similarity.
FT DISULFID 419 428 By similarity.
FT DISULFID 435 446 By similarity.
FT DISULFID 440 455 By similarity.
FT DISULFID 457 466 By similarity.
SQ SEQUENCE 589 AA; 61424 MW; A17B3BF9B95EC17F CRC64;

Query Match 34.2%; Score 55; DB 1; Length 589;
Best Local Similarity 37.9%; Pred. No. 97;
Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

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QY 1 CR--IXNOKCFQHLDDCCSRKCNFNKCV 27
 DB 381 CRAGFAGPRCEHDLDDCAGACANGGTCV 409

RESULT 56
 DLL3 MOUSE
 ID DLL3 MOUSE STANDARD; PRT; 592 AA.
 AC O88516; O35675; O9QWL9; O9QWZ7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Delta-like protein 3 precursor (Drosophila Delta homolog 3) (M-Delta-3).
 DE Name=Dll3;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6 X DBA; TISSUE=Embryo;
 RX MEDLINE=97417575; PubMed=9272948;
 RA Dunwoodie S.L., Henrique D.M.P., Harrison S.M., Beddington R.S.P.;
 RT "Mouse Dll3: a novel divergent Delta gene which may complement the function of other Delta homologues during early pattern formation in the mouse embryo."
 RL Nat. Genet. 19:274-278(1998).
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=129/SVJ;
 RX MEDLINE=98324780; PubMed=9662403; DOI=10.1038/961;
 RA Kusumi K., Sun E.S., Kerrebrock A.W., Bronson R.T., Chi D.-C., Bulotsky M.S., Spencer J.B., Birren B.W., Frankel W.N., Lander E.S.;
 RT "The mouse pudgy mutation disrupts Delta homologue Dll3 and initiation of early somite boundaries."
 RL Nat. Genet. 19:274-278(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Neural tube;
 RA Nakayama K., Nakayama N., Tomooka Y., Hayashi Y., Takahashi M.;
 RT "Specific expression of a divergent type of Delta in a set of earliest generated neurons including the prospective subplate neurons."
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in the formation of somite boundaries during segmentation of the paraxial mesoderm.
 CC -1- SUBUNIT: Can bind and activate Notch-1 or another Notch receptor (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=2;
 CC IsoId=O88516-1; Sequence=Displayed;
 CC Name=1;
 CC IsoId=O88516-2; Sequence=VSP_001376;
 CC TISSUE SPECIFICITY: Predominantly expressed in the neuroectoderm and paraxial mesoderm during embryogenesis.
 CC -1- DOMAIN: The DSL domain is required for binding to the Notch receptor.
 CC -1- DISEASE: A truncating mutation in Dll3 is the cause of the pudgy (pu) phenotype. Pudgy mice exhibit patterning defects at the earliest stages of somitogenesis. Adult pudgy mice present severe vertebral and rib deformities.
 CC -1- SIMILARITY: Contains 1 DSL domain.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
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 CC EMBL; AF068865; AAC40170.1; --
 CC EMBL; AF068865; AAC40169.1; --
 CC EMBL; Y11895; CAA72637.1; --
 CC EMBL; AB013440; BAA33716.1; --
 CC HSPB; P00740; IEDM.
 CC MGD; MGI:1096877; Dll3.
 CC GO; GO:0005112; F-Notch binding; NAS.
 CC GO; GO:0001709; P:cell fate determination; NAS.
 CC GO; GO:0007386; P:compartment specification; IMP.
 CC GO; GO:0001701; P:embryonic development (sensu Mammalia); NAS.
 CC GO; GO:0007399; P:neurogenesis; NAS.
 CC GO; GO:0007219; P:Notch signaling pathway; NAS.
 CC GO; GO:0001501; P:skeletal development; IMP.
 CC InterPro; IPR000742; EGF 2.
 CC InterPro; IPR001438; EGF-II.
 CC InterPro; IPR006209; EGF_like.
 CC Pfam; PF00008; EGF; 5.
 CC PRINTS; PRO0010; EGFLOOD.
 CC PROSITE; PS00022; EGF 1; 6.
 CC PROSITE; PS01186; EGF 2; 6.
 CC PROSITE; PS00026; EGF 3; 6.
 KW Alternative splicing; Developmental protein; Differentiation;
 KW EGF-like domain; Notch signaling pathway; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 592 Delta-like protein 3.
 FT DOMAIN 33 490 Extracellular (Potential).
 FT TRANSMEM 491 511 Potential.
 FT DOMAIN 512 592 Cytoplasmic (Potential).
 FT DOMAIN 174 213 DSL.
 FT DOMAIN 214 247 EGF-like 1.
 FT DOMAIN 272 308 EGF-like 2.
 FT DOMAIN 310 349 EGF-like 3.
 FT DOMAIN 351 387 EGF-like 4.
 FT DOMAIN 389 425 EGF-like 5.
 FT DOMAIN 427 463 EGF-like 6.
 FT DISULFID 218 229 By similarity.
 FT DISULFID 222 235 By similarity.
 FT DISULFID 237 246 By similarity.
 FT DISULFID 276 287 By similarity.
 FT DISULFID 281 296 By similarity.
 FT DISULFID 298 307 By similarity.
 FT DISULFID 314 325 By similarity.
 FT DISULFID 319 337 By similarity.
 FT DISULFID 339 348 By similarity.
 FT DISULFID 355 366 By similarity.
 FT DISULFID 360 375 By similarity.
 FT DISULFID 377 386 By similarity.
 FT DISULFID 393 404 By similarity.
 FT DISULFID 398 413 By similarity.
 FT DISULFID 415 424 By similarity.
 FT DISULFID 431 442 By similarity.
 FT DISULFID 436 451 By similarity.
 FT DISULFID 453 462 By similarity.
 FT VARSPLIC 585 592 DMLIQVLF-->A (in isoform 1).
 FT CONFLICT 94 94 E->K (in Ref. 3).
 FT CONFLICT 401 401 G->A (in Ref. 1).
 SQ SEQUENCE 592 AA; 62069 MW; 1A84F8022E7E7DCC CRC64;
 Query Match 34.2%; Score 55; DB 1; Length 592;
 Best Local Similarity 37.9%; Pred. No. 98;
 Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;
 QY 1 CR--IXNOKCFQHLDDCCSRKCNFNKCV 27
 DB 377 CRAGFAGPRCEHDLDDCAGACANGGTCV 405


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RESULT 57
DL33_HUMAN
ID   DLL3_HUMAN          STANDARD;          PRT;          618 AA.
AC   Q9NYJ7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-JAN-2005 (Rel. 46, Last annotation update)
DE   Delta-like protein 3 precursor (Drosophila Delta homolog 3).
GN   Name=DLL3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT SC001 ASP-385.
RX   MEDLINE=20206573; PubMed=10742114; DOI=10.1038/74307;
RA   Bulman M.P., Kusumi K., Frayling T.M., McKeown C., Garrett C.,
RA   Lander E.S., Krumlauf R., Hattersley A.T., Ellard S., Turpenny P.D.,
RT   "Mutations in the human delta homologue, DLL3, cause axial skeletal
RT   defects in spondylocostal dysostosis."
RL   Nat. Genet. 24:438-441(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klugner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheck T.E.,
RA   Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywicki M.I., Skolala U., Smalls D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences."
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -1- FUNCTION: Inhibits primary neurogenesis. May be required to divert
CC   neurons along a specific differentiation pathway. Play a role in
CC   the formation of somite boundaries during segmentation of the
CC   paraxial mesoderm (By similarity).
CC   -1- SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
CC   (By similarity).
CC   -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -1- DOMAIN: The DSL domain is required for binding to the Notch
CC   receptor.
CC   -1- DISEASE: Defects in DLL3 are the cause of autosomal recessive
CC   spondylocostal dysostosis type 1 (SC001) [MIM:277300]. SC001 is
CC   characterized by multiple hemivertebrae, rib fusions and deletions
CC   with a non-progressive kyphoscoliosis.
CC   -1- SIMILARITY: Contains 1 DSL domain.
CC   -1- SIMILARITY: Contains 6 EGF-like domains.
-----
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EMBL; AF241373; AAF62542.1; -.
DR EMBL; AF241367; AAF62542.1; JOINED.
DR EMBL; AF241368; AAF62542.1; JOINED.
DR EMBL; AF241369; AAF62542.1; JOINED.

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DR EMBL; AF241370; AAF62542.1; JOINED.
DR EMBL; AF241371; AAF62542.1; JOINED.
DR EMBL; AF241372; AAF62542.1; JOINED.
DR EMBL; BC000218; AAF00218.1; -.
DR HSSP; P00740; LEDM.
DR Genew; HGNC:2909; DLL3.
DR H-INVD; HIX0015121; -.
DR MIM; 602768; -.
DR MIM; 277300; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005112; F:Notch binding; NAS.
DR GO; GO:0001709; P:cell fate determination; ISS.
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
DR GO; GO:0007399; P:neurogenesis; ISS.
DR GO; GO:0007219; P:Notch signaling pathway; ISS.
DR GO; GO:0001501; P:skeletal development; IMP.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 5.
DR PRINTS; PR0010; EGFBL00.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00026; EGF_3; 6.
KW Developmental protein; Differentiation; Disease mutation; Repeat;
KW EGF-like domain; Notch signaling pathway; Polymorphism; Repeat;
FT SIGNAL 1 26 Potential.
FT CHAIN 27 618 Delta-like protein 3.
FT DOMAIN 27 492 Extracellular (Potential).
FT TRANSMEM 493 513 Potential.
FT DOMAIN 514 618 Cytoplasmic (Potential).
FT DOMAIN 176 215 DSL.
FT DOMAIN 216 249 EGF-like 1.
FT DOMAIN 274 310 EGF-like 2.
FT DOMAIN 312 351 EGF-like 3.
FT DOMAIN 353 389 EGF-like 4.
FT DOMAIN 391 427 EGF-like 5.
FT DOMAIN 429 465 EGF-like 6.
FT DISULFID 220 231 By similarity.
FT DISULFID 224 217 By similarity.
FT DISULFID 239 248 By similarity.
FT DISULFID 278 289 By similarity.
FT DISULFID 283 298 By similarity.
FT DISULFID 300 309 By similarity.
FT DISULFID 316 327 By similarity.
FT DISULFID 321 339 By similarity.
FT DISULFID 341 350 By similarity.
FT DISULFID 357 368 By similarity.
FT DISULFID 362 377 By similarity.
FT DISULFID 379 388 By similarity.
FT DISULFID 395 406 By similarity.
FT DISULFID 400 415 By similarity.
FT DISULFID 417 426 By similarity.
FT DISULFID 433 444 By similarity.
FT DISULFID 438 453 By similarity.
FT DISULFID 455 464 By similarity.
FT VARIANT 218 218 L -> P (in dbSNP:1110627).
FT VARIANT 385 385 /FTID=VAR_016776.
FT VARIANT 385 385 G -> D (in SC001).
FT FTID=VAR_009952.
SQ SEQUENCE 618 AA; 64617 MW; 58A9BC0A7DEAD1A0 CRC64;
Query Match 34.2%; Score 55; DB 1; Length 618;
Best Local Similarity 37.9%; Pred. No. 1e+02;
Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;
QY 1 CR--IXNQKCFQHLDDCCSRKCNKFNKCV 27
||| : |||||
Db 379 CRAGFAGRCRCHDLDDCCAGACANGTCV 407
||| : |||||
RESULT 58

```


Q812A6
ID Q812A6 PRELIMINARY; PRT; 1620 AA.
AC Q812A6
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein PFA0170C.
GN Name=PFA0170C; Synonyms=MAL1P1.74b;
OS Plasmodium falciparum (isolate 3D7)
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Barriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Kontorov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitz E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
DR EMBL; AL031745; CAB48994.1;
DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000834; Peptidase_M14.
DR Pfam; PF00246; Peptidase_M14; 1.
KW Hypothetical protein.
SQ SEQUENCE 1620 AA; 19196 MW; 31A7292B814ACE0F CRC64;
Nature 419:527-531(2002).
Query Match 34.2%; Score 55; DB 2; Length 1620;
Best Local Similarity 37.9%; Pred. No. 2.4e+02;
Matches 11; Conservative 5; Mismatches 7; Indels 6; Gaps 1;
QY 4 XNQCFOHLDCCSRKCNRF-----NKC 26
Db 161 YTNKCNQYNDYTNKCNQYNDYTNKC 189
RESULT 59
Q7RR73
ID Q7RR73 PRELIMINARY; PRT; 5309 AA.
AC Q7RR73
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY00634;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAL01000171; EAA17439.1; -;
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR006162; Ppantne S.
DR InterPro; IPR002078; Sig54_interact.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN_1.
DR PROSITE; PS00675; SIGMAS4_INTERACT_1; 1.
KW Hypothetical protein.
FT NON_TER 5309 5309
SQ SEQUENCE 5309 AA; 628397 MW; 2406AC52CF2F5A93 CRC64;
Query Match 34.2%; Score 55; DB 2; Length 5309;
Best Local Similarity 32.4%; Pred. No. 6.8e+02;
Matches 12; Conservative 5; Mismatches 10; Indels 10; Gaps 2;
QY 1 CR-IXNQCFOH-----LDDCCSRKCNRFNKC 27
Db 3900 CRIKNCSCFTTEKQNNVCFEDICKNNVKNKICI 3936
RESULT 60
CXOA_CONMA
ID CXOA_CONMA STANDARD; PRT; 71 AA.
AC P05484;
DT 01-NOV-1988 (Rel. 09, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Omega-conotoxin MVIIa precursor (SNX-111) (Ziconotide).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Neogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom duct;
RX MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002252200;
RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
RT "Novel omega-conotoxins from Conus catus discriminate among neuronal
RT calcium channel subtypes.";
RL J. Biol. Chem. 275:35335-35344(2000).
RN [2]
RP SEQUENCE OF 46-70.
RX MEDLINE=86070213; PubMed=4071055;
RA Olivera B.M., Gray W.R., Zeikus R.D., McIntosh J.M., Varga J.,
RA Rivier J.E., de Santos V., Cruz L.J.;
RT "Peptide neurotoxins from fish-hunting cone snails.";
RL Science 230:1338-1343(1985).
RN [3]
RP SEQUENCE OF 46-70.
RX MEDLINE=87299637; PubMed=2441741;
RA Olivera B.M., Cruz L.J., de Santos V., Lechmanant G.W., Griffin D.,
RA Zeikus R.D., McIntosh J.M., Galyean R., Varga J., Gray W.R.,
RA Rivier J.E.;
RT "Neuronal calcium channel antagonists. Discrimination between calcium
RT channel subtypes using omega-conotoxin from Conus magus venom.";
RL Biochemistry 26:2086-2090(1987).
RN [4]
RP DISULFIDE BONDS.
RX MEDLINE=96122182; PubMed=8537186;
RA Chung D., Gaur S., Bell J.R., Ramachandran J., Nadaesi L.;
RT "Determination of disulfide bridge pattern in omega-conopeptides.";
RL Int. J. Pept. Protein Res. 46:320-325(1995).
RN [5]

RP SYNTHESIS, AND MUTAGENESIS OF LYS-47 AND TYR-58.
 RX MEDLINE=95126930; PubMed=7826361;
 RA Kim J.I., Takahashi M., Ohtake A., Wakamiya A., Sato K.;
 RT "Tyrl3 is essential for the activity of omega-conotoxin MVIIA and
 GVIA, specific N-type calcium channel blockers.";
 RL Biochem. Biophys. Res. Commun. 206:449-454(1995).
 RN [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95367555; PubMed=7640281;
 RA Kohno T., Kim J.-I., Kobayashi K., Kodera Y., Maeda T., Sato K.;
 RT "Three-dimensional structure in solution of the calcium channel
 blocker omega-conotoxin MVIIA.";
 RL Biochemistry 34:10256-10265(1995).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95385787; PubMed=7656969; DOI=10.1016/0014-5793(95)00819-U;
 RA Basus V.J., Nadasdi L., Ramachandran J., Miljanich G.P.;
 RT "Solution structure of omega-conotoxin MVIIA using 2D NMR
 spectroscopy.";
 RL FEBS Lett. 370:163-169(1995).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97070382; PubMed=8913308; DOI=10.1006/jmbi.1996.0576;
 RA Nielsen K.J., Thomas L., Lewis R.J., Alewood P.F., Craik D.J.;
 RT "A consensus structure for omega-conotoxins with different
 selectivities for voltage-sensitive calcium channel subtypes:
 comparison of MVIIA, SVIB and SNX-202.";
 RL J. Mol. Biol. 263:297-310(1996).
 RN [9]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99303703; PubMed=10373375; DOI=10.1006/jmbi.1999.2817;
 RA Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
 RA Lewis R.J.;
 RT "Structure-activity relationships of omega-conotoxins MVIIA, MVIIIC and
 J4 loop splice hybrids at N and P/Q-type calcium channels.";
 RL J. Mol. Biol. 289:1405-1421(1999).
 RN [10]
 RP STRUCTURE BY NMR.
 RX MEDLINE=20212338; PubMed=10747778; DOI=10.1021/bi992651h;
 RA Atkinson R.A., Kieffer B., Dejaegere A., Sirockin F., Lefevre J.-F.;
 RT "Structural and dynamic characterization of omega-conotoxin MVIIA: the
 binding loop exhibits slow conformational exchange.";
 RL Biochemistry 39:3908-3919(2000).
 RN [11]
 RP STRUCTURE BY NMR.
 RX MEDLINE=21243158; PubMed=11344322; DOI=10.1110/ps.30701;
 RA Goldenberg D.P., Koehn R.E., Gilbert D.E., Wagner G.;
 RT "Solution structure and backbone dynamics of an omega-conotoxin
 precursor.";
 RL Protein Sci. 10:538-550(2001).
 CC -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 and block voltage-sensitive calcium channels (VSCC). This toxin
 blocks N-type calcium channels.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- PHARMACEUTICAL: Is under clinical trial by Neurex. It blocks acute
 pain in patients who no longer obtain relief from opiate drugs. It
 is 100 to 1000 times more potent than morphine. By blocking
 calcium channels it disable nerves that transmit pain signals.
 CC -1- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
 family.
 CC -1- DATABASE: NAME=ziconotide Source; NOTE=web site on ziconotide;
 WWW="http://docmd.com/ziconotide/".
 CC PIR; JH0700; JH0700.
 DR PDB; 1DW4; NMR; A=1-25.
 DR PDB; 1DW5; NMR; A=1-25.
 DR PDB; 1FEO; NMR; A=1-25.
 DR PDB; 1MVI; NMR; @=1-25.
 DR PDB; 1OMG; NMR; @=1-25.
 DR InterPro; IPR004214; Conotoxin.
 DR Pfam; PF02950; Conotoxin; 1.
 DR 3D-structure; Amidation; Calcium channel inhibitor;
 KW Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;

KW Pharmaceutical; Presynaptic neurotoxin; Signal; Toxin.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 45 Omega-conotoxin MVIIA.
 FT PEPTIDE 46 70
 FT DISULFID 46 61
 FT DISULFID 53 65
 FT DISULFID 60 70
 FT MOD_RES 70 70
 FT MUTAGEN 47 47 Cysteine amide (G-71 provides amide
 group).
 FT MUTAGEN 58 58 K->A: Little decrease in activity.
 FT SEQUENCE 71 AA; 7587 MW; E2A32725C81AF31D CRC64; Y->A: Strong decrease in activity.
 SQ
 Query Match 33.9%; Score 54.5; DB 1; Length 71;
 Best Local Similarity 38.5%; Pred. No. 17;
 Matches 10; Conservative 5; Mismatches 10; Indels 1; Gaps 1;
 QY 1 CRXNQKCFQHLDDCCSRKCNRFNK 26
 Db 46 CRGKAGKCSRLMYDCTGSC-RSGKC 70
 RESULT 61
 Q646V4 PRELIMINARY; PRT; 74 AA.
 AC Q646V4
 ID Q646V4; (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Phytotoxin-like SCR74.
 OS Phytophthora infestans (Potato late blight fungus).
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 OC Phytophthora.
 OX NCBI_TaxID=4787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
 RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
 RA Kamoun S.;
 RT "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene
 Family of Phytophthora infestans.";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY723713; AAU21454.1; -
 SQ SEQUENCE 74 AA; 7942 MW; CE020986B607E796 CRC64;
 Query Match 33.9%; Score 54.5; DB 2; Length 74;
 Best Local Similarity 37.0%; Pred. No. 18;
 Matches 10; Conservative 4; Mismatches 6; Indels 7; Gaps 1;
 QY 7 KCFQHLDDCCSRKCNRFNK 26
 Db 45 KCCQAINPVPVAFYDCCSKSCNTGSPC 71
 RESULT 62
 Q646V5 PRELIMINARY; PRT; 74 AA.
 AC Q646V5
 ID Q646V5; (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Phytotoxin-like SCR74.
 OS Phytophthora infestans (Potato late blight fungus).
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 OC Phytophthora.
 OX NCBI_TaxID=4787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
 RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
 RA Kamoun S.;
 RT "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene
 Family of Phytophthora infestans.";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY723711; AAU21452.1; -
 SQ SEQUENCE 74 AA; 7825 MW; 537318AAPP612545 CRC64;

Query Match 33.9%; Score 54.5; DB 2; Length 74;
 Best Local Similarity 37.0%; Pred. No. 18;
 Matches 10; Conservative 4; Mismatches 6; Indels 7; Gaps 1;

QY 7 KCFQHLDD-----DCCSRKCNRFNKC 26
 |||:::|||||:
 Db 45 KCCQAINADPIAFHDCCKSKCNTGSPC 71

RESULT 63

Q646W1
 ID Q646W1 PRELIMINARY; PRT; 74 AA.
 AC Q646W1;
 DT 25-OCT-2004 (TREMELrel. 28, Created)
 DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
 DE Phytoxin-like SCR74.
 OS Phytoththora infestans (Potato late blight fungus)
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 OC Phytoththora
 NCBI_TaxID=4787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
 RA Torto-Alalibo T., Min J., Avrova A.O., Wright F., Birch P.R.J.,
 RA Kamoun S.;
 RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
 RT Family of Phytoththora infestans";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY723705; AAU21446.1; -
 SQ SEQUENCE 74 AA; 7885 MW; 98D110005D613927 CRC64;

Query Match 33.9%; Score 54.5; DB 2; Length 74;
 Best Local Similarity 37.0%; Pred. No. 18;
 Matches 10; Conservative 4; Mismatches 6; Indels 7; Gaps 1;

QY 7 KCFQHLDD-----DCCSRKCNRFNKC 26
 |||:::|||||:
 Db 45 KCCQAINADPIAFHDCCKSKCNTGSPC 71

RESULT 64

O18052
 ID O18052 PRELIMINARY; PRT; 247 AA.
 AC O18052;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Hypothetical protein T06G6.6.
 GN ORFNames=T06G6.6;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Kershaw J.K.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z81587; CAB04705.2; -
 WormBase; WBGene00011548; T06G6.6.

DR WormPep; T06G6.6; CE13343.
 KW Hypothetical protein.
 SQ SEQUENCE 247 AA; 27954 MW; 26FAB589C121PBEB CRC64;

Query Match 33.9%; Score 54.5; DB 2; Length 247;
 Best Local Similarity 33.3%; Pred. No. 52;
 Matches 10; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 3 IXNOKCFQHLDD-----DCCSRKCNRFNKC 25
 |||:::|||||:
 Db 77 INDNGCFMHFDCKLESIELCLPQCFNE 106

RESULT 65

Q97GL5
 ID Q97GL5 PRELIMINARY; PRT; 252 AA.
 AC Q97GL5;
 DT 01-OCT-2001 (TREMELrel. 18, Created)
 DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Glycosyltransferase.
 GN OrderedLocusNames=CAC2351;
 OS Clostridium acetobutylicum
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium
 NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RX DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R.L., Lee H.M., Dubois J., Glu D., Hitti J., Wolf Y.I.,
 RA Tatsov R., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum";
 RL J. Bacteriol. 183:4823-4838 (2001).
 DR EMBL; AE007735; AAK80307.1; -
 DR FIR; H97189; H97189.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR001173; Glyco trans 2.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 252 AA; 29892 MW; C7A45BA39F534DE9 CRC64;

Query Match 33.9%; Score 54.5; DB 2; Length 252;
 Best Local Similarity 37.0%; Pred. No. 53;
 Matches 10; Conservative 5; Mismatches 5; Indels 7; Gaps 2;

QY 3 IXNOKCFQHLDDCCSR-----KCNRFN 24
 |||:::|||||:
 Db 188 LAEDACF--IEDCKQGIKIYSCNRFN 212

RESULT 66

O18720
 ID O18720 PRELIMINARY; PRT; 1282 AA.
 AC O18720;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Gal/GalNAc-inhibitable adherence lectin.
 GN Name=dhg12;
 OS Entamoeba dispar.
 OC Eukaryota; Entamoebidae; Entamoeba.
 NCBI_TaxID=46681;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SAW760;
 RX MEDLINE=97376907; PubMed=9233678; DOI=10.1016/S0166-6851(97)00047-9;
 RA Pillai D.R., Britten D., Ackers J.P., Ravdin J.I., Kain K.C.;
 RT "A gene homologous to hgl2 of Entamoeba histolytica is present and
 RT expressed in Entamoeba dispar.";


```
RL Mol. Biochem. Parasitol. 87:101-105(1997).
DR EMBL; U73710; AAC47580.1; -.
DR GO; GO:0005529; F: sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
KW Lectin.
SQ SEQUENCE 1282 AA; 143481 MW; 48BD2FA64140C33E CRC64;

Query Match 33.9%; Score 54.5; DB 2; Length 1282;
Best Local Similarity 38.1%; Pred. No. 2.2e+02;
Matches 11; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KC 26
DB 708 CSMGTDNVI SYCEDCASRKSCQCGNFNGKC 736

RESULT 67
CXOD_CONCT STANDARD; PRT; 73 AA.
AC PS8920;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Omega-conotoxin CVID precursor.
OS Conus catus (Cat cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 46-72, SYNTHESIS, AND STRUCTURE BY
RP NNR.
RC TISSUE=Venom, and Venom duct;
RX MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002252200;
RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
RT "Novel omega-conotoxins from Conus catus discriminate among neuronal
RT calcium channel subtypes."
RL J. Biol. Chem. 275:35335-35344(2000).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
CC and block voltage-sensitive calcium channels (VSCC) (By
CC similarity). This toxin blocks N-type calcium channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
CC family.
DR HSSP; P05484; 1D44.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
KW Amidation; Calcium channel inhibitor; Direct protein sequencing;
KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Signal;
KW Toxin.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 45
FT PEPTIDE 46 72 Omega-conotoxin CVID.
FT DISULFID 46 61 By similarity.
FT DISULFID 53 65 By similarity.
FT DISULFID 60 72 By similarity.
FT MOD_RES 72 72 Cysteine amide (G-73 provides amide
FT group).
SQ SEQUENCE 73 AA; 7748 MW; C4CEBD30C77DAEC3 CRC64;

Query Match 33.5%; Score 54; DB 1; Length 73;
Best Local Similarity 38.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCN 21
DB 46 CKSKGAKCSKLMWDCCSGSCS 66

RESULT 68
ID Q80LT7 PRELIMINARY; PRT; 247 AA.
AC Q80LT7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Adoxophyes honmai nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=224399;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ADN001;
RX MEDLINE=22963401; PubMed=14599801; DOI=10.1016/j.virol.2003.08.002;
RA Nakai M., Goto C., Kang W., Shikata M., Luque T., Kunimi Y.;
RT "Genome sequence and organization of a nucleopolyhedrovirus isolated
RT from the smaller tea tortrix, Adoxophyes honmai."
RL Virology 316:171-183(2003).
DR EMBL; AF006270; BAC67260.1; -.
KW Hypothetical protein.
SQ SEQUENCE 247 AA; 28773 MW; 9E53E54D3E022C25 CRC64;

Query Match 33.5%; Score 54; DB 2; Length 247;
Best Local Similarity 40.7%; Pred. No. 60;
Matches 11; Conservative 3; Mismatches 9; Indels 4; Gaps 1;

QY 4 XNQKCFQ----HLDDCCSRKCNRFNKC 26
DB 168 CEKKCFAPRLHLDGLVCDKCGNFNC 194

RESULT 69
LHX1_BRARE
ID LHX1_BRARE STANDARD; PRT; 405 AA.
AC Q90476;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE LIM/homeobox protein Lhx1 (Homeobox protein LIM-1).
GN Name=Lhx1a; Synonyms=lhx1, lim1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gastrula, and Neurula;
RX MEDLINE=95285760; PubMed=7768180;
RA Toyama R., O'Connell M.L., Wright C.V.E., Kuehn M.R., Dawid I.B.;
RT "Nodal induces ectopic goosecoid and lim1 expression and axis
RT duplication in zebrafish."
RL Development 121:383-391(1995).
CC -!- FUNCTION: Seems to play a role in dorsal axis formation.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- DEVELOPMENTAL STAGE: Detected 4 hours after fertilization, maximum
CC levels are seen in 6-hours embryos. Expression then declines
CC during gastrulation (6-10 hours), but is still detectable in 24-
CC and 30-hours embryos. The spatial distribution also vary during
CC embryogenesis: at the beginning, expression is localized in deep
CC cells, and absent from the enveloping layer. The pattern then
CC becomes asymmetric, restricted to the forming embryonic shield. By
CC the shield stage, it is highly localized in the axial hypoblast.
CC As gastrulation proceeds, expression still continues in the
CC involuting cells, extending from the margin towards the anterior.
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; L37802; AAA92157.1; -.
CC HSSP; P06601; 1FJL.
CC ZFIN; ZDB-GENE-980526-347; lxh1a.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR009057; Homeodomain_like.
CC InterPro; IPR001781; LIM.
CC InterPro; IPR007107; LIM homeo.
CC Pfam; PF00046; Homeobox; 1.
CC Pfam; PF00412; LIM; 2.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC ProDom; PD000094; LIM; 2.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC PROSITE; PS00478; LIM DOMAIN_1; 2.
CC PROSITE; PS00023; LIM DOMAIN_2; 2.
CC Developmental protein; DNA-binding; Homeobox; LIM domain;
KW Metal-binding; Nuclear protein; Repeat; Zinc.
FT DOMAIN 4 54 LIM 1.
FT DOMAIN 63 117 LIM 2.
FT DNA BIND 179 238 Homeobox.
SQ SEQUENCE 405 AA; 45153 MW; 186EBEB59C88123 CRC64;

Query Match 33.5%; Score 54; DB 1; Length 405;
Best Local Similarity 44.0%; Pred. No. 93;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNQKCFQHLDDCCSRKCNRFNK 26
DB 22 RAWHIKCVQ---CCECKNLTEKC 42

RESULT 70
Q45117 ID 045117 PRELIMINARY; PRT; 552 AA.
AC 045117;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ultraspiracle.
GN Names=USP-1;
OS Chironomus tentans (Midge).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7153;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99457719; PubMed=10528412; DOI=10.1016/S0965-1748(99)00068-5;
RA Vogtli M., Imhof M.O., Brown N.E., Rauch P., Spindler-Barth M.,
RA Lezzi M., Henrich V.C.;
RT "Functional characterization of two Ultraspiracle forms (CtUSP-1 and
RT CtUSP-2) from Chironomus tentans.";
RL Insect Biochem. Mol. Biol. 29:931-942(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Vogtli M.O., Henrich V.C., Imhof M.O., Lezzi M.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBSJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AF045891; AAC03056.1; -.
DR HSSP; P20153; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000536; Hrmn_recept_lig.

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DR InterPro; IPR000003; Rtnoidx_receptor.
DR InterPro; IPR001723; Stdhrn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; Zf-C4; 1.
DR PRINTS; PR00545; RETINOIDXR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 552 AA; 61882 MW; 3261341C2BD0A98E CRC64;

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Query Match 33.5%; Score 54; DB 2; Length 552;
Best Local Similarity 40.0%; Pred. No. 1.2e+02;
Matches 10; Conservative 6; Mismatches 7; Indels 2; Gaps 1;

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QY 1 CRXNQKCFQHLDDCCSRKCNRFNK 25
DB 345 CAVNKKVQFQHMDFC--RLPHFTK 367

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RESULT 71
Q68KF8 ID 068KF8 PRELIMINARY; PRT; 911 AA.
AC 068KF8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Subtilisin-like protease SPC6A.
GN Name=spc6a;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas J.T., Weih K.A., Prakash D., Moos M. Jr.;
RT "Vgl and CDMF-1/GDF5 Have Specific Processing Requirements That
RT Restrict their Sites of Action to Body Axis and Joint Patterning
RT Centers.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY685229; AAT99305.1; -.
GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR006210; IEGF_
DR InterPro; IPR000209; Rept_S8_S53.
DR InterPro; IPR009020; Prot_inh_propt.
DR InterPro; IPR002884; PrototnconvertSP.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF01483; P_protease; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; PrototnconvertSP; 1.
DR SMART; SM00181; EGF; 4.
DR SMART; SM00261; FU; 5.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE 911 AA; 101427 MW; E75C63CB60D3B82F CRC64;

```

Query Match 33.5%; Score 54; DB 2; Length 911;
Best Local Similarity 38.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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QY 6 QKCFQHLDDCCSRKCNRFNK 26
DB 683 KKCFCQHCDCVGSRTDQCTAC 703

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RESULT 72
P91526 PRELIMINARY; PRT; 1372 AA.
AC P91526;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein W02C12.1.
GN Names=W02C12.1; ORFNames=W02C12.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99089613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99089613; PubMed=9851916;
RG WormBase Consortium;
RT "The sequence of C. elegans cosmid W02C12."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99089613; PubMed=9851916;
RG WormBase Consortium;
RT "The sequence of C. elegans cosmid W02C12."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80815; AAB37995.1; -.
DR PIR; T25933; T25933.
DR HSSP; Q12780; IHAE.
DR WormBase; WBGene0020928; W02C12.1.
DR WormPep; W02C12.1; CEI4412.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR003410; HyalIn.
DR InterPro; IPR001759; Pentaxin.
DR InterPro; IPR000436; Sushi_SCR_ccp.
DR Pfam; PF00008; EGF; 10.
DR Pfam; PF02494; HYR; 1.
DR PRINTS; PR00010; EGFBL00D.
DR ProDom; PD002153; Pentaxin; 1.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00179; EGF CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS00022; EGF_1; 11.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 12.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00825; HYR; 1.
DR PROSITE; PS0923; SUSHI; 1.
KW EGF-like domain; Hypothetical protein.
SQ SEQUENCE 1372 AA; 150561 MW; 0537FA79BA0576C5 CRC64;
```

Query Match 33.5%; Score 54; DB 2; Length 1372;
Best Local Similarity 29.2%; Pred. No. 2.7e+02;

```
Matches 7; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY 4 XNQKCFQHLDDCCSRKCNFRKCV 27
: : : : : : : : : : : : : : : :
Db 95 TGENCQNDIDCAASPCQNDKCI 118

RESULT 73
Q9DE37 PRELIMINARY; PRT; 1515 AA.
ID Q9DE37;
AC Q9DE37;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Slit3.
GN Name=slit3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Michigan;
RX MEDLINE=21098742; PubMed=11161558; DOI=10.1006/dbio.2000.0105;
RA Yeo S.Y., Little M.H., Yamada T., Miyashita T., Halloran M.C.,
RA Kuwada J.Y., Huh T.L., Okamoto H.;
RT "Overexpression of a slit homologue impairs convergent extension of
the mesoderm and causes cyclopia in embryonic zebrafish.";
RL Dev. Biol. 230:11-17(2001).
DR EMBL; AF210320; AAG36772.1; -.
DR HSSP; P01132; 1GK5.
DR ZFIN; ZDB-GENE-010306-4; slit3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00008; EGF; 7.
DR Pfam; PF02210; Laminin_G_2; 1.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR Pfam; PF00560; LRR_1; 19.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00274; FOLN; 3.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_Typ; 9.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 8.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00025; LAM_G_DOMAIN; 1.
KW EGF-like domain.
SQ SEQUENCE 1515 AA; 166871 MW; 12FD111277D18D5B CRC64;
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Query Match      33.5%; Score 54; DB 2; Length 1515;
Best Local Similarity 37.5%; Pred. No. 3e+02;
Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKCNRENK 27
DB 1059 VQCCFQDYNDCLNKCQHGACV 1082

RESULT 74
HSPC_ELECI
ID HSPC_ELECI STANDARD; PRT; 84 AA.
AC P83183;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Cysteine-rich protamine.
DE Cysteine-rich protamine.
OS Eleione cirrhosa (Curled octopus) (Ozaena cirrhosa).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eleione.
OX NCBI_TaxID=102876;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE-Sperm;
RX MEDLINE=22108191; PubMed=12113475;
RA Gimenez-Bonafe P., Ribes E., Sautiere P., Gonzalez A., Kasinsky H.E.,
RA Kouach M., Sautiere P.-E., Ausio J., Chiva M.;
RT "Chromatin condensation, cysteine-rich protamine, and establishment of
RT disulphide interprotamine bonds during spermiogenesis of Eleione
RT cirrhosa (Cephalopoda).";
RL Eur. J. Cell Biol. 81:341-349 (2002).
CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC This protamine condenses spermiogenic chromatin in a pattern which
CC comprises fibres with a progressively larger diameter and lamellae
CC that finally undergo definitive coalescence.
CC -!- SUBUNIT: Cross-linked by interchain disulfide bonds around the
CC DNA-helix (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
DR InterPro: IPR001212; Somatomedin B.
KW Chromosomal protein; Direct protein sequencing; DNA condensation;
KW DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis.
FT DISULFID 12 12 Interchain (with C-31) (By similarity).
FT DISULFID 16 24 By similarity.
FT DISULFID 31 31 Interchain (with C-12) (By similarity).
FT DISULFID 63 63 Interchain (with C-63) (By similarity).
FT DISULFID 64 80 By similarity.
SQ SEQUENCE 84 AA; 10612 MW; 70932DAC3C71837E CRC64;

Query Match      33.2%; Score 53.5; DB 1; Length 84;
Best Local Similarity 31.0%; Pred. No. 27;
Matches 9; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

QY 1 CRXNOKCFQHLDDCCSRK---CNRENK 26
DB 24 CRRRCRCRIVKCCRRRSCRRRRRC 52

RESULT 75
Q693N8
ID Q693N8 PRELIMINARY; PRT; 476 AA.
AC Q693N8;
DT 25-OCT-2004 (TRMBLrel. 28, Created)
DT 25-OCT-2004 (TRMBLrel. 28, Last sequence update)
DE 3-hydroxy-3-methylglutaryl-CoA synthase (EC 2.3.3.10).
OS Taxus x media.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.
OX NCBI_TaxID=85957;
RN [1]

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SEQUENCE FROM N.A.
Kai G., Miao Z., Tang K.;
"Cloning and expression analyses of a new gene encoding 3-hydroxy-3-
methylglutaryl-CoA synthase from Taxus x media.";
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AY644708; AAT73206.1; -.
GO: GO:0008415; F:acetyltransferase activity; IEA.
GO: GO:0016740; F:hydroxymethylglutaryl-CoA synthase activity; IEA.
GO: GO:0006084; P:acetyl-CoA metabolism; IEA.
InterPro: IPR008260; HMG CoA synth.
InterPro: IPR010122; HMG CoA synth.
PFam: PF01154; HMG CoA synt; 1.
TIGRFAMS: TIGR01833; HMG-CoA-S_euk; 1.
KW Acyltransferase; Transferase.
SQ SEQUENCE 476 AA; 52863 MW; 973883623142EE0D CRC64;

Query Match      33.2%; Score 53.5; DB 2; Length 476;
Best Local Similarity 43.5%; Pred. No. 1.2e+02;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 4 XNOKCF-QHLDDCCSRKCNRENK 25
DB 211 LSQTCYLKALDSCYKRFCKFEK 233

RESULT 76
NH25_CAEEL
ID NH25_CAEEL STANDARD; PRT; 572 AA.
AC Q19345; Q9NJ95; Q9NJ96; Q9NJ97;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nuclear hormone receptor family member nhr-25.
GN Name=nhr-25; ORFNames=F11C1.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND CHARACTERIZATION.
RC STRAIN=Bristol N2;
RX MEDLINE=20237592; PubMed=1072806; DOI=10.1006/dbio.2000.9679;
RA Gissendanner C.R., Sludner A.E.;
RT "nhr-25, the Caenorhabditis elegans ortholog of ftz-fl, is required
RT for epidermal and somatic gonad development.";
RL Dev. Biol. 221:259-272 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
CC -!- FUNCTION: Orphan nuclear receptor. Seems to be required during
CC development. Disruption of nhr-25 function leads to embryonic
CC arrest due to failure of the epidermally mediated process of
CC embryo elongation.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=Q19345-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=Q19345-2; Sequence=VSP_003723;
CC -!- TISSUE SPECIFICITY: Expressed in the epidermis, the developing
CC somatic gonad, and a subset of other epithelial cells.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
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 CC -----
 DR EMBL; AF179214; AAF67038.1; -
 DR EMBL; AF179215; AAF67039.1; -
 DR EMBL; AF179216; AAF67040.1; -
 DR EMBL; Z54270; CAA91028.1; -
 DR PIR; T20764; T20764.
 DR HSSP; P19793; 2NLL.
 DR WormBase; WBGene00003623; F11C1.6.
 DR WormPep; F11C1.6; CE03191.
 DR InterPro; IPR000536; Hmon_recept_lig.
 DR InterPro; IPR001723; Strdhmn_receptor.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR000324; Vitd_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00398; STRDHMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR PRINTS; PR00350; VITAMINDR.
 DR PRODOM; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOL1; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 KW Alternative splicing; Developmental protein; DNA-binding;
 KW Nuclear protein; Receptor; Transcription regulation; Zinc-finger.
 FT DNA_BIND 18 83
 FT ZN_FING 18 38
 FT ZN_FING 54 78
 FT VARSPLIC 1 80
 FT Missing (in Isoform Beta).
 FT /FTID=VSP_003723.
 FT CONFLICT 100 100 F > L (in Ref. 2; AAF67039).
 FT CONFLICT 540 540 R > Q (in Ref. 2; AAF67039).
 SQ SEQUENCE 572 AA; 64772 MW; D3092AES33092D7A CRC64;
 Query Match 33.2%; Score 53.5; DB 1; Length 572;
 Best Local Similarity 32.4%; Pred. No. 1.4e+02;
 Matches 11; Conservative 8; Mismatches 6; Indels 9; Gaps 2;
 QY 3 IXNQKCFQ-----HLDCCSRKCN--RFNKC V 27
 Db 46 VQNKQVQCSAEANCHVDRTCKRCPCRCQKCL 79
 RESULT 77
 ID ITXA_PANIM STANDARD; PRT; 33 AA.
 AC PS9868;
 DT 10-OCT-2003 (Rel. 42, Last Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Imperatoxin A (ipTxa) (Imperatoxin activator).
 OS Pandinus imperator (Emperor scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Urida; Scorpionidea; Scorpionidae; Scorpioninae; Pandinus.
 OX NCBI_TaxID=55084;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=97261909; PubMed=9108323; DOI=10.1016/S0014-5793(97)00227-5;
 RA Zamudio F.Z., Gurrola G.B., Arevalo C., Sreekumar R., Walker J.W.,
 RA Valdivia H.H., Possani L.D.;
 RT "Primary structure and synthesis of Imperatoxin A (IpTx(a)), a peptide
 RT activator of Ca2+ release channels/ryanodine receptors.";
 RL FEBS Lett. 405:385-389 (1997).
 RN [2]
 RP IDENTIFICATION.
 RX MEDLINE=93101692; PubMed=1334561;
 RA Valdivia H.H., Kirby M.S., Lederer W.J., Coronado R.;
 RT "Scorpion toxins targeted against the sarcoplasmic reticulum Ca(2+)-

RT release channel of skeletal and cardiac muscle.";
 RN Proc. Natl. Acad. Sci. U.S.A. 89:12185-12189 (1992).
 RL [3]
 RP FUNCTION ON RYR1 AND RYR2.
 RX MEDLINE=98232523; PubMed=9565405;
 RA Tripathy A., Resch W., Xu L., Valdivia H.H., Meissner G.;
 RT "Imperatoxin A induces subconductance states in Ca2+ release channels
 RT (ryanodine receptors) of cardiac and skeletal muscle.";
 RL J. Gen. Physiol. 111:679-690 (1998).
 RN [4]
 RP FUNCTION ON RYR3.
 RX MEDLINE=21855933; PubMed=11867448;
 RA Nabhani T., Zhu X., Simeoni I., Sorrentino V., Valdivia H.H.,
 RA Garcia J.;
 RT "Imperatoxin A enhances Ca(2+) release in developing skeletal muscle
 RT containing ryanodine receptor type 3.";
 RL Biophys. J. 82:1319-1328 (2002).
 CC -1- FUNCTION: Strong agonist of ryanodine receptors (calcium release
 CC channels). Induces voltage- and concentration-dependent
 CC subconductance states in both skeletal (RYR1 and RYR3) and cardiac
 CC (RYR2) ryanodine receptors by binding to a single, cytosolically
 CC accessible site different from the ryanodine binding site.
 CC Enhances calcium release.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the scorpion calcine family.
 KW Calcium channel inhibitor; Direct protein sequencing;
 KW Ionic channel inhibitor; Neurotoxin; Toxin.
 FT DISULFID 3 17 By similarity.
 FT DISULFID 10 21 By similarity.
 FT DISULFID 16 32 By similarity.
 SQ SEQUENCE 33 AA; 3764 MW; D0DF8EFFE294537 CRC64;
 Query Match 32.9%; Score 53; DB 1; Length 33;
 Best Local Similarity 42.9%; Pred. No. 13;
 Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;
 QY 8 CFQHL-----DDCCSRKCNR 22
 Db 3 CLPHLKRCKADNDCCGKKCKR 23
 RESULT 78
 Q8YXK8
 ID Q8YXK8 PRELIMINARY; PRT; 85 AA.
 AC Q8YXK8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein CPE1386.
 GN OrderedLocusNames=CPE1386;
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13;
 RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
 RA Shimizu T., Ohtani K., Hirakawa H., Onshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
 DR EMBL; AF003190; BAB81092.1; -
 DR PRINTS; PR00003; 4DISULPHORE.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 85 AA; 9440 MW; 90EA0381B8D681 CRC64;
 Query Match 32.9%; Score 53; DB 2; Length 85;
 Best Local Similarity 37.5%; Pred. No. 31;
 Matches 12; Conservative 5; Mismatches 9; Indels 6; Gaps 2;

RC TISSUE=whole plant;
RX MEDLINE=22598051; PubMed=12679534; DOI=10.1093/molbev/meg088;
RA Heim M.A., Jakoby M., Werber M., Martin C., Weissshaar B., Bailey P.C.;
RT "The basic helix-loop-helix transcription factor family in plants: a
genome-wide study of protein structure and functional diversity";
RL Mol. Biol. Evol. 20:735-747(2003).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole plant;
RA Jakob M.J., Heim M.A., Bailey P., Martin C., Weissshaar B.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR ENBL; Z97336; CAB10220.1; -;
DR ENBL; AL161538; CAB78483.1; -;
DR ENBL; AF486628; AAM10963.1; -;
DR PIR; B71406; B71406.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PSS0888; HLH; 1.
KW Hypothetical protein.
SQ SEQUENCE 277 AA; 31190 MW; 17D79957B8B77B48 CRC64;
Query Match 32.9%; Score 53; DB 2; Length 277;
Best Local Similarity 58.8%; Pred. No. 88;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 10 QHLDCCSRKCNRFNC 26
Db 106 EHLDDCSRKARTGSC 122
RESULT 83
Q8L467
ID Q8L467 PRELIMINARY; PRT; 283 AA.
AC Q8L467
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AT4914410/dl3245w (Hypothetical protein).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
Ecker J.R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
annotation";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR ENBL; AY102106; AAM26676.1; -;
DR ENBL; AY088053; AAM65599.1; -;
DR ENBL; AY133565; AAM91395.1; -;
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PSS0888; HLH; 1.
KW Hypothetical protein.
SQ SEQUENCE 283 AA; 31995 MW; AB758D25A07E12BB CRC64;
Query Match 32.9%; Score 53; DB 2; Length 283;
Best Local Similarity 58.8%; Pred. No. 89;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 10 QHLDCCSRKCNRFNC 26
Db 112 EHLDDCSRKARTGSC 128
RESULT 84
Q44635
ID Q44635 PRELIMINARY; PRT; 421 AA.
AC Q44635
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F16B4.9.
GN Name=F16B4.9; ORFNames=F16B4.9;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequencing of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Davidson S., Wohlmann P., Bauer C., O'Neal D.;
RT "The sequence of C. elegans cosmid F16B4";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.


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RN  SEQUENCE FROM N.A.
RP  STRAIN=Bristol N2.
RG  WormBase Consortium;
RL  Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC  -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC  -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR  EMBL; AF039048; AAB94240.2; -.
DR  PIR; T32670; T32670.
DR  HSSP; P06536; 1LAT.
DR  WormBase; WEGene00017510; F16B4.9.
DR  WormPep; F16B4.9; CEI7680.
DR  GO; GO:0005634; C:nucleus; IEA.
DR  GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR  GO; GO:0003700; F:transcription factor activity; IEA.
DR  GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR  InterPro; IPR000536; Hmon_recept_lig.
DR  InterPro; IPR008946; Str_ncl_receptor.
DR  Pfam; PF00105; zf-C4; 1.
DR  SMART; SM00430; HOL1_1.
DR  ProDom; PD000035; Znf C4steroid; 1.
DR  SMART; SM00393; Znf C4; 1.
KW  DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
KW  Receptor; Transcription; Transcription regulation; Zinc; Zinc-finger.
SQ  SEQUENCE 421 AA; 48753 MW; 04720B0520F4F59C CRC64;

Query Match 32.9%; Score 53; DB 2; Length 421;
Best Local Similarity 40.7%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY  1 CRXNKCQFQHLDDCCSRKCNRFNKCVCV 27
DB  62 CRGGMNKCIIVNTNDRYQCLRFNKCVCV 98

RESULT 85
QY  Q7QCT2 PRELIMINARY; PRT; 1286 AA.
AC  Q7QCT2;
DT  01-MAR-2004 (TrEMBLrel. 26, Created)
DT  01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE  AGCP1804 (Fragment).
GN  Name=agCGS1928; ORFNames=ENSAANGG00000014325;
OS  Anopheles gambiae str. PEST.
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX  NCBI_TaxID=180454;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=PEST;
RA  Anopheles Genome Sequencing Consortium;
RL  Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; AAB0100859; EAA07783.1; -.
DR  HSSP; P00740; IEDM.
DR  GO; GO:0005509; F:calcium ion binding; IEA.
DR  InterPro; IPR000152; Asx_hydroxyl_S.
DR  InterPro; IPR008985; ConA_like_lig_g1.
DR  InterPro; IPR006207; Cys Knot_C.
DR  InterPro; IPR000742; EGF-2.
DR  InterPro; IPR001881; EGF-Ca.
DR  InterPro; IPR001438; EGF-11.
DR  InterPro; IPR006209; EGF-like.
DR  InterPro; IPR001791; Laminin G.
DR  InterPro; IPR001611; LRR.
DR  InterPro; IPR000483; LRR Cterm.
DR  InterPro; IPR000372; LRR Nterm.
DR  InterPro; IPR003591; LRR_tyr.

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DR  InterPro; IPR001211; PhospholipaseA2.
DR  Pfam; PF00008; EGF; 7.
DR  Pfam; PF01463; LRRCT; 3.
DR  Pfam; PF01462; LRRNT; 3.
DR  Pfam; PF00560; LRR_1; 14.
DR  PRINTS; PR00010; EGFBL00D.
DR  PRINTS; PR00019; LEURICHRPT.
DR  PROSITE; PS00010; ASX_HYDROXYL; 3.
DR  PROSITE; PS01185; CTCK_1; 1.
DR  PROSITE; PS01225; CTCK_2; 1.
DR  PROSITE; PS00022; EGF_1; 7.
DR  PROSITE; PS01186; EGF-2; 4.
DR  PROSITE; PS00026; EGF-3; 7.
DR  PROSITE; PS01187; EGF CA; 2.
DR  PROSITE; PS00025; LAM_G_DOMAIN; 1.
DR  PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
KW  EGF-like domain.
FT  NON_TER 1
SQ  SEQUENCE 1286 AA; 144156 MW; EE919D876B21BB3E CRC64;

Query Match 32.9%; Score 53; DB 2; Length 1286;
Best Local Similarity 33.3%; Pred. No. 3.4e+02;
Matches 8; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY  4 XNQCQFQHLDDCCSRKCNRFNKCVCV 27
DB  801 TGSRCVNIIDDCVGHKQNNGTVCV 824

RESULT 86
QY  Q16004 PRELIMINARY; PRT; 2531 AA.
AC  Q16004;
DT  01-JAN-1998 (TrEMBLrel. 05, Created)
DT  01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE  Notch homolog.
OS  Lytechinus variegatus (Sea urchin).
OC  Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC  Echinoidea; Euechinoidea; Echinacea; Temnopneuroidea; Toxopneustidae;
OC  Lytechinus.
OX  NCBI_TaxID=7654;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=97454256; PubMed=9310331;
RA  Sherwood D.R., McClay D.R.;
RT  "Identification and localization of a sea urchin Notch homolog:
RT  insights into vegetal plate regionalization and Notch receptor
RT  regulation.";
RL  Development 124:3363-3374(1997).
DR  EMBL; AF000634; AAB82088.1; -.
DR  PIR; T31070; T31070.
DR  HSSP; P01132; 1EGF.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0005509; F:calcium ion binding; IEA.
DR  GO; GO:0030154; P:cell differentiation; IEA.
DR  GO; GO:0050793; P:regulation of development; IEA.
DR  InterPro; IPR002110; ANK.
DR  InterPro; IPR000152; Asx_hydroxyl_S.
DR  InterPro; IPR000742; EGF-2.
DR  InterPro; IPR001881; EGF-Ca.
DR  InterPro; IPR001438; EGF-11.
DR  InterPro; IPR006209; EGF-like.
DR  InterPro; IPR008297; Notch.
DR  InterPro; IPR000800; Notch_region.
DR  Pfam; PF00023; Ank; 6.
DR  Pfam; PF00008; EGF; 31.
DR  Pfam; PF07645; EGF CA; 4.
DR  Pfam; PF00086; Notch; 3.
DR  PIRSF; PIRSF002279; Notch; 1.
DR  PRINTS; PR01415; ANKYRIN.
DR  PRINTS; PR00010; EGFBL00D.
DR  PRINTS; PR01452; NOTCH.

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DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF CA; 23.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 5.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 21.
 DR PROSITE; PS00022; EGF_1; 33.
 DR PROSITE; PS01186; EGF_2; 25.
 DR PROSITE; PS50026; EGF_3; 35.
 DR PROSITE; PS01187; EGF CA; 20.
 KW ANK repeat; EGF-like domain.
 SQ SEQUENCE 2531 AA; 273982 MW; 5BP42BEC627CA303 CRC64;
 Query Match 32.9%; Score 53; DB 2; Length 2531;
 Best Local Similarity 45.0%; Pred. No. 6.2e+02;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 OY 8 CFQHLDDCCSRKCNRENKCV 27
 DB 662 CEDIDDCESRPCHNGTCV 681
 RESULT 87
 NTCL_HUMAN
 ID_NTCL_HUMAN STANDARD; PRT; 2556 AA.
 AC P46531;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (hnl)
 DE (Translocation-associated notch protein TAN-1).
 GN Name=NOTCH1; Synonyms=TAN1;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Mann R.S., Blaumueller C.M., Zagouras P.;
 RT "Complete human notch 1 (hnl) cDNA sequence";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 1-2444 FROM N.A.
 RX MEDLINE=91347367; PubMed=1831692; DOI=10.1016/0092-9674(91)90111-B;
 RA Ellisen L.W., Bird J., West D.C., Soreng A.L., Reynolds T.C.,
 RA Smith S.D., Sklar J.;
 RT "TAN-1, the human homolog of the Drosophila notch gene, is broken by
 RT chromosomal translocations in T lymphoblastic neoplasms.";
 RL Cell 66:649-661(1991).
 RN [3]
 RP IDENTIFICATION OF LIGANDS
 RX MEDLINE=99180745; PubMed=10079256;
 RA Gray G.E., Mann R.S., Mitsiades E., Henrique D., Carcangiu M.L.,
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Teakonas S.;
 RT "Human ligands of the Notch receptor";
 RL Am. J. Pathol. 154:785-794(1999).
 RN [4]
 RP INTERACTION WITH DTX1
 RX MEDLINE=98250176; PubMed=9590294;
 RA Matsuno K., Eastman D., Mitsiades T., Quinn A.M., Carcangiu M.L.,
 RA Ordentlich P., Kadesch T., Artavanis-Teakonas S.;
 RT "Human deltex is a conserved regulator of Notch signalling";
 RL Nat. Genet. 19:74-78(1998).
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
 CC Jagged1, Jagged2 and Deltal to regulate cell-face determination.
 CC Upon ligand activation through the released notch intracellular
 CC domain (NICD) it forms a transcriptional activator complex with
 CC RBP-J kappa and activates genes of the enhancer of split locus.
 CC affects the implementation of differentiation, proliferation and
 CC apoptotic programs. May be important for normal lymphocyte
 CC function. In altered form, may contribute to transformation or
 CC progression in some T-cell neoplasms. Involved in the maturation

of both CD4+ and CD8+ cells in the thymus (By similarity).
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 CC terminal fragment N(EC) which are probably linked by disulfide
 CC bonds (By similarity). Interacts with DTX1 and DTX2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: In fetal tissues most abundant in spleen,
 CC brain stem and lung. Also present in most adult tissues where it
 CC is found mainly in lymphoid tissues.
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane (By similarity).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- DISEASE: NOTCH1 truncation is associated with T-cell acute
 CC lymphoblastic leukemia.
 CC -1- SIMILARITY: Belongs to the NOTCH family.
 CC -1- SIMILARITY: Contains 5 ANK repeats.
 CC -1- SIMILARITY: Contains 36 EGF-like domains.
 CC -1- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -----
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 CC -----
 DR EMBL; AF308602; AAG33848.1; -.
 DR EMBL; M73980; AAA60614.1; -.
 DR PDB; 1PB5; NMR; A=1447-1481.
 DR Genew; HGNC:7881; NOTCH1.
 DR MIM; 190198; -.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx_hydroxyl_s.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR001438; EGF_11.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR010660; NOD.
 DR InterPro; IPR008297; Notch.
 DR InterPro; IPR000800; Notch_region.
 DR Pfam; PF00023; Ank; 6.
 DR Pfam; PF00008; EGF; 35.
 DR Pfam; PF06816; NOD; 1.
 DR Pfam; PF00066; Notch; 3.
 DR PIRSF; PIRSF002279; Notch; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00010; EGFLOOD.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF CA; 23.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 20.
 DR PROSITE; PS00022; EGF_1; 34.
 DR PROSITE; PS01186; EGF_2; 26.
 DR PROSITE; PS50026; EGF_3; 36.
 DR PROSITE; PS01187; EGF_CA; 18.
 KW 3D-structure; Activator; ANK repeat; Developmental protein;
 KW Differentiation; EGF-like domain; Glycoprotein;

KW Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal;
 KW Transcription regulation; Transmembrane.
 FT SIGNAL 1 18 Potential.
 FT CHAIN 19 2556 Neurogenic locus notch homolog protein 1.
 FT CHAIN 1722 2556 Notch extracellular truncation (By
 FT similarity).
 FT CHAIN 1755 2556 Notch intracellular domain (By
 FT similarity).
 FT DOMAIN 19 1736 Extracellular (Potential).
 FT TRANSMEM 1737 1757 Potential.
 FT DOMAIN 1758 2556 Cytoplasmic
 FT DOMAIN 20 58 EGF-like 1.
 FT DOMAIN 59 99 EGF-like 2.
 FT DOMAIN 102 139 EGF-like 3.
 FT DOMAIN 140 176 EGF-like 4.
 FT DOMAIN 178 216 EGF-like 5.
 FT DOMAIN 218 255 EGF-like 6.
 FT DOMAIN 257 293 EGF-like 7.
 FT DOMAIN 295 333 EGF-like 8.
 FT DOMAIN 335 371 EGF-like 9.
 FT DOMAIN 372 410 EGF-like 10.
 FT DOMAIN 412 450 EGF-like 11.
 FT DOMAIN 452 488 EGF-like 12.
 FT DOMAIN 490 528 EGF-like 13.
 FT DOMAIN 528 564 EGF-like 14.
 FT DOMAIN 566 601 EGF-like 15.
 FT DOMAIN 603 639 EGF-like 16.
 FT DOMAIN 641 676 EGF-like 17.
 FT DOMAIN 678 714 EGF-like 18.
 FT DOMAIN 716 751 EGF-like 19.
 FT DOMAIN 753 789 EGF-like 20.
 FT DOMAIN 791 827 EGF-like 21.
 FT DOMAIN 829 868 EGF-like 22.
 FT DOMAIN 870 906 EGF-like 23.
 FT DOMAIN 908 944 EGF-like 24.
 FT DOMAIN 946 982 EGF-like 25.
 FT DOMAIN 984 1020 EGF-like 26.
 FT DOMAIN 1022 1058 EGF-like 27.
 FT DOMAIN 1060 1096 EGF-like 28.
 FT DOMAIN 1098 1144 EGF-like 29.
 FT DOMAIN 1146 1182 EGF-like 30.
 FT DOMAIN 1184 1220 EGF-like 31.
 FT DOMAIN 1222 1266 EGF-like 32.
 FT DOMAIN 1268 1306 EGF-like 33.
 FT DOMAIN 1308 1347 EGF-like 34.
 FT DOMAIN 1349 1385 EGF-like 35.
 FT DOMAIN 1388 1427 EGF-like 36.
 FT REPEAT 1446 1481 Lin/Notch 1.
 FT REPEAT 1482 1523 Lin/Notch 2.
 FT REPEAT 1524 1563 Lin/Notch 3.
 FT REPEAT 1564 1597 ANK 1.
 FT REPEAT 1598 1636 ANK 2.
 FT REPEAT 1637 1675 ANK 3.
 FT REPEAT 1676 1714 ANK 4.
 FT REPEAT 1715 1753 ANK 5.
 FT DOMAIN 1754 1792 Poly-Val.
 FT DOMAIN 1793 1831 Poly-Arg.
 FT DOMAIN 1832 1870 Poly-Pro.
 FT DOMAIN 1871 1909 Poly-Ala.
 FT DOMAIN 1910 1948 Poly-Glu.
 FT DOMAIN 1949 1987 Poly-Gly.
 FT DOMAIN 1988 2026 Poly-Gln.
 FT DOMAIN 2027 2065 Poly-Pro.
 FT DOMAIN 2066 2104 Poly-Ser.
 FT SITE 2105 2143 Cleavage (by furin-like protease) (By
 FT similarity).
 FT DISULFID 24 37 By similarity.
 FT DISULFID 31 46 By similarity.
 FT DISULFID 48 57 By similarity.
 FT DISULFID 63 74 By similarity.
 FT DISULFID 88 99 By similarity.
 FT DISULFID 106 117 By similarity.

FT DISULFID 111 127 By similarity.
 FT DISULFID 129 138 By similarity.
 FT DISULFID 144 155 By similarity.
 FT DISULFID 149 164 By similarity.
 FT DISULFID 166 175 By similarity.
 Query Match 32.9%; Score 53; DB 1; Length 2556;
 Best Local Similarity 33.3%; Pred. No. 6.3e+02;
 Matches 8; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
 QY 4 XNKKCFQHLDDCCSRKCNRFNKC 27
 DB 250 TQNCBENIDDCPGNNCKNGGACV 273
 RESULT 88
 HSPI_PLETO STANDARD; PRT; 47 AA.
 ID _HSPI_PLETO
 AC QPWNZO
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Sperm protamine P1.
 GN Name=PRM1;
 OS Plecotus townsendii (Townsend's big-eared bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Vespertilionidae;
 OC Corynorhinus.
 OC NCBI_TaxID=124745;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21881971; PubMed-11894158; DOI=10.1006/mpsv.2001.1051;
 RA Van Den Bussche R.A., Hofer S.R., Hansen E.W.;
 RT "Characterization and phylogenetic utility of the mammalian protamine
 P1 gene."
 RL Mol. Phylogenet. Evol. 22:333-341(2002).
 CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
 CC sperm during the haploid phase of spermatogenesis. They compact
 CC sperm DNA into a highly condensed, stable and inactive complex (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- TISSUE SPECIFICITY: Testis.
 CC -!- SIMILARITY: Belongs to the protamine P1 family.
 CC -----
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 CC -----
 DR EMBL; AF435940; AALJ3574.1; -.
 DR InterPro; IPR000221; Protamine P1.
 DR Pfam; PF00260; Protamine P1; 1.
 DR PROSITE; PS00048; PROTAMINE P1; 1.
 KW Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
 KW Nucleosome core; Spermatogenesis; Testis.
 FT INIT_MET 0 By similarity.
 SQ SEQUENCE 47 AA; 6530 MW; B4670EB86CEDB19 CRC64;
 Query Match 32.6%; Score 52.5; DB 1; Length 47;
 Best Local Similarity 26.7%; Pred. No. 21;
 Matches 8; Conservative 8; Mismatches 9; Indels 5; Gaps 1;
 QY 1 CRXNKKCFQHLDDCCSRK-----CNRFNK 25
 DB 14 CRRRRRCYRRRRRCRRRRRCRRRYTR 43
 RESULT 89
 Q646U5 PRELIMINARY; PRT; 74 AA.
 ID Q646U5


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AC Q646U5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Phytotoxin-like SCR74.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RN SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene
RT Family of Phytophthora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723722; AAU21463.1;
DR EMBL; AY723721; AAU21462.1;
SQ SEQUENCE 74 AA; 7702 MW; 294DCIA85D1D9FF0 CRC64;

Query Match 32.6%; Score 52.5; DB 2; Length 74;
Best Local Similarity 34.6%; Pred. No. 32;
Matches 9; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNK 26
: : : : :
Db 47 CKAINAEPPVA-FNDCCSKCNTGSPC 71

RESULT 90
Q646U7
ID Q646U7 PRELIMINARY; PRT; 74 AA.
AC Q646U7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Phytotoxin-like SCR74.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RN SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene
RT Family of Phytophthora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723720; AAU21461.1;
SQ SEQUENCE 74 AA; 7802 MW; 57A8231D29AB5F8F CRC64;

Query Match 32.6%; Score 52.5; DB 2; Length 74;
Best Local Similarity 34.6%; Pred. No. 32;
Matches 9; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNK 26
: : : : :
Db 47 CKAINAEPPVA-FNDCCSKCNTGSPC 71

RESULT 91
Q6PYV0
ID Q6PYV0 PRELIMINARY; PRT; 92 AA.
AC Q6PYV0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Egg protein CP422.
GN Names=CP422;
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;

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OC Schistosomatoidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RN SEQUENCE FROM N.A.
RA Yu C., Zhang F., Mihoko K., Masahiro I., Zhu Y., Hirayama K.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570752; AAS68257.1;
SQ SEQUENCE 92 AA; 10345 MW; 052F01B53D379FSF CRC64;

Query Match 32.6%; Score 52.5; DB 2; Length 92;
Best Local Similarity 41.7%; Pred. No. 38;
Matches 10; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFN 24
: : : : :
Db 66 CLPDKQCCRRN-KDCCSKSCYRGN 88

RESULT 92
P93773
ID P93773 PRELIMINARY; PRT; 474 AA.
AC P93773;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 3-hydroxy-3-methylglutaryl-CoA-synthase.
OS Pinus sylvestris (Scots pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3349;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Needles;
RX MEDLINE=97214637; PubMed=9061017; DOI=10.1016/S0005-2760(96)00161-0;
RA Wegener A., Gimbel W., Werner T., Hani J., Ernst D., Sandermann H.;
RT "Molecular cloning of ozone-inducible protein from Pinus sylvestris L.
RT with high sequence similarity to vertebrate 3-hydroxy-3-methylglutaryl-
RT CoA-synthase.";
RL Biochim. Biophys. Acta 1350:247-252 (1997).
DR EMBL; X96386; CAA65250.1;
DR PIR; T09688; T09688.
DR GO; GO:0004421; F:hydroxymethylglutaryl-CoA synthase activity; IEA.
DR GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
DR InterPro; IPR000886; ER target S.
DR InterPro; IPR008260; HMG CoA synth.
DR InterPro; IPR010122; HMG CoA synth.
DR Pfam; PF01154; HMG CoA synt. 1.
DR TIGRFAMs; TIGR01833; HMG-CoA-S-euk. 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN.1.
SQ SEQUENCE 474 AA; 52998 MW; 3ECB48E5F23D37BA CRC64;

Query Match 32.6%; Score 52.5; DB 2; Length 474;
Best Local Similarity 43.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 4 XNQKCF-QHLDDCCSRKCNRFNK 25
: : : : :
Db 211 LSQTCYLMALDSCYKFCNKEK 233

RESULT 93
Q6K5W7
ID Q6K5W7 PRELIMINARY; PRT; 764 AA.
AC Q6K5W7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative wall-associated kinase.
GN Name=P0016F11.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.

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OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AP005503; BAD22031.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004674; F:protein-serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR001881; EGF CA.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000719; prot kinase.
DR InterPro: IPR002290; Ser Thr_pkinase.
DR InterPro: IPR008271; Ser Thr_pkinase.
DR Pfam: PF07645; EGF CA; 1.
DR ProDom: PD000001; Prot kinase; 1.
DR SMART: SM00179; EGF CA; 1.
DR SMART: SM00220; S_TKG; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE: PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 764 AA; 85266 MW; 5ECAB51B666C88C7 CRC64;

Query Match 32.6%; Score 52.5; DB 2; Length 764;
Best Local Similarity 26.2%; Pred. No. 2.5e+02;
Matches 11; Conservative 6; Mismatches 10; Indels 15; Gaps 2;

QY 1 CRXNKCQFQHLDDCCSRK--CNRFN-KC 27
DB 280 CRSTNSECFDTIDGGVRCNCCQGVGNPYLDGCTDINECL 321

RESULT 94
SL17_ENTHI
ID SL17_ENTHI STANDARD; PRT; 1285 AA.
AC F23502;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 170 kDa surface lectin precursor.
GN Name=CEL-170/4;
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 16-33.
RA MEDLINE=91156704; PubMed=2000392;
RA Tannich E., Ebert F., Horstmann R.D.;
RT "Primary structure of the 170-kDa surface lectin of pathogenic
RT Entamoeba histolytica."
RL Proc. Natl. Acad. Sci. U.S.A. 88:1849-1853 (1991).
RN [2]
RP REVISIONS TO N-TERMINUS.
RA Tannich E., Nickel R., Ebert F., Horstmann R.D.;
RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 16-30.
RX MEDLINE=89123408; PubMed=2536731;
RA Petri W.A. Jr., Chapman M.D., Snodgrass T., Mann B.J., Broman J.,
RA Ravdin J.I.;
RT Inhibitable adherence lectin of Entamoeba histolytica."
RL J. Biol. Chem. 264:3007-3012 (1989).
CC -!- FUNCTION: Mediates adherence of E. histolytica to colonic mucins,
CC an essential step for pathogenic tissue invasion.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Phosphorylated regions may have a role in signal

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transduction.

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EMBL: M60498; AAA29106.1; -.
EMBL: X61003; CA43321.1; -.
KW Direct protein sequencing; Glycoprotein; Lectin; Phosphorylation;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 15
FT CHAIN 16 1285 170 kDa surface lectin.
FT DOMAIN 16 1218 Extracellular (Potential).
FT TRANSMEM 1219 1247 Potential.
FT DOMAIN 1248 1285 Cytoplasmic (Potential).
FT DOMAIN 378 1208 Cys-rich.
FT REPEAT 378 407 9 X approximate tandem repeats.
FT REPEAT 408 438 1.
FT REPEAT 439 464 2.
FT REPEAT 465 497 3.
FT REPEAT 498 525 4.
FT REPEAT 526 554 5.
FT REPEAT 555 584 6.
FT REPEAT 585 620 7.
FT REPEAT 621 653 8.
FT CARBOHYD 200 200 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 236 236 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 383 383 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 461 461 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 651 651 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 882 882 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1196 1196 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1206 1206 N-linked (GlcNAc. .) (Potential).
FT CONFLICT 16 16 D -> G (in Ref. 3).
SQ SEQUENCE 1285 AA; 144410 MW; 64BB2DFD2AD8ECBA CRC64;

Query Match 32.6%; Score 52.5; DB 1; Length 1285;
Best Local Similarity 41.4%; Pred. No. 3.9e+02;
Matches 12; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNKCQFQHLDDCCSRK--CNRFN-KC 26
DB 710 CSMGTDNVITYHDDCDRSKSCGNGKGC 738

RESULT 95

Q9XV21 PRELIMINARY; PRT; 354 AA.
ID Q9XV21
AC Q9XV21
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F46B3.9.
DE ORFNames=F46B3.9;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Poloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
RN [2]

SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blasej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ball J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendell J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhakdani D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brokter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

DR GO: GO:0016327; C1apicolateral plasma membrane; IDA.
 DR GO: GO:0007163; P:establishment and/or maintenance of cell po. . . ; IMP.
 DR GO: GO:0016332; P:establishment and/or maintenance of polarit. . . ; IMP.
 DR GO: GO:0016334; P:establishment and/or maintenance of polarit. . . ; IMP.
 DR GO: GO:0002009; P:morphogenesis of an epithelium; NAS.
 DR GO: GO:0045494; P:photoreceptor maintenance; IMP.
 DR GO: GO:0042052; P:rhabdome development; NAS.
 DR GO: GO:0045186; P:zonula adherens assembly; IMP.
 DR GO: GO:0045218; P:zonula adherens maintenance; IMP.
 DR InterPro: IPR000152; Asx_hydroxyl_S.
 DR InterPro: IPR008985; ConA_like_1ec_g1.
 DR InterPro: IPR000742; EGF 2.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR001438; EGF II.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR001791; Laminin_G.
 DR Pfam: PF00008; EGF; 26.
 DR Pfam: PF00054; Laminin_G; 3.
 DR PRINTS: PR00054; Laminin_G; 3.
 DR SMART: SM00179; EGF_BLOOD.
 DR SMART: SM00282; LamG; 3.
 DR PROSITE: PS00010; ASX_HYDROXYL; 15.
 DR PROSITE: PS00022; EGF 1; 26.
 DR PROSITE: PS01186; EGF 2; 17.
 DR PROSITE: PS50026; EGF 3; 27.
 DR PROSITE: PS01187; EGF_Ca; 12.
 DR PROSITE: PS50025; LAM_G DOMAIN; 3.
 KW Differentiation; EGF-like domain; Glycoprotein; Phosphorylation;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 90
 FT CHAIN 91 2139
 FT DOMAIN 91 2084 Crumbs protein.
 FT TRANSMEM 2085 2111 Extracellular (Potential).
 FT DOMAIN 2112 2139 Potential.
 FT DOMAIN 267 303 Cytoplasmic (Potential).
 FT DOMAIN 306 343 EGF-like 1.
 FT DOMAIN 348 386 EGF-like 2.
 FT DOMAIN 388 425 EGF-like 3.
 FT DOMAIN 427 463 EGF-like 4, calcium-binding (Potential).
 FT DOMAIN 464 500 EGF-like 5.
 FT DOMAIN 501 532 EGF-like 6.
 FT DOMAIN 545 581 EGF-like 7.
 FT DOMAIN 582 611 EGF-like 8.
 FT DOMAIN 609 646 EGF-like 9.
 FT DOMAIN 648 685 EGF-like 10.
 FT DOMAIN 687 723 EGF-like 11, calcium-binding (Potential).
 FT DOMAIN 725 761 EGF-like 12, calcium-binding (Potential).
 FT DOMAIN 802 838 EGF-like 13, calcium-binding (Potential).
 FT DOMAIN 840 902 EGF-like 14, calcium-binding (Potential).
 FT DOMAIN 904 940 EGF-like 15, calcium-binding (Potential).
 FT DOMAIN 942 978 EGF-like 16.
 FT DOMAIN 980 1021 EGF-like 17, calcium-binding (Potential).
 FT DOMAIN 1023 1205 EGF-like 18, calcium-binding (Potential).
 FT DOMAIN 1207 1243 Laminin G-like 1.
 FT DOMAIN 1250 1480 EGF-like 20.
 FT DOMAIN 1481 1517 Laminin G-like 2.
 FT DOMAIN 1558 1758 EGF-like 21.
 FT DOMAIN 1759 1795 Laminin G-like 3.
 FT DOMAIN 1797 1833 EGF-like 22.
 FT DOMAIN 1835 1871 EGF-like 23, calcium-binding (Potential).
 FT DOMAIN 1874 1915 EGF-like 24, calcium-binding (Potential).
 FT DOMAIN 1915 1951 EGF-like 25.
 FT DOMAIN 1953 1989 EGF-like 26.
 FT DOMAIN 1991 2029 EGF-like 27, calcium-binding (Potential).
 FT DOMAIN 2030 2070 EGF-like 28, calcium-binding (Potential).
 FT DISULFID 271 282 By similarity.
 FT DISULFID 276 291 By similarity.
 FT DISULFID 293 302 By similarity.
 FT DISULFID 310 321 By similarity.
 FT DISULFID 331 331 By similarity.
 FT DISULFID 333 342 By similarity.
 FT DISULFID 352 363 By similarity.

FT DISULFID 357 374 By similarity.
 FT DISULFID 376 385 By similarity.
 FT DISULFID 392 403 By similarity.
 FT DISULFID 397 412 By similarity.
 FT DISULFID 414 424 By similarity.
 FT DISULFID 431 442 By similarity.
 FT DISULFID 436 451 By similarity.
 FT DISULFID 453 462 By similarity.
 FT DISULFID 468 479 By similarity.
 FT DISULFID 473 488 By similarity.
 FT DISULFID 490 499 By similarity.
 FT DISULFID 505 515 By similarity.
 FT DISULFID 509 520 By similarity.
 FT DISULFID 522 531 By similarity.
 FT DISULFID 549 562 By similarity.
 FT DISULFID 556 569 By similarity.
 FT DISULFID 571 580 By similarity.
 FT DISULFID 586 597 By similarity.
 FT DISULFID 591 602 By similarity.
 FT DISULFID 604 610 By similarity.
 FT DISULFID 613 624 By similarity.
 FT DISULFID 618 634 By similarity.
 FT DISULFID 636 645 By similarity.
 FT DISULFID 652 664 By similarity.
 FT DISULFID 659 673 By similarity.
 FT DISULFID 675 684 By similarity.
 FT DISULFID 691 702 By similarity.
 FT DISULFID 696 711 By similarity.
 FT DISULFID 713 722 By similarity.

Query Match 32.3%; Score 52; DB 1; Length 2139;
 Best Local Similarity 30.4%; Pred. No. 7.1e+02;

Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

OY 4 XNQCFOHLDCCSRKCNRFNC 26

Db 1828 EGQCEQNIDECADQPCHNGNC 1850

Search completed: April 18, 2005, 20:37:49
 Job time : 120 secs